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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 13, 2005, 00:43:34 ; Search time 490 Seconds  
(without alignments)  
3072.291 Million cell updates/sec

Perfect score: 1343  
Sequence: 1 MTQVPRLSPVPAALGSA.....VRVYISLLPLGDTLAFKI 262

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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Query

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70	1343	100.0	989	16	US-10-307-817-125	Sequence 125, App
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74	884	65.8	787	16	US-10-307-817-123	Sequence 123, App
c 75	707	52.6	620	16	US-10-240-425-182	Sequence 182, App
76	509	37.9	458	10	US-09-918-995-23102	Sequence 23102, A
77	509	37.9	474	10	US-09-918-995-22407	Sequence 22407, A
78	428.5	31.9	1512	18	US-10-739-930-3516	Sequence 3516, Ap
c 79	425.5	31.7	84428	16	US-10-229-1489-1	Sequence 1, Appli
80	413	30.8	849	16	US-10-425-114-25410	Sequence 25410, A
81	413	30.8	1159	16	US-10-425-114-2777	Sequence 2777, Ap
82	413	30.8	1218	15	US-10-361-460-77	Sequence 77, Appl
83	411	30.6	86941	16	US-10-461-194-2	Sequence 2, Appli
84	409.5	30.5	85692	16	US-10-461-194-1	Sequence 1, Appli
85	407	30.3	901	16	US-10-425-114-27082	Sequence 27082, A
86	407	30.3	2381	18	US-10-425-115-138013	Sequence 138013, A
87	406	30.2	1257	18	US-10-425-115-66941	Sequence 66941, A
88	405.5	30.2	980	9	US-09-452-239-21	Sequence 21, Appl
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91	398.5	29.7	744	16	US-10-239-463-1	Sequence 1, Appli
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93	396	29.5	1058	9	US-09-452-239-11	Sequence 11, Appl
94	396	29.5	1060	17	US-10-437-963-62449	Sequence 62449, A
c 95	396	29.5	3759	17	US-10-437-963-23149	Sequence 23149, A
96	394	29.3	1078	9	US-09-452-239-41	Sequence 41, Appl
97	392.5	29.2	962	9	US-09-452-239-23	Sequence 23, Appl
98	392.5	29.2	1023	9	US-09-452-239-25	Sequence 25, Appl
99	392.5	29.2	1044	16	US-10-424-599-95805	Sequence 95805, A
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101	392.5	29.2	1059	15	US-10-289-757-36	Sequence 36, App
102	392	29.2	975	17	US-10-437-963-61696	Sequence 61696, A
c 103	391.5	29.2	1072	9	US-09-770-445-132	Sequence 132, App
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111	387	28.8	1443	17	US-10-767-701-14336	Sequence 14336, A
112	386	28.7	1012	15	US-10-174-693-94	Sequence 94, Appl
113	386	28.7	1026	15	US-10-174-693-6	Sequence 6, Appli
114	386	28.7	1088	16	US-10-425-114-12284	Sequence 12284, A
115	386	28.7	1097	16	US-10-425-114-3691	Sequence 3691, Ap
116	386	28.7	1118	9	US-09-452-239-37	Sequence 37, Appl
117	386	28.7	1146	9	US-09-452-239-3	Sequence 3, Appli
118	386	28.7	1160	15	US-10-361-460-31	Sequence 31, Appl
119	385.5	28.7	931	15	US-09-452-239-17	Sequence 17, Appl
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124	385	28.7	1200	18	US-10-425-115-138010	Sequence 138010, A
125	385	28.7	1506	18	US-10-425-115-113176	Sequence 113176, A
126	385	28.7	1890	18	US-10-739-930-2642	Sequence 2642, Ap
127	383.5	28.6	1003	15	US-10-361-460-33	Sequence 33, Appl
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129	383.5	28.6	1059	9	US-09-452-239-5	Sequence 5, Appli
130	383.5	28.6	1089	16	US-10-425-114-2526	Sequence 2526, Ap
131	382.5	28.5	929	9	US-09-452-239-19	Sequence 19, Appl
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133	381	28.4	876	17	US-10-437-963-41905	Sequence 41905, A
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135	380.5	28.3	1114	16	US-10-425-114-3140	Sequence 3140, Ap



136	378	28.1	944	15	US-10-361-460-32	Sequence 32, Appl	209	174	13.0	296	15	US-10-174-693-195	Sequence 195, App
137	378	28.1	1066	18	US-10-425-115-179664	Sequence 179664, A	210	173.5	12.9	584	18	US-10-425-115-53810	Sequence 53810, A
138	377.5	28.1	905	17	US-10-437-963-41715	Sequence 41715, A	211	172.5	12.8	522	15	US-10-156-761-3105	Sequence 3105, App
139	377	28.1	1233	17	US-10-767-795-6335	Sequence 6335, App	212	172	12.8	2355	16	US-10-424-599-18324	Sequence 18324, A
140	376	28.0	923	9	US-09-452-239-7	Sequence 7, Appl	213	172	12.8	2256646	17	US-10-470-565-1	Sequence 53, Appl
141	376	28.0	1006	16	US-10-425-114-27818	Sequence 27818, A	214	171.5	12.8	562	15	US-10-174-693-53	Sequence 4334, App
142	376	28.0	1146	16	US-10-425-115-53825	Sequence 53825, A	215	170	12.7	447	11	US-09-732-627A-4334	Sequence 646, App
143	373	27.8	1146	18	US-10-425-115-138015	Sequence 138015, A	C 216	170	12.7	75216	17	US-10-080-170-646	Sequence 646, App
144	372.5	27.7	1281	17	US-10-767-701-12827	Sequence 12827, A	C 217	170	12.7	75216	17	US-10-468-356-646	Sequence 646, App
145	369	27.5	966	18	US-10-739-930-382	Sequence 382, App	C 218	169	12.6	1289	18	US-10-398-221-1713	Sequence 1713, App
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151	356.5	26.5	1052	16	US-10-425-114-24738	Sequence 24738, A	C 224	160	11.9	554	16	US-10-425-114-17961	Sequence 481, App
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154	354	26.4	912	9	US-09-452-239-27	Sequence 27, Appl	C 227	156	11.6	19024	9	US-09-070-927A-179	Sequence 179, Appl
155	351.5	26.2	813	18	US-10-425-115-108865	Sequence 108865, A	C 228	149.5	11.1	508	9	US-09-452-239-15	Sequence 15, Appl
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180	279	20.8	651	11	US-09-758-759-84	Sequence 84, App	C 253	114	8.5	468	16	US-10-424-599-133784	Sequence 133784, A
181	278.5	20.7	546	17	US-10-021-323-10069	Sequence 10069, A	C 254	112.5	8.4	371	17	US-10-437-963-67549	Sequence 67549, A
182	276.5	20.6	343	9	US-09-917-800A-298	Sequence 275, App	C 255	112	8.3	2086	9	US-09-935-757-5	Sequence 5, Appl
183	276.5	20.6	343	16	US-10-152-319A-298	Sequence 298, App	C 256	111.5	8.3	602	18	US-10-425-115-172234	Sequence 172234, A
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186	231.5	17.2	1159	18	US-10-425-115-53828	Sequence 53828, A	C 259	110	8.2	236	15	US-10-174-693-175	Sequence 3232, App
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188	224	16.7	534	9	US-09-452-239-47	Sequence 47, Appl	C 261	109	8.1	521	16	US-10-424-599-35115	Sequence 35007, A
189	220	16.4	575	18	US-10-425-115-140243	Sequence 140243, A	C 262	109	8.1	521	16	US-10-424-599-35115	Sequence 35007, A
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192	215	16.0	672	15	US-10-156-761-5814	Sequence 5814, App	C 265	107.5	8.0	1206	17	US-10-283-975A-192	Sequence 192, App
193	215	16.0	9025608	15	US-10-156-761-1	Sequence 1, Appl	C 266	107.5	8.0	1311	13	US-10-087-192-1325	Sequence 1325, App
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207	176	13.1	9025608	15	US-10-156-761-1	Sequence 1, Appl	C 280	102	7.6	328	16	US-10-425-114-6556	Sequence 6556, App
208	175.5	13.1	9025608	15	US-10-156-761-1	Sequence 1, Appl	C 281	102	7.6	328	16	US-10-425-114-6556	Sequence 6556, App



C 282	101.5	7.6	2505	15	US-10-303-110A-1	Sequence 1, Appli	355	93	6.9	5032	17	US-10-473-576-26	Sequence 26, Appli
C 283	101.5	7.6	2505	15	US-10-303-110A-4	Sequence 4, Appli	356	93	6.9	5591	15	US-10-170-385-14	Sequence 14, Appli
C 284	101	7.5	1602	17	US-10-437-963-102014	Sequence 102014, A	357	93	6.9	7788	15	US-10-329-079-8	Sequence 8, Appli
C 285	101	7.5	1786	16	US-10-302-172-657	Sequence 657, App	358	93	6.9	37360	15	US-10-329-079-6	Sequence 6, Appli
C 286	100.5	7.5	1815	15	US-10-327-813-3	Sequence 3, Appli	c 359	92.5	6.9	1107	15	US-10-156-761-6131	Sequence 6131, Ap
C 287	100.5	7.5	1815	15	US-10-329-668-3	Sequence 3, Appli	c 360	92.5	6.9	2433	10	US-09-864-636A-587	Sequence 587, App
C 288	100.5	7.5	1815	17	US-10-717-049-3	Sequence 3, Appli	c 361	92.5	6.9	2433	11	US-09-864-426A-587	Sequence 587, App
C 289	100	7.4	8460	14	US-10-237-271-2	Sequence 2, Appli	c 362	92.5	6.9	2433	15	US-10-084-839-587	Sequence 587, App
C 290	100	7.4	8460	15	US-10-191-997-115	Sequence 115, App	c 363	92.5	6.9	2445	10	US-09-864-636A-571	Sequence 571, App
C 291	100	7.4	8460	16	US-10-274-085-4	Sequence 4, Appli	c 364	92.5	6.9	2445	10	US-09-864-636A-571	Sequence 571, App
C 292	100	7.4	8460	17	US-10-717-597-192	Sequence 192, App	c 365	92.5	6.9	2445	10	US-09-864-636A-579	Sequence 579, App
C 293	99	7.4	2010	16	US-10-159-563-379	Sequence 379, App	c 366	92.5	6.9	2445	10	US-09-864-636A-581	Sequence 581, App
C 294	99	7.4	2010	16	US-10-418-007-3	Sequence 3, Appli	c 367	92.5	6.9	2445	11	US-09-864-426A-571	Sequence 571, App
C 295	99	7.4	2010	18	US-10-641-325-7	Sequence 7, Appli	c 368	92.5	6.9	2445	11	US-09-864-426A-575	Sequence 575, App
C 296	99	7.4	2430	17	US-10-437-963-10627	Sequence 10627, A	c 369	92.5	6.9	2445	11	US-09-864-426A-579	Sequence 579, App
C 297	99	7.4	2685	16	US-10-401-403-147	Sequence 147, App	c 370	92.5	6.9	2445	11	US-09-864-426A-581	Sequence 581, App
C 298	99	7.4	2685	16	US-10-401-403-171	Sequence 171, App	c 371	92.5	6.9	2445	11	US-09-864-426A-581	Sequence 581, App
C 299	98.5	7.3	1338	15	US-10-156-761-3240	Sequence 3240, Ap	c 372	92.5	6.9	2445	15	US-10-084-839-571	Sequence 571, App
C 300	98.5	7.3	1338	15	US-10-104-047-567	Sequence 567, App	c 373	92.5	6.9	2445	15	US-10-084-839-575	Sequence 575, App
C 301	98.5	7.3	3147	9	US-09-741-669-216	Sequence 216, App	c 374	92.5	6.9	2445	15	US-10-084-839-579	Sequence 579, App
C 302	98.5	7.3	3147	9	US-09-815-242-5965	Sequence 5965, Ap	c 375	92.5	6.9	2445	15	US-10-084-839-581	Sequence 581, App
C 303	98.5	7.3	3147	15	US-10-301-997-84	Sequence 84, Appl	c 376	92.5	6.9	2445	15	US-10-084-839-2818	Sequence 2818, Ap
C 304	98.5	7.3	3147	16	US-10-282-122A-20260	Sequence 20260, A	c 377	92.5	6.9	2445	15	US-10-084-839-2822	Sequence 2822, Ap
C 305	98.5	7.3	3147	17	US-10-818-509-84	Sequence 84, Appl	c 378	92.5	6.9	2445	15	US-10-084-839-2826	Sequence 2826, Ap
C 306	98.5	7.3	77536	10	US-09-940-316B-1	Sequence 1, Appli	c 379	92.5	6.9	2493	10	US-09-864-636A-589	Sequence 589, App
C 307	98	7.3	828	16	US-10-282-122A-31998	Sequence 31998, A	c 380	92.5	6.9	2493	11	US-09-864-426A-589	Sequence 589, App
C 308	97.5	7.3	2505	15	US-10-303-110A-2	Sequence 2, Appli	c 381	92.5	6.9	2493	15	US-10-084-839-589	Sequence 589, App
C 309	97.5	7.3	2505	15	US-10-303-110A-3	Sequence 3, Appli	c 382	92.5	6.9	2493	15	US-10-084-839-589	Sequence 589, App
C 310	97.5	7.3	2505	15	US-10-303-110A-5	Sequence 5, Appli	c 383	92.5	6.9	2493	15	US-10-084-839-585	Sequence 585, App
C 311	97.5	7.3	2505	15	US-10-303-110A-6	Sequence 6, Appli	c 384	92.5	6.9	2493	11	US-09-864-426A-585	Sequence 585, App
C 312	97.5	7.3	2505	15	US-10-303-110A-7	Sequence 7, Appli	c 385	92.5	6.9	2493	15	US-10-084-839-585	Sequence 585, App
C 313	97.5	7.3	2505	15	US-10-303-110A-10	Sequence 10, Appl	c 386	92.5	6.9	2508	10	US-09-864-636A-401	Sequence 401, App
C 314	97.5	7.3	5208	17	US-10-437-963-69592	Sequence 69592, A	c 387	92.5	6.9	2508	10	US-09-864-636A-405	Sequence 405, App
C 315	97	7.2	421	16	US-10-424-599-1595	Sequence 1595, Ap	c 388	92.5	6.9	2508	10	US-09-864-636A-407	Sequence 407, App
C 316	97	7.2	1104	16	US-10-282-122A-33573	Sequence 33573, A	c 389	92.5	6.9	2508	10	US-09-864-636A-409	Sequence 409, App
C 317	97	7.2	2867	17	US-10-437-963-195	Sequence 195, App	c 390	92.5	6.9	2508	10	US-09-864-636A-411	Sequence 411, App
C 318	96.5	7.2	1454	18	US-10-425-115-126435	Sequence 126435, A	c 391	92.5	6.9	2508	10	US-09-864-636A-415	Sequence 415, App
C 319	96.5	7.2	2227	18	US-10-425-115-3967	Sequence 3967, Ap	c 392	92.5	6.9	2508	10	US-09-864-636A-417	Sequence 417, App
C 320	96.5	7.2	5397	17	US-10-437-963-69644	Sequence 69644, A	c 393	92.5	6.9	2508	10	US-09-864-636A-419	Sequence 419, App
C 321	96	7.1	1322	18	US-10-425-115-122270	Sequence 122270, A	c 394	92.5	6.9	2508	10	US-09-864-636A-423	Sequence 423, App
C 322	96	7.1	1952	14	US-10-171-311-51	Sequence 51, Appl	c 395	92.5	6.9	2508	10	US-09-864-636A-426	Sequence 426, App
C 323	95.5	7.1	348	15	US-10-424-599-30454	Sequence 30454, A	c 396	92.5	6.9	2508	10	US-09-864-636A-431	Sequence 431, App
C 324	95.5	7.1	1272	15	US-10-369-493-37699	Sequence 37699, A	c 397	92.5	6.9	2508	10	US-09-864-636A-439	Sequence 439, App
C 325	95.5	7.1	1565	18	US-10-739-930-2155	Sequence 2155, Ap	c 398	92.5	6.9	2508	11	US-09-864-426A-401	Sequence 401, App
C 326	95.5	7.1	2261	17	US-10-437-963-15102	Sequence 15102, A	c 399	92.5	6.9	2508	11	US-09-864-426A-405	Sequence 405, App
C 327	95.5	7.1	2553	9	US-09-815-242-7690	Sequence 7690, Ap	c 400	92.5	6.9	2508	11	US-09-864-426A-407	Sequence 407, App
C 328	95.5	7.1	2553	16	US-10-282-122A-29994	Sequence 29994, A	c 401	92.5	6.9	2508	11	US-09-864-426A-409	Sequence 409, App
C 329	95	7.1	553	15	US-10-264-049-1169	Sequence 1169, Ap	c 402	92.5	6.9	2508	11	US-09-864-426A-411	Sequence 411, App
C 330	95	7.1	717	15	US-10-156-761-4336	Sequence 4336, Ap	c 403	92.5	6.9	2508	11	US-09-864-426A-415	Sequence 415, App
C 331	95	7.1	1062	18	US-10-739-930-1766	Sequence 1766, Ap	c 404	92.5	6.9	2508	11	US-09-864-426A-417	Sequence 417, App
C 332	95	7.1	1948	16	US-10-282-122A-15101	Sequence 15101, A	c 405	92.5	6.9	2508	11	US-09-864-426A-419	Sequence 419, App
C 333	95	7.1	2597	15	US-10-094-749-246	Sequence 246, App	c 406	92.5	6.9	2508	11	US-09-864-426A-423	Sequence 423, App
C 334	95	7.1	4184	10	US-09-927-827-42	Sequence 42, Appl	c 407	92.5	6.9	2508	11	US-09-864-426A-426	Sequence 426, App
C 335	94.5	7.0	373	16	US-10-424-599-109508	Sequence 109508, A	c 408	92.5	6.9	2508	11	US-09-864-426A-431	Sequence 431, App
C 336	94.5	7.0	1243	18	US-10-739-930-2839	Sequence 2839, Ap	c 409	92.5	6.9	2508	11	US-09-864-426A-439	Sequence 439, App
C 337	94	7.0	717	16	US-10-282-122A-31785	Sequence 31785, A	c 410	92.5	6.9	2508	15	US-10-084-839-401	Sequence 401, App
C 338	94	7.0	4618	18	US-10-723-860-4935	Sequence 4935, Ap	c 411	92.5	6.9	2508	15	US-10-084-839-405	Sequence 405, App
C 339	94	7.0	14101	16	US-10-197-824-6	Sequence 6, Appli	c 412	92.5	6.9	2508	15	US-10-084-839-407	Sequence 407, App
C 340	94	7.0	17589	15	US-10-197-824-3	Sequence 3, Appli	c 413	92.5	6.9	2508	15	US-10-084-839-409	Sequence 409, App
C 341	93.5	7.0	1107	15	US-10-156-761-1969	Sequence 1969, Ap	c 414	92.5	6.9	2508	15	US-10-084-839-411	Sequence 411, App
C 342	93.5	7.0	1807	15	US-10-156-761-4441	Sequence 4441, Ap	c 415	92.5	6.9	2508	15	US-10-084-839-415	Sequence 415, App
C 343	93.5	7.0	2505	15	US-10-303-110A-8	Sequence 8, Appli	c 416	92.5	6.9	2508	15	US-10-084-839-417	Sequence 417, App
C 344	93.5	7.0	2505	15	US-10-303-110A-9	Sequence 9, Appli	c 417	92.5	6.9	2508	15	US-10-084-839-419	Sequence 419, App
C 345	93.5	7.0	2505	15	US-10-303-110A-11	Sequence 11, Appl	c 418	92.5	6.9	2508	15	US-10-084-839-423	Sequence 423, App
C 346	93.5	7.0	2505	15	US-10-303-110A-12	Sequence 12, Appl	c 419	92.5	6.9	2508	15	US-10-084-839-426	Sequence 426, App
C 347	93.5	7.0	125746	15	US-10-156-761-15102	Sequence 15102, A	c 420	92.5	6.9	2508	15	US-10-084-839-431	Sequence 431, App
C 348	93.5	7.0	154746	10	US-09-827-688-8	Sequence 8, Appli	c 421	92.5	6.9	2508	15	US-10-084-839-439	Sequence 439, App
C 349	93	6.9	1524	18	US-10-425-115-114038	Sequence 114038, A	c 422	92.5	6.9	2508	15	US-10-084-839-2737	Sequence 2737, Ap
C 350	93	6.9	1908	15	US-10-369-493-33780	Sequence 33780, A	c 423	92.5	6.9	2508	15	US-10-084-839-2739	Sequence 2739, Ap
C 351	93	6.9	2176	8	US-08-808-031A-1	Sequence 1, Appli	c 424	92.5	6.9	2508	15	US-10-084-839-2741	Sequence 2741, Ap
C 352	93	6.9	3744	16	US-10-302-172-585	Sequence 585, App	c 425	92.5	6.9	2508	15	US-10-084-839-2743	Sequence 2743, Ap
C 353	93	6.9	4018	15	US-10-172-118-508	Sequence 308, App	c 426	92.5	6.9	2508	15	US-10-084-839-2745	Sequence 2745, Ap
C 354	93	6.9	4018	16	US-10-342-188-308	Sequence 308, App	c 427	92.5	6.9	2508	15	US-10-084-839-2747	Sequence 2747, Ap



C 428	92.5	6.9	2508	15	US-10-084-839-2749	Sequence 2749, Ap	C 501	92.5	6.9	2517	15	US-10-084-839-529	Sequence 529, App
C 429	92.5	6.9	2508	15	US-10-084-839-2751	Sequence 2751, Ap	C 502	92.5	6.9	2517	15	US-10-084-839-533	Sequence 533, App
C 430	92.5	6.9	2508	15	US-10-084-839-2753	Sequence 2753, Ap	C 503	92.5	6.9	2517	15	US-10-084-839-537	Sequence 537, App
C 431	92.5	6.9	2508	15	US-10-084-839-2755	Sequence 2755, Ap	C 504	92.5	6.9	2517	15	US-10-084-839-2675	Sequence 2675, Ap
C 432	92.5	6.9	2508	15	US-10-084-839-2757	Sequence 2757, Ap	C 505	92.5	6.9	2517	15	US-10-084-839-2706	Sequence 2706, Ap
C 433	92.5	6.9	2508	15	US-10-084-839-2761	Sequence 2761, Ap	C 506	92.5	6.9	2517	15	US-10-084-839-2779	Sequence 2779, Ap
C 434	92.5	6.9	2511	9	US-09-777-430A-12	Sequence 12, Appl	C 507	92.5	6.9	2517	15	US-10-084-839-2784	Sequence 2784, Ap
C 435	92.5	6.9	2511	10	US-09-940-244-258	Sequence 258, App	C 508	92.5	6.9	2517	15	US-10-084-839-2790	Sequence 2790, Ap
C 436	92.5	6.9	2511	10	US-09-864-636A-262	Sequence 262, App	C 509	92.5	6.9	2517	15	US-10-084-839-2796	Sequence 2796, Ap
C 437	92.5	6.9	2511	10	US-09-758-282-59	Sequence 59, Appl	C 510	92.5	6.9	2517	15	US-10-084-839-2798	Sequence 2798, Ap
C 438	92.5	6.9	2511	11	US-09-864-426A-262	Sequence 262, App	C 511	92.5	6.9	2517	15	US-10-084-839-2800	Sequence 2800, Ap
C 439	92.5	6.9	2511	15	US-10-084-839-2715	Sequence 2715, Ap	C 512	92.5	6.9	2517	15	US-10-084-839-2802	Sequence 2802, Ap
C 440	92.5	6.9	2511	15	US-10-084-839-2834	Sequence 2834, Ap	C 513	92.5	6.9	2517	15	US-10-084-839-2806	Sequence 2806, Ap
C 441	92.5	6.9	2511	15	US-10-084-839-2834	Sequence 2834, Ap	C 514	92.5	6.9	2517	15	US-10-084-839-2808	Sequence 2808, Ap
C 442	92.5	6.9	2511	18	US-10-309-584-258	Sequence 258, App	C 515	92.5	6.9	2517	15	US-10-084-839-2808	Sequence 2808, Ap
C 443	92.5	6.9	2514	10	US-09-864-636A-133	Sequence 133, App	C 516	92.5	6.9	2517	15	US-10-084-839-2856	Sequence 2856, Ap
C 444	92.5	6.9	2514	10	US-09-864-636A-454	Sequence 454, App	C 517	92.5	6.9	2520	10	US-09-864-636A-222	Sequence 222, App
C 445	92.5	6.9	2514	10	US-09-864-636A-475	Sequence 475, App	C 518	92.5	6.9	2520	10	US-09-864-636A-505	Sequence 505, App
C 446	92.5	6.9	2514	10	US-09-864-636A-499	Sequence 499, App	C 519	92.5	6.9	2520	10	US-09-864-636A-541	Sequence 541, App
C 447	92.5	6.9	2514	10	US-09-758-282-260	Sequence 260, App	C 520	92.5	6.9	2520	10	US-09-864-636A-543	Sequence 543, App
C 448	92.5	6.9	2514	11	US-09-864-426A-133	Sequence 133, App	C 521	92.5	6.9	2520	10	US-09-864-636A-573	Sequence 573, App
C 449	92.5	6.9	2514	11	US-09-864-426A-454	Sequence 454, App	C 522	92.5	6.9	2520	10	US-09-864-636A-577	Sequence 577, App
C 450	92.5	6.9	2514	11	US-09-864-426A-475	Sequence 475, App	C 523	92.5	6.9	2520	10	US-09-864-636A-583	Sequence 583, App
C 451	92.5	6.9	2514	11	US-09-864-426A-499	Sequence 499, App	C 524	92.5	6.9	2520	10	US-09-864-636A-583	Sequence 583, App
C 452	92.5	6.9	2514	15	US-10-084-839-133	Sequence 133, App	C 525	92.5	6.9	2520	10	US-09-758-282-279	Sequence 279, App
C 453	92.5	6.9	2514	15	US-10-084-839-454	Sequence 454, App	C 526	92.5	6.9	2520	11	US-09-864-426A-222	Sequence 222, App
C 454	92.5	6.9	2514	15	US-10-084-839-475	Sequence 475, App	C 527	92.5	6.9	2520	11	US-09-864-426A-505	Sequence 505, App
C 455	92.5	6.9	2514	15	US-10-084-839-2708	Sequence 2708, App	C 528	92.5	6.9	2520	11	US-09-864-426A-541	Sequence 541, App
C 456	92.5	6.9	2514	15	US-10-084-839-2764	Sequence 2764, Ap	C 529	92.5	6.9	2520	11	US-09-864-426A-543	Sequence 543, App
C 457	92.5	6.9	2514	15	US-10-084-839-2775	Sequence 2775, Ap	C 530	92.5	6.9	2520	11	US-09-864-426A-573	Sequence 573, App
C 458	92.5	6.9	2514	15	US-10-084-839-2788	Sequence 2788, Ap	C 531	92.5	6.9	2520	11	US-09-864-426A-577	Sequence 577, App
C 459	92.5	6.9	2514	15	US-10-084-839-2850	Sequence 2850, Ap	C 532	92.5	6.9	2520	11	US-09-864-426A-583	Sequence 583, App
C 460	92.5	6.9	2514	15	US-10-084-839-2850	Sequence 2850, Ap	C 533	92.5	6.9	2520	15	US-10-084-839-222	Sequence 222, App
C 461	92.5	6.9	2514	15	US-10-084-839-2854	Sequence 2854, Ap	C 534	92.5	6.9	2520	15	US-10-084-839-505	Sequence 505, App
C 462	92.5	6.9	2517	10	US-09-864-636A-69	Sequence 69, Appl	C 535	92.5	6.9	2520	15	US-10-084-839-541	Sequence 541, App
C 463	92.5	6.9	2517	10	US-09-864-636A-128	Sequence 128, App	C 536	92.5	6.9	2520	15	US-10-084-839-543	Sequence 543, App
C 464	92.5	6.9	2517	10	US-09-864-636A-484	Sequence 484, App	C 537	92.5	6.9	2520	15	US-10-084-839-573	Sequence 573, App
C 465	92.5	6.9	2517	10	US-09-864-636A-495	Sequence 495, App	C 538	92.5	6.9	2520	15	US-10-084-839-577	Sequence 577, App
C 466	92.5	6.9	2517	10	US-09-864-636A-501	Sequence 501, App	C 539	92.5	6.9	2520	15	US-10-084-839-583	Sequence 583, App
C 467	92.5	6.9	2517	10	US-09-864-636A-509	Sequence 509, App	C 540	92.5	6.9	2520	15	US-10-084-839-2711	Sequence 2711, Ap
C 468	92.5	6.9	2517	10	US-09-864-636A-513	Sequence 513, App	C 541	92.5	6.9	2520	15	US-10-084-839-2792	Sequence 2792, Ap
C 469	92.5	6.9	2517	10	US-09-864-636A-517	Sequence 517, App	C 542	92.5	6.9	2520	15	US-10-084-839-2810	Sequence 2810, Ap
C 470	92.5	6.9	2517	10	US-09-864-636A-521	Sequence 521, App	C 543	92.5	6.9	2520	15	US-10-084-839-2812	Sequence 2812, Ap
C 471	92.5	6.9	2517	10	US-09-864-636A-525	Sequence 525, App	C 544	92.5	6.9	2520	15	US-10-084-839-2820	Sequence 2820, Ap
C 472	92.5	6.9	2517	10	US-09-864-636A-529	Sequence 529, App	C 545	92.5	6.9	2520	15	US-10-084-839-2824	Sequence 2824, Ap
C 473	92.5	6.9	2517	10	US-09-864-636A-533	Sequence 533, App	C 546	92.5	6.9	2520	15	US-10-084-839-2830	Sequence 2830, Ap
C 474	92.5	6.9	2517	10	US-09-864-636A-537	Sequence 537, App	C 547	92.5	6.9	2526	9	US-09-777-430A-14	Sequence 14, Appl
C 475	92.5	6.9	2517	10	US-09-758-282-74	Sequence 74, Appl	C 548	92.5	6.9	2526	9	US-09-777-430A-19	Sequence 19, Appl
C 476	92.5	6.9	2517	10	US-09-758-282-238	Sequence 238, App	C 549	92.5	6.9	2526	9	US-09-777-430A-22	Sequence 22, Appl
C 477	92.5	6.9	2517	11	US-09-864-426A-69	Sequence 69, Appl	C 550	92.5	6.9	2526	9	US-09-777-430A-25	Sequence 25, Appl
C 478	92.5	6.9	2517	11	US-09-864-426A-128	Sequence 128, App	C 551	92.5	6.9	2526	10	US-09-864-636A-103	Sequence 103, App
C 479	92.5	6.9	2517	11	US-09-864-426A-484	Sequence 484, App	C 552	92.5	6.9	2526	10	US-09-864-636A-104	Sequence 104, App
C 480	92.5	6.9	2517	11	US-09-864-426A-495	Sequence 495, App	C 553	92.5	6.9	2526	10	US-09-864-636A-117	Sequence 117, App
C 481	92.5	6.9	2517	11	US-09-864-426A-501	Sequence 501, App	C 554	92.5	6.9	2526	10	US-09-864-636A-118	Sequence 118, App
C 482	92.5	6.9	2517	11	US-09-864-426A-509	Sequence 509, App	C 555	92.5	6.9	2526	10	US-09-864-636A-119	Sequence 119, App
C 483	92.5	6.9	2517	11	US-09-864-426A-513	Sequence 513, App	C 556	92.5	6.9	2526	10	US-09-864-636A-132	Sequence 132, App
C 484	92.5	6.9	2517	11	US-09-864-426A-517	Sequence 517, App	C 557	92.5	6.9	2526	10	US-09-864-636A-137	Sequence 137, App
C 485	92.5	6.9	2517	11	US-09-864-426A-521	Sequence 521, App	C 558	92.5	6.9	2526	10	US-09-864-636A-273	Sequence 273, App
C 486	92.5	6.9	2517	11	US-09-864-426A-525	Sequence 525, App	C 559	92.5	6.9	2526	10	US-09-864-636A-349	Sequence 349, App
C 487	92.5	6.9	2517	11	US-09-864-426A-529	Sequence 529, App	C 560	92.5	6.9	2526	10	US-09-864-636A-373	Sequence 373, App
C 488	92.5	6.9	2517	11	US-09-864-426A-533	Sequence 533, App	C 561	92.5	6.9	2526	10	US-09-864-636A-375	Sequence 375, App
C 489	92.5	6.9	2517	11	US-09-864-426A-537	Sequence 537, App	C 562	92.5	6.9	2526	10	US-09-864-636A-379	Sequence 379, App
C 490	92.5	6.9	2517	15	US-10-084-839-69	Sequence 69, Appl	C 563	92.5	6.9	2526	10	US-09-864-636A-383	Sequence 383, App
C 491	92.5	6.9	2517	15	US-10-084-839-128	Sequence 128, App	C 564	92.5	6.9	2526	10	US-09-864-636A-387	Sequence 387, App
C 492	92.5	6.9	2517	15	US-10-084-839-484	Sequence 484, App	C 565	92.5	6.9	2526	10	US-09-864-636A-391	Sequence 391, App
C 493	92.5	6.9	2517	15	US-10-084-839-495	Sequence 495, App	C 566	92.5	6.9	2526	10	US-09-864-636A-395	Sequence 395, App
C 494	92.5	6.9	2517	15	US-10-084-839-501	Sequence 501, App	C 567	92.5	6.9	2526	10	US-09-864-636A-399	Sequence 399, App
C 495	92.5	6.9	2517	15	US-10-084-839-509	Sequence 509, App	C 568	92.5	6.9	2526	10	US-09-864-636A-452	Sequence 452, App
C 496	92.5	6.9	2517	15	US-10-084-839-513	Sequence 513, App	C 569	92.5	6.9	2526	10	US-09-864-636A-455	Sequence 455, App
C 497	92.5	6.9	2517	15	US-10-084-839-517	Sequence 517, App	C 570	92.5	6.9	2526	10	US-09-864-636A-459	Sequence 459, App
C 498	92.5	6.9	2517	15	US-10-084-839-521	Sequence 521, App	C 571	92.5	6.9	2526	10	US-09-864-636A-471	Sequence 471, App
C 499	92.5	6.9	2517	15	US-10-084-839-525	Sequence 525, App	C 572	92.5	6.9	2526	10	US-09-864-636A-497	Sequence 497, App
C 500	92.5	6.9	2517	15	US-10-084-839-525	Sequence 525, App	C 573	92.5	6.9	2526	10	US-09-864-636A-558	Sequence 558, App



C 574	92.5	6.9	2526	10	US-09-758-282-64	Sequence 64, Appl	C 647	92.5	6.9	2526	15	US-10-084-839-2767	Sequence 2767, Ap
C 575	92.5	6.9	2526	10	US-09-758-282-70	Sequence 70, Appl	C 648	92.5	6.9	2526	15	US-10-084-839-2773	Sequence 2773, Ap
C 576	92.5	6.9	2526	10	US-09-758-282-162	Sequence 162, Appl	C 649	92.5	6.9	2526	15	US-10-084-839-2786	Sequence 2786, Ap
C 577	92.5	6.9	2526	10	US-09-758-282-165	Sequence 165, Appl	C 650	92.5	6.9	2526	15	US-10-084-839-2832	Sequence 2832, Ap
C 578	92.5	6.9	2526	10	US-09-758-282-211	Sequence 211, Appl	C 651	92.5	6.9	2526	15	US-10-084-839-2838	Sequence 2838, Ap
C 579	92.5	6.9	2526	10	US-09-758-282-213	Sequence 213, Appl	C 652	92.5	6.9	2526	15	US-10-084-839-2840	Sequence 2840, Ap
C 580	92.5	6.9	2526	10	US-09-758-282-215	Sequence 215, Appl	C 653	92.5	6.9	2526	15	US-10-084-839-2842	Sequence 2842, Ap
C 581	92.5	6.9	2526	10	US-09-758-282-258	Sequence 258, Appl	C 654	92.5	6.9	2526	15	US-10-084-839-2844	Sequence 2844, Ap
C 582	92.5	6.9	2526	11	US-09-864-426A-103	Sequence 103, Appl	C 655	92.5	6.9	2526	15	US-10-084-839-2846	Sequence 2846, Ap
C 583	92.5	6.9	2526	11	US-09-864-426A-104	Sequence 104, Appl	C 656	92.5	6.9	2526	15	US-10-084-839-2848	Sequence 2848, Ap
C 584	92.5	6.9	2526	11	US-09-864-426A-117	Sequence 117, Appl	C 657	92.5	6.9	2532	10	US-09-864-426A-463	Sequence 463, App
C 585	92.5	6.9	2526	11	US-09-864-426A-118	Sequence 118, Appl	C 658	92.5	6.9	2532	10	US-09-864-426A-467	Sequence 467, App
C 586	92.5	6.9	2526	11	US-09-864-426A-119	Sequence 119, Appl	C 659	92.5	6.9	2532	11	US-09-864-426A-463	Sequence 463, App
C 587	92.5	6.9	2526	11	US-09-864-426A-132	Sequence 132, Appl	C 660	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 588	92.5	6.9	2526	11	US-09-864-426A-167	Sequence 167, Appl	C 661	92.5	6.9	2532	11	US-10-084-839-463	Sequence 463, App
C 589	92.5	6.9	2526	11	US-09-864-426A-273	Sequence 273, Appl	C 662	92.5	6.9	2532	15	US-10-084-839-467	Sequence 467, App
C 590	92.5	6.9	2526	11	US-09-864-426A-349	Sequence 349, Appl	C 663	92.5	6.9	2532	15	US-10-084-839-2769	Sequence 2769, Ap
C 591	92.5	6.9	2526	11	US-09-864-426A-373	Sequence 373, Appl	C 664	92.5	6.9	2532	15	US-10-084-839-2771	Sequence 2771, Ap
C 592	92.5	6.9	2526	11	US-09-864-426A-375	Sequence 375, Appl	C 665	92.5	6.9	2619	10	US-09-864-426A-563	Sequence 563, App
C 593	92.5	6.9	2526	11	US-09-864-426A-379	Sequence 379, Appl	C 666	92.5	6.9	2619	11	US-09-864-426A-563	Sequence 563, App
C 594	92.5	6.9	2526	11	US-09-864-426A-383	Sequence 383, Appl	C 667	92.5	6.9	2619	15	US-10-084-839-563	Sequence 563, App
C 595	92.5	6.9	2526	11	US-09-864-426A-387	Sequence 387, Appl	C 668	92.5	6.9	2619	15	US-10-084-839-2816	Sequence 2816, Ap
C 596	92.5	6.9	2526	11	US-09-864-426A-391	Sequence 391, Appl	C 669	92.5	6.9	2643	10	US-09-864-426A-559	Sequence 559, App
C 597	92.5	6.9	2526	11	US-09-864-426A-395	Sequence 395, Appl	C 670	92.5	6.9	2643	11	US-09-864-426A-559	Sequence 559, App
C 598	92.5	6.9	2526	11	US-09-864-426A-399	Sequence 399, Appl	C 671	92.5	6.9	2643	15	US-10-084-839-559	Sequence 559, App
C 599	92.5	6.9	2526	11	US-09-864-426A-452	Sequence 452, Appl	C 672	92.5	6.9	2643	15	US-10-084-839-2814	Sequence 2814, Ap
C 600	92.5	6.9	2526	11	US-09-864-426A-455	Sequence 455, Appl	C 673	92.5	6.9	3135	10	US-09-864-426A-481	Sequence 481, App
C 601	92.5	6.9	2526	11	US-09-864-426A-459	Sequence 459, Appl	C 674	92.5	6.9	3135	11	US-09-864-426A-481	Sequence 481, App
C 602	92.5	6.9	2526	11	US-09-864-426A-471	Sequence 471, Appl	C 675	92.5	6.9	3135	15	US-10-084-839-481	Sequence 481, App
C 603	92.5	6.9	2526	11	US-09-864-426A-497	Sequence 497, Appl	C 676	92.5	6.9	3135	15	US-10-084-839-2777	Sequence 2777, Ap
C 604	92.5	6.9	2526	11	US-09-864-426A-558	Sequence 558, Appl	C 677	92	6.9	813	15	US-10-369-493-33103	Sequence 33103, A
C 605	92.5	6.9	2526	15	US-10-084-839-104	Sequence 103, Appl	C 678	92	6.9	942	10	US-09-942-025-8	Sequence 8, Appl
C 606	92.5	6.9	2526	15	US-10-084-839-117	Sequence 117, Appl	C 679	92	6.9	1130	16	US-10-282-122A-19437	Sequence 19437, A
C 607	92.5	6.9	2526	15	US-10-084-839-119	Sequence 119, Appl	C 680	92	6.9	1932	16	US-10-267-502-88	Sequence 88, Appl
C 608	92.5	6.9	2526	15	US-10-084-839-118	Sequence 118, Appl	C 681	92	6.9	67311	10	US-09-942-025-1	Sequence 1, Appl
C 609	92.5	6.9	2526	15	US-10-084-839-132	Sequence 132, Appl	C 682	91.5	6.8	903	15	US-10-156-761-642	Sequence 642, App
C 610	92.5	6.9	2526	15	US-10-084-839-267	Sequence 267, Appl	C 683	91.5	6.8	1092	17	US-10-437-963-97637	Sequence 97637, A
C 611	92.5	6.9	2526	15	US-10-084-839-273	Sequence 273, Appl	C 684	91.5	6.8	1116	16	US-10-282-122A-32148	Sequence 32148, A
C 612	92.5	6.9	2526	15	US-10-084-839-349	Sequence 349, Appl	C 685	91.5	6.8	1149	15	US-10-156-761-5745	Sequence 5745, A
C 613	92.5	6.9	2526	15	US-10-084-839-373	Sequence 373, Appl	C 686	91.5	6.8	1896	15	US-10-156-761-5658	Sequence 5658, Ap
C 614	92.5	6.9	2526	15	US-10-084-839-375	Sequence 375, Appl	C 687	91.5	6.8	2253	16	US-10-282-122A-30610	Sequence 30610, A
C 615	92.5	6.9	2526	15	US-10-084-839-379	Sequence 379, Appl	C 688	91.5	6.8	2499	10	US-09-864-426A-79	Sequence 79, Appl
C 616	92.5	6.9	2526	15	US-10-084-839-383	Sequence 383, Appl	C 689	91.5	6.8	2499	10	US-09-758-282-94	Sequence 94, Appl
C 617	92.5	6.9	2526	15	US-10-084-839-387	Sequence 387, Appl	C 690	91.5	6.8	2499	11	US-09-864-426A-79	Sequence 79, Appl
C 618	92.5	6.9	2526	15	US-10-084-839-391	Sequence 391, Appl	C 691	91.5	6.8	2499	15	US-10-084-839-79	Sequence 79, Appl
C 619	92.5	6.9	2526	15	US-10-084-839-395	Sequence 395, Appl	C 692	91.5	6.8	2499	15	US-10-084-839-2682	Sequence 2682, Ap
C 620	92.5	6.9	2526	15	US-10-084-839-399	Sequence 399, Appl	C 693	91.5	6.8	2505	10	US-09-864-426A-155	Sequence 155, App
C 621	92.5	6.9	2526	15	US-10-084-839-452	Sequence 452, Appl	C 694	91.5	6.8	2505	11	US-09-758-282-266	Sequence 266, App
C 622	92.5	6.9	2526	15	US-10-084-839-455	Sequence 455, Appl	C 695	91.5	6.8	2505	11	US-09-864-426A-155	Sequence 155, App
C 623	92.5	6.9	2526	15	US-10-084-839-459	Sequence 459, Appl	C 696	91.5	6.8	2505	15	US-10-084-839-155	Sequence 155, App
C 624	92.5	6.9	2526	15	US-10-084-839-471	Sequence 471, Appl	C 697	91.5	6.8	2505	15	US-10-084-839-2709	Sequence 2709, Ap
C 625	92.5	6.9	2526	15	US-10-084-839-497	Sequence 497, Appl	C 698	91.5	6.8	2511	9	US-09-777-430A-9	Sequence 9, Appl
C 626	92.5	6.9	2526	15	US-10-084-839-558	Sequence 558, Appl	C 699	91.5	6.8	2511	10	US-09-864-426A-244	Sequence 244, App
C 627	92.5	6.9	2526	15	US-10-084-839-2701	Sequence 2701, Appl	C 700	91.5	6.8	2511	10	US-09-758-282-3	Sequence 3, Appl
C 628	92.5	6.9	2526	15	US-10-084-839-2702	Sequence 2702, Appl	C 701	91.5	6.8	2511	11	US-09-864-426A-244	Sequence 244, App
C 629	92.5	6.9	2526	15	US-10-084-839-2718	Sequence 2718, Appl	C 702	91.5	6.8	2511	11	US-10-084-839-244	Sequence 244, App
C 630	92.5	6.9	2526	15	US-10-084-839-2720	Sequence 2720, Appl	C 703	91.5	6.8	2511	15	US-10-084-839-2713	Sequence 2713, Ap
C 631	92.5	6.9	2526	15	US-10-084-839-2704	Sequence 2704, Appl	C 704	91.5	6.8	2653	17	US-10-469-858-1	Sequence 1, Appl
C 632	92.5	6.9	2526	15	US-10-084-839-2705	Sequence 2705, Appl	C 705	91.5	6.8	2731748	17	US-10-297-465A-1	Sequence 1, Appl
C 633	92.5	6.9	2526	15	US-10-084-839-2707	Sequence 2707, Appl	C 706	91.5	6.8	2731748	17	US-10-297-465A-1	Sequence 1, Appl
C 634	92.5	6.9	2526	15	US-10-084-839-2716	Sequence 2716, Appl	C 707	91	6.8	798	18	US-10-425-115-60646	Sequence 60646, A
C 635	92.5	6.9	2526	15	US-10-084-839-2718	Sequence 2718, Appl	C 708	91	6.8	846	16	US-10-282-122A-23727	Sequence 23727, A
C 636	92.5	6.9	2526	15	US-10-084-839-2720	Sequence 2720, Appl	C 709	91	6.8	1209	16	US-10-425-114-16417	Sequence 16417, A
C 637	92.5	6.9	2526	15	US-10-084-839-2721	Sequence 2721, Appl	C 710	91	6.8	1400	17	US-10-437-963-22255	Sequence 22255, A
C 638	92.5	6.9	2526	15	US-10-084-839-2723	Sequence 2723, Appl	C 711	91	6.8	1590	16	US-10-282-122A-41291	Sequence 41291, A
C 639	92.5	6.9	2526	15	US-10-084-839-2725	Sequence 2725, Appl	C 712	91	6.8	2064	15	US-10-156-761-2902	Sequence 2902, Ap
C 640	92.5	6.9	2526	15	US-10-084-839-2727	Sequence 2727, Appl	C 713	91	6.8	2259	17	US-10-466-531-49	Sequence 49, Appl
C 641	92.5	6.9	2526	15	US-10-084-839-2729	Sequence 2729, Appl	C 714	91	6.8	2494	15	US-10-156-761-2410	Sequence 2410, App
C 642	92.5	6.9	2526	15	US-10-084-839-2731	Sequence 2731, Appl	C 715	91	6.8	2749	14	US-09-997-428-516	Sequence 516, App
C 643	92.5	6.9	2526	15	US-10-084-839-2733	Sequence 2733, Appl	C 716	91	6.8	2749	14	US-10-140-002-385	Sequence 385, App
C 644	92.5	6.9	2526	15	US-10-084-839-2735	Sequence 2735, Appl	C 717	91	6.8	2749	14	US-10-167-749-215	Sequence 215, App
C 645	92.5	6.9	2526	15	US-10-084-839-2763	Sequence 2763, Appl	C 718	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl
C 646	92.5	6.9	2526	15	US-10-084-839-2765	Sequence 2765, Appl	C 719	91	6.8	2749	15	US-10-223-084-59	Sequence 59, Appl



967	6.8	2749	15	US-10-223-088-59	Sequence 59, Appl	cl393	88.5	6.6	3289	18	US-10-723-860-6374	Sequence 6374, Ap
968	6.8	2749	15	US-10-223-090-59	Sequence 59, Appl	1394	88.5	6.6	3413	16	US-10-424-599-52304	Sequence 52304, A
969	6.8	2749	15	US-10-223-087-59	Sequence 59, Appl	1395	88.5	6.6	22459	11	US-09-973-278-883	Sequence 883, App
971	6.8	2749	15	US-10-223-083-59	Sequence 59, Appl	cl396	88.5	6.6	30350	13	US-10-118-328-3	Sequence 3, Appl1
972	6.8	2749	15	US-10-175-590-385	Sequence 385, App	cl397	88.5	6.6	30350	17	US-10-694-438-3	Sequence 3, Appl1
973	6.8	2749	15	US-10-223-089-59	Sequence 59, Appl	1398	88.5	6.6	37116	15	US-10-107-431-279	Sequence 279, App
1145	6.8	2749	15	US-10-223-081-59	Sequence 59, Appl	1399	88.5	6.6	84428	16	US-10-229-1488-1	Sequence 1, Appl1
1155	6.8	2749	15	US-10-223-082-59	Sequence 59, Appl	1400	88.5	6.6	109519	11	US-09-758-759-1	Sequence 35, Appl
1234	6.8	2749	15	US-10-170-481A-215	Sequence 215, App	cl401	88.5	6.6	160361	16	US-10-369-493-33037	Sequence 33037, A
1236	6.8	2749	15	US-10-160-028-215	Sequence 215, App	1402	88	6.6	813	16	US-10-369-493-33037	Sequence 34, Appl
1236	6.8	2749	15	US-10-162-521A-215	Sequence 215, App	1403	88	6.6	852	17	US-10-389-647-34	Sequence 2040, Ap
1236	6.8	2749	15	US-10-305-654-59	Sequence 59, Appl	1404	88	6.6	934	17	US-10-767-701-2040	Sequence 14306, A
1305	6.8	2749	16	US-10-081-056-59	Sequence 59, Appl	1405	88	6.6	1087	18	US-10-425-115-143306	Sequence 140838, A
1318	6.8	2749	16	US-10-081-056-59	Sequence 31552, A	1406	88	6.6	1281	15	US-10-425-115-140838	Sequence 44399, A
cl333	6.8	3459	15	US-10-369-493-31552	Sequence 96859, A	cl407	88	6.6	1461	15	US-10-156-761-1666	Sequence 1666, Ap
1334	6.7	1023	17	US-10-437-963-96859	Sequence 1741, Ap	1408	88	6.6	1464	16	US-10-424-599-128274	Sequence 128274, A
1335	6.7	1248	15	US-10-156-761-1741	Sequence 1534, Ap	cl409	88	6.6	1694	17	US-10-437-963-97638	Sequence 97638, A
cl335	6.7	1611	16	US-10-260-238-1534	Sequence 49451, A	cl410	88	6.6	2006	17	US-10-437-963-18431	Sequence 18431, A
cl336	6.7	1820	17	US-10-437-963-49451	Sequence 102, App	1411	88	6.6	2402	15	US-10-369-493-32004	Sequence 32004, A
1337	6.7	2526	10	US-09-864-636A-102	Sequence 159, App	1412	88	6.6	2487	16	US-10-282-122A-32996	Sequence 12996, A
cl338	6.7	2526	10	US-09-758-282-159	Sequence 102, App	cl413	88	6.6	2517	10	US-09-864-636A-127	Sequence 127, App
cl339	6.7	2526	11	US-09-864-426A-102	Sequence 102, App	cl414	88	6.6	2517	11	US-09-864-426A-127	Sequence 127, App
cl341	6.7	2526	15	US-10-084-839-102	Sequence 2700, Ap	cl415	88	6.6	2517	15	US-10-084-839-127	Sequence 127, App
cl342	6.7	2526	15	US-10-084-839-2700	Sequence 174346, A	cl416	88	6.6	2528	17	US-10-437-963-81418	Sequence 81418, A
1343	6.7	2538	18	US-10-425-115-174346	Sequence 1, Appl1	cl417	88	6.6	2565	15	US-10-156-761-3914	Sequence 3914, Ap
1344	6.7	135638	15	US-10-314-657-1	Sequence 1, Appl1	cl418	88	6.6	3426	15	US-10-156-761-5493	Sequence 5493, Ap
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Run on: January 12, 2005, 22:45:23 ; Search time 93 Seconds

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 93	99	7.4	636	4	US-09-252-991A-9822	Sequence 9822, App	C 166	92.5	6.9	2526	4	US-09-758-282B-165	Sequence 165, App
C 94	99	7.4	1275	4	US-09-252-991A-9915	Sequence 9915, App	C 167	92.5	6.9	2526	4	US-09-758-282B-211	Sequence 211, App
C 95	99	7.4	1443	4	US-09-252-991A-10160	Sequence 10160, App	C 168	92.5	6.9	2526	4	US-09-758-282B-213	Sequence 213, App
C 96	99	7.4	2030	1	US-08-330-283-1	Sequence 1, Appli	C 169	92.5	6.9	2526	4	US-09-758-282B-258	Sequence 258, App
C 97	99	7.4	2030	2	US-08-646-248-1	Sequence 1, Appli	C 170	92.5	6.9	2526	4	US-09-577-304A-64	Sequence 64, Appl
C 98	99	7.4	2030	5	PCT-US95-13924-1	Sequence 1, Appli	C 171	92.5	6.9	2526	4	US-09-577-304A-70	Sequence 70, Appl
C 99	99	7.4	2030	5	PCT-US95-13931-1	Sequence 1, Appli	C 172	92.5	6.9	2526	4	US-09-577-304A-162	Sequence 162, App
C 100	99	7.4	2505	1	US-07-977-434-7	Sequence 7, Appli	C 173	92.5	6.9	2526	4	US-09-577-304A-165	Sequence 165, App
C 101	99	7.4	2505	1	US-08-458-819-7	Sequence 7, Appli	C 174	92.5	6.9	2526	4	US-09-577-304A-211	Sequence 211, App
C 102	99	7.4	2505	5	PCT-US91-07035-7	Sequence 1, Appli	C 175	92.5	6.9	2526	4	US-09-577-304A-213	Sequence 213, App
C 103	99	7.4	8519	3	US-09-261-907-1	Sequence 1, Appli	C 176	92.5	6.9	2526	4	US-09-577-304A-215	Sequence 215, App
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C 105	98.5	7.3	855	4	US-09-252-991A-9455	Sequence 9455, App	C 178	92.5	6.9	2526	4	US-09-777-430C-14	Sequence 14, Appl
C 106	98.5	7.3	1101	4	US-09-252-991A-9455	Sequence 84, Appl	C 179	92.5	6.9	2526	4	US-09-777-430C-19	Sequence 19, Appl
C 107	98.5	7.3	3147	4	US-08-887-534A-84	Sequence 84, Appl	C 180	92.5	6.9	2526	4	US-09-777-430C-22	Sequence 22, Appl
C 108	98.5	7.3	3147	4	US-09-527-431-84	Sequence 84, Appl	C 181	92.5	6.9	2526	4	US-09-777-430C-25	Sequence 25, Appl
C 109	98.5	7.3	3147	4	US-09-446-861-84	Sequence 1, Appli	C 182	92.5	6.9	2526	4	US-09-252-991A-6737	Sequence 6737, App
C 110	98.5	7.3	77536	4	US-09-940-316B-1	Sequence 1, Appli	C 183	92.5	6.9	1407	4	US-09-252-991A-13018	Sequence 13018, A
C 111	98.5	7.3	77536	4	US-09-252-991A-109	Sequence 109, App	C 184	91.5	6.8	1137	4	US-09-252-991A-6952	Sequence 6952, App
C 112	98	7.3	657	4	US-09-252-991A-9351	Sequence 14, Appl	C 185	91.5	6.8	1272	4	US-09-252-991A-6782	Sequence 6782, App
C 113	97.5	7.3	657	4	US-09-351-150A-14	Sequence 14, Appl	C 186	91.5	6.8	2346	4	US-09-758-282B-94	Sequence 94, Appl
C 114	97.5	7.3	1632	4	US-09-252-991A-11756	Sequence 11756, A	C 187	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 115	97.5	7.3	2232	4	US-09-252-991A-11756	Sequence 11756, A	C 188	91.5	6.8	2499	4	US-07-977-434-9	Sequence 9, Appli
C 116	97.5	7.3	2274	4	US-09-252-991A-11609	Sequence 11836, A	C 189	91.5	6.8	2505	1	US-08-458-819-9	Sequence 159, App
C 117	97.5	7.3	2613	1	US-07-642-734C-3	Sequence 3, Appli	C 190	91.5	6.8	2505	1	US-09-308-825A-159	Sequence 159, App
C 118	97.5	7.3	20235	3	US-08-439-009A-3	Sequence 3, Appli	C 191	91.5	6.8	2505	4	US-09-758-282B-286	Sequence 286, App
C 119	97.5	7.3	20235	3	US-08-439-009A-3	Sequence 1, Appli	C 192	91.5	6.8	2505	4	US-09-577-304A-266	Sequence 266, App
C 120	97.5	7.3	24494	4	US-09-351-150A-1	Sequence 10259, A	C 193	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appli
C 121	97	7.2	1086	4	US-09-252-991A-10259	Sequence 10259, A	C 194	91.5	6.8	2505	4	US-09-684-938-161	Sequence 161, App
C 122	97	7.2	1101	4	US-09-252-991A-10597	Sequence 10597, A	C 195	91.5	6.8	2511	4	US-09-308-825A-161	Sequence 161, App
C 123	96.5	7.2	783	4	US-09-252-991A-12098	Sequence 12098, A	C 196	91.5	6.8	2511	4	US-09-578-282B-3	Sequence 3, Appli
C 124	96.5	7.2	984	4	US-09-252-991A-12173	Sequence 12173, A	C 197	91.5	6.8	2511	4	US-09-578-282B-3	Sequence 3, Appli
C 125	96.5	7.2	1254	4	US-09-252-991A-12420	Sequence 12420, A	C 198	91.5	6.8	2511	4	US-09-577-430C-9	Sequence 9, Appli
C 126	96	7.1	3135	4	US-09-252-991A-5922	Sequence 5922, App	C 199	91.5	6.8	2511	4	US-09-777-430C-9	Sequence 30, Appl
C 127	95.5	7.1	852	4	US-09-252-991A-7607	Sequence 7607, App	C 200	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl
C 128	95.5	7.1	1452	4	US-09-252-991A-3933	Sequence 3933, App	C 201	91.5	6.8	2640	1	US-08-459-383-30	Sequence 4, Appli
C 129	95.5	7.1	1794	5	PCT-US95-14148-3	Sequence 3, Appli	C 202	91.5	6.8	2943	4	US-09-379-530B-4	Sequence 4, Appli
C 130	95.5	7.1	1794	5	PCT-US95-15327-3	Sequence 1, Appli	C 203	91.5	6.8	2943	4	US-09-252-991A-9720	Sequence 9720, App
C 131	95.5	7.1	3048	5	PCT-US95-14418-1	Sequence 1, Appli	C 204	91.5	6.8	3660	4	US-09-252-991A-12269	Sequence 12269, A
C 132	95.5	7.1	3048	5	PCT-US95-15327-1	Sequence 1, Appli	C 205	91.5	6.8	3660	4	US-09-252-991A-13269	Sequence 13269, A
C 133	95.5	7.1	4284	4	US-09-252-991A-4006	Sequence 4006, App	C 206	91	6.8	906	4	US-09-489-039A-3080	Sequence 3080, App
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C 136	94.5	7.0	2304	1	US-08-464-514-1	Sequence 1, Appli	C 209	91	6.8	1200	4	US-09-252-991A-14709	Sequence 14709, A
C 137	94.5	7.0	2304	3	US-08-486-403-1	Sequence 1, Appli	C 210	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 138	94	7.0	1527	4	US-09-252-991A-12042	Sequence 12042, A	C 211	91	6.8	1299	4	US-09-252-991A-14277	Sequence 14277, A
C 139	94	7.0	1962	4	US-09-252-991A-231	Sequence 231, App	C 212	91	6.8	1428	4	US-09-252-991A-14277	Sequence 14277, A
C 140	94	7.0	2313	4	US-09-252-991A-11939	Sequence 11939, A	C 213	91	6.8	1449	4	US-09-252-991A-1326	Sequence 1326, A
C 141	93.5	7.0	1233	4	US-09-252-991A-8712	Sequence 8712, App	C 214	91	6.8	1515	4	US-09-252-991A-14307	Sequence 14307, A
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C 144	93	6.9	1848	4	US-09-252-991A-1910	Sequence 1910, App	C 217	90.5	6.7	2526	4	US-09-758-282B-159	Sequence 159, App
C 145	93	6.9	2169	4	US-09-252-991A-2045	Sequence 2045, App	C 218	90.5	6.7	2526	4	US-09-577-304A-159	Sequence 159, App
C 146	93	6.9	2946	4	US-09-799-451-585	Sequence 585, App	C 219	90.5	6.7	2622	4	US-09-252-991A-13933	Sequence 13933, A
C 147	93	6.9	3744	4	US-09-252-991A-250	Sequence 250, App	C 220	90.5	6.7	2685	4	US-09-252-991A-13826	Sequence 13826, A
C 148	92.5	6.9	1200	4	US-09-252-991A-3649	Sequence 3649, App	C 221	90.5	6.7	3065	3	US-09-171-710-3	Sequence 3, Appli
C 149	92.5	6.9	1311	4	US-09-252-991A-163	Sequence 163, App	C 222	90.5	6.7	3065	3	US-09-614-912-203	Sequence 203, App
C 150	92.5	6.9	2511	4	US-09-308-825A-163	Sequence 163, App	C 223	90	6.7	1929	4	US-09-252-991A-7017	Sequence 7017, App
C 151	92.5	6.9	2511	4	US-09-758-282B-59	Sequence 59, App	C 224	90	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 152	92.5	6.9	2511	4	US-09-940-444-258	Sequence 59, App	C 225	90	6.7	962	3	US-08-765-907A-16	Sequence 16, Appl
C 153	92.5	6.9	2511	4	US-09-577-304A-59	Sequence 59, App	C 226	89.5	6.7	1052	2	US-08-403-852D-10	Sequence 10, Appl
C 154	92.5	6.9	2511	4	US-09-777-430C-12	Sequence 12, App	C 227	89.5	6.7	1052	2	US-08-510-646B-10	Sequence 10, Appl
C 155	92.5	6.9	2514	4	US-09-758-282B-260	Sequence 260, App	C 228	89.5	6.7	1052	3	US-09-231-818-10	Sequence 10, Appl
C 156	92.5	6.9	2514	4	US-09-577-304A-260	Sequence 260, App	C 229	89.5	6.7	1052	3	US-09-635-359B-10	Sequence 10, Appl
C 157	92.5	6.9	2514	4	US-09-758-282B-74	Sequence 74, Appl	C 230	89.5	6.7	1266	4	US-09-252-991A-13397	Sequence 13397, A
C 158	92.5	6.9	2517	4	US-09-758-282B-238	Sequence 238, App	C 231	89.5	6.7	1359	4	US-09-252-991A-13492	Sequence 13492, A
C 159	92.5	6.9	2517	4			C 232	89.5	6.7				



C 233	89.5	6.7	1605	4	US-09-252-991A-3610	Sequence 3610, Ap	C 306	85.5	6.4	909	4	US-09-252-991A-12929	Sequence 12929, A
C 234	89.5	6.7	3270	4	US-09-252-991A-3763	Sequence 3763, Ap	C 307	85.5	6.4	1269	4	US-09-252-991A-8698	Sequence 8698, Ap
C 235	88.5	6.6	969	4	US-09-252-991A-8841	Sequence 8841, Ap	C 308	85.5	6.4	1944	4	US-09-252-991A-9081	Sequence 9081, Ap
C 236	88.5	6.6	1008	4	US-09-252-991A-8953	Sequence 8953, Ap	C 309	85.5	6.4	29598	3	US-09-341-587-6	Sequence 6, Appli
C 237	88.5	6.6	1035	4	US-09-252-991A-185	Sequence 185, Ap	C 310	85	6.3	666	4	US-09-252-991A-7202	Sequence 7202, Ap
C 238	88.5	6.6	1074	4	US-09-252-991A-162	Sequence 162, Ap	C 311	85	6.3	798	4	US-09-543-681A-2640	Sequence 2640, Ap
C 239	88.5	6.6	1293	4	US-09-252-991A-12484	Sequence 12484, A	C 312	85	6.3	53165	4	US-09-214-808-1	Sequence 1, Appli
C 240	88.5	6.6	1422	4	US-09-252-991A-12989	Sequence 12989, A	C 313	84.5	6.3	1260	4	US-09-252-991A-6317	Sequence 6317, Ap
C 241	88.5	6.6	1455	4	US-09-252-991A-158	Sequence 158, Ap	C 314	84.5	6.3	1524	4	US-09-252-991A-9472	Sequence 9472, Ap
C 242	88.5	6.6	1696	4	US-09-774-528-151	Sequence 151, Ap	C 315	84.5	6.3	2406	4	US-09-252-991A-11239	Sequence 11239, A
C 243	88.5	6.6	2413	3	US-09-367-066B-1	Sequence 2, Appli	C 316	84.5	6.3	2517	4	US-09-758-282B-80	Sequence 80, Appli
C 244	88.5	6.6	2507	2	US-08-471-066B-1	Sequence 1, Appli	C 317	84.5	6.3	2517	4	US-09-577-304A-80	Sequence 80, Appli
C 245	88.5	6.6	2511	4	US-09-252-991A-9132	Sequence 9132, Ap	C 318	84.5	6.3	2526	4	US-09-758-282B-92	Sequence 92, Appli
C 246	88.5	6.6	30350	4	US-10-118-328-3	Sequence 3, Appli	C 319	84.5	6.3	2526	4	US-09-577-304A-92	Sequence 92, Appli
C 247	88	6.6	2517	4	US-09-758-282B-235	Sequence 235, Ap	C 320	84.5	6.3	3358	3	US-09-248-571-2	Sequence 2, Appli
C 248	88	6.6	2517	4	US-09-577-304A-235	Sequence 235, Ap	C 321	84.5	6.3	3358	4	US-09-553-736-2	Sequence 2, Appli
C 249	87.5	6.5	849	4	US-09-252-991A-617	Sequence 617, Ap	C 322	84.5	6.3	3358	4	US-09-103-330-35	Sequence 35, Appli
C 250	87.5	6.5	1575	4	US-09-252-991A-3100	Sequence 3100, Ap	C 323	84	6.3	34446	3	US-09-060-756-582	Sequence 582, App
C 251	87.5	6.5	1866	4	US-09-252-991A-16213	Sequence 16213, A	C 324	84	6.3	314	3	US-09-670-314-582	Sequence 582, App
C 252	87.5	6.5	1956	4	US-09-252-991A-3189	Sequence 3189, Ap	C 325	84	6.3	314	4	US-09-583-110-637	Sequence 637, App
C 253	87.5	6.5	2379	4	US-09-252-991A-686	Sequence 686, Ap	C 326	84	6.3	759	4	US-08-253-155A-11	Sequence 11, Appli
C 254	87.5	6.5	2499	4	US-09-252-991A-696	Sequence 696, Ap	C 327	84	6.3	1065	4	US-09-252-991A-16320	Sequence 16320, A
C 255	87.5	6.5	2526	4	US-09-758-282B-156	Sequence 156, Ap	C 328	84	6.3	1332	4	US-09-252-991A-15961	Sequence 15961, A
C 256	87.5	6.5	2526	4	US-09-577-304A-156	Sequence 156, Ap	C 329	84	6.3	1341	4	US-09-252-991A-16544	Sequence 16544, A
C 257	87	6.5	930	4	US-09-252-991A-6618	Sequence 6618, Ap	C 330	84	6.3	1405	1	US-08-035-558-3	Sequence 3, Appli
C 258	87	6.5	1074	4	US-09-351-150A-36	Sequence 36, Appli	C 331	84	6.3	1405	2	US-08-682-876-5	Sequence 5, Appli
C 259	87	6.5	1158	4	US-09-252-991A-14214	Sequence 14214, A	C 332	84	6.3	1405	3	US-09-063-676-1	Sequence 1, Appli
C 260	87	6.5	1308	4	US-09-252-991A-6649	Sequence 6649, Ap	C 333	84	6.3	1785	1	US-07-865-662F-4	Sequence 4, Appli
C 261	87	6.5	1377	4	US-09-351-150A-12	Sequence 12, Appli	C 334	84	6.3	1785	3	US-08-374-219B-4	Sequence 4, Appli
C 262	87	6.5	1535	1	US-08-910-973-10	Sequence 10, Appli	C 335	84	6.3	2055	4	US-08-252-991A-1845	Sequence 1845, Ap
C 263	87	6.5	1625	4	US-09-499-227-10	Sequence 10, Appli	C 336	84	6.3	2067	4	US-09-252-991A-1398	Sequence 1398, Ap
C 264	87	6.5	1625	4	US-09-799-451-594	Sequence 594, Ap	C 337	84	6.3	2100	4	US-09-252-991A-1209	Sequence 1209, Ap
C 265	87	6.5	1650	4	US-09-252-991A-10150	Sequence 10150, A	C 338	84	6.3	2480	4	US-08-064-199-15	Sequence 15, Appli
C 266	87	6.5	1725	4	US-09-252-991A-9926	Sequence 9926, Ap	C 339	84	6.3	3393	1	US-08-295-502-1	Sequence 1, Appli
C 267	87	6.5	2145	4	US-09-252-991A-13235	Sequence 13235, A	C 340	84	6.3	3393	5	PCT-US95-10691-1	Sequence 1, Appli
C 268	87	6.5	3390	4	US-09-489-039A-3029	Sequence 3029, Ap	C 341	84	6.3	3884	4	US-10-140-002-145	Sequence 145, App
C 269	87	6.5	3741	4	US-09-252-991A-6569	Sequence 6569, Ap	C 342	84	6.3	4346	4	US-09-064-199-12	Sequence 12, Appli
C 270	87	6.5	4431	4	US-09-252-991A-12856	Sequence 12856, A	C 343	84	6.3	4366	4	US-09-064-199-14	Sequence 14, Appli
C 271	87	6.5	10095	3	US-08-822-586-45	Sequence 45, Appli	C 344	84	6.3	4418	4	US-09-064-199-13	Sequence 13, Appli
C 272	87	6.5	24494	4	US-09-351-150A-1	Sequence 1, Appli	C 345	84	6.3	4431	4	US-09-064-199-8	Sequence 8, Appli
C 273	86.5	6.4	888	4	US-09-540-236-1514	Sequence 1514, Ap	C 346	84	6.3	4441	3	US-09-641-999-2	Sequence 2, Appli
C 274	86.5	6.4	1086	4	US-09-252-991A-11554	Sequence 11554, A	C 347	84	6.3	4441	4	US-08-064-199-10	Sequence 10, Appli
C 275	86.5	6.4	1251	4	US-09-252-991A-3770	Sequence 3770, Ap	C 348	84	6.3	4543	2	US-08-519-547A-5	Sequence 5, Appli
C 276	86.5	6.4	1425	4	US-09-252-991A-6019	Sequence 6019, Ap	C 349	84	6.3	4549	4	US-09-064-199-9	Sequence 9, Appli
C 277	86.5	6.4	1707	4	US-09-489-039A-2690	Sequence 2690, Ap	C 350	84	6.3	4564	4	US-09-064-199-2	Sequence 2, Appli
C 278	86.5	6.4	1989	4	US-09-252-991A-6290	Sequence 6290, Ap	C 351	84	6.3	4649	4	US-09-064-199-11	Sequence 11, Appli
C 279	86.5	6.4	2367	4	US-09-252-991A-726	Sequence 726, Ap	C 352	84	6.3	4745	4	US-09-064-199-7	Sequence 7, Appli
C 280	86.5	6.4	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	C 353	84	6.3	5105	4	US-09-064-199-3	Sequence 3, Appli
C 281	86.5	6.4	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	C 354	84	6.3	5463	4	US-09-064-199-1	Sequence 1, Appli
C 282	86.5	6.4	7001	1	US-08-258-261B-1	Sequence 1, Appli	C 355	83.5	6.2	1251	4	US-09-252-991A-8004	Sequence 8004, Ap
C 283	86.5	6.4	7001	1	US-08-456-837-1	Sequence 1, Appli	C 356	83.5	6.2	1308	4	US-09-252-991A-7182	Sequence 7182, Ap
C 284	86.5	6.4	7001	1	US-08-457-342-1	Sequence 1, Appli	C 357	83.5	6.2	1344	4	US-09-252-991A-6363	Sequence 6363, Ap
C 285	86.5	6.4	7001	1	US-08-457-646A-1	Sequence 1, Appli	C 358	83.5	6.2	1550	3	US-09-234-332-3	Sequence 3, Appli
C 286	86.5	6.4	7001	1	US-08-458-076A-1	Sequence 1, Appli	C 359	83.5	6.2	1671	4	US-09-252-991A-6188	Sequence 6188, Ap
C 287	86.5	6.4	7001	1	US-08-457-335A-1	Sequence 1, Appli	C 360	83.5	6.2	1767	1	US-08-399-646-1	Sequence 1, Appli
C 288	86.5	6.4	7001	1	US-08-457-258-6	Sequence 6, Appli	C 361	83.5	6.2	1767	1	US-08-607-321-1	Sequence 1, Appli
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C 290	86.5	6.4	7001	2	US-08-977-306-6	Sequence 6, Appli	C 363	83.5	6.2	1767	2	US-08-605-501-1	Sequence 1, Appli
C 291	86.5	6.4	7001	3	US-09-028-934-1	Sequence 1, Appli	C 364	83.5	6.2	2161	1	US-08-399-646-11	Sequence 11, Appli
C 292	86.5	6.4	8037	4	US-09-774-528-209	Sequence 209, Ap	C 365	83.5	6.2	2161	2	US-08-607-321-11	Sequence 11, Appli
C 293	86.5	6.4	53500	4	US-09-266-965-76	Sequence 76, Appli	C 366	83.5	6.2	2161	2	US-08-961-240-11	Sequence 11, Appli
C 294	86.5	6.4	62909	4	US-09-596-002-32	Sequence 32, Appli	C 367	83.5	6.2	2161	2	US-08-605-501-11	Sequence 11, Appli
C 295	86	6.4	822	4	US-09-252-991A-6178	Sequence 6178, Ap	C 368	83.5	6.2	2484	4	US-09-252-991A-7462	Sequence 7462, Ap
C 296	86	6.4	1221	4	US-09-252-991A-7107	Sequence 7107, Ap	C 369	83.5	6.2	2499	4	US-09-758-282B-98	Sequence 98, Appli
C 297	86	6.4	1488	4	US-09-252-991A-9231	Sequence 9231, Ap	C 370	83.5	6.2	2499	3	US-09-577-304A-98	Sequence 98, Appli
C 298	86	6.4	2019	4	US-09-252-991A-8818	Sequence 8818, Ap	C 371	83.5	6.2	3251	3	US-09-085-199B-6	Sequence 6, Appli
C 299	86	6.4	2094	4	US-09-252-991A-7438	Sequence 7438, Ap	C 372	83.5	6.2	3876	4	US-09-849-602-4	Sequence 4, Appli
C 300	86	6.4	2517	4	US-09-758-282B-174	Sequence 174, Ap	C 373	83.5	6.2	11219	1	US-07-642-734C-1	Sequence 1, Appli
C 301	86	6.4	2517	4	US-09-577-304A-174	Sequence 174, Ap	C 374	83.5	6.2	11219	3	US-08-439-009A-1	Sequence 1, Appli
C 302	86	6.4	2814	4	US-09-252-991A-15765	Sequence 15765, A	C 375	83	6.2	774	4	US-09-252-991A-13331	Sequence 13331, A
C 303	86	6.4	3012	4	US-09-252-991A-7498	Sequence 7498, Ap	C 376	83	6.2	933	4	US-09-252-991A-10917	Sequence 10917, A
C 304	86	6.4	3357	4	US-09-252-991A-15868	Sequence 15868, A	C 377	83	6.2	964	4	US-09-513-999C-14934	Sequence 14934, A
C 305	86	6.4	47981	4	US-09-679-279-1	Sequence 1, Appli	C 378	83	6.2	1152	4	US-09-252-991A-5237	Sequence 5237, Ap



379	83	6.2	1617	4	US-09-265-013-2	Sequence 2, Appli	C 452	82	6.1	1068	4	US-09-252-991A-6432	Sequence 6432, Ap
380	83	6.2	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	C 453	82	6.1	1737	4	US-09-252-991A-2085	Sequence 2085, Ap
381	83	6.2	2046	4	US-09-252-991A-5266	Sequence 5266, Ap	C 454	82	6.1	2517	4	US-09-758-282B-138	Sequence 138, App
382	83	6.2	2328	4	US-09-252-991A-11890	Sequence 11890, A	C 455	82	6.1	2517	4	US-09-577-304A-138	Sequence 138, App
383	83	6.2	4143	4	US-09-252-991A-9151	Sequence 9151, Ap	C 456	82	6.1	3186	4	US-09-489-039A-5569	Sequence 5569, Ap
384	83	6.2	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	C 457	82	6.1	3236	4	US-08-961-527-222	Sequence 222, App
385	83	6.2	7308	3	US-09-252-991A-8929	Sequence 3, Appli	C 458	82	6.1	3378	4	US-09-252-991A-2158	Sequence 2158, Ap
386	83	6.2	7308	3	US-09-011-745-3	Sequence 4, Appli	C 459	82	6.1	5661	3	US-08-938-105-2	Sequence 2, Appli
387	83	6.2	7616	3	US-09-011-745-4	Sequence 4, Appli	C 460	82	6.1	7861	4	US-09-774-528-305	Sequence 305, App
388	83	6.2	8202	1	US-08-850-961-1	Sequence 1, Appli	C 461	81.5	6.1	744	4	US-09-252-991A-15563	Sequence 15563, A
389	83	6.2	8332	3	US-08-850-961-1	Sequence 1, Appli	C 462	81.5	6.1	837	4	US-09-252-991A-5702	Sequence 5702, Ap
390	83	6.2	8332	3	US-08-479-776-1	Sequence 1, Appli	C 463	81.5	6.1	1080	4	US-09-248-766A-4099	Sequence 4099, Ap
391	83	6.2	8332	4	US-09-309-572-11	Sequence 11, Appli	C 464	81.5	6.1	1161	4	US-09-892-188B-1	Sequence 1, Appli
392	83	6.2	8332	4	US-09-315-127-1	Sequence 1, Appli	C 465	81.5	6.1	1221	4	US-09-252-991A-7990	Sequence 7990, Ap
393	83	6.2	8332	4	US-09-265-013-1	Sequence 1, Appli	C 466	81.5	6.1	1233	4	US-09-252-991A-8268	Sequence 8268, Ap
394	83	6.2	8332	4	US-09-554-572-25	Sequence 25, Appli	C 467	81.5	6.1	1245	4	US-09-252-991A-8268	Sequence 8268, Ap
395	83	6.2	8332	4	US-09-718-096-11	Sequence 11, Appli	C 468	81.5	6.1	1302	4	US-09-252-991A-8677	Sequence 8677, Ap
396	83	6.2	8332	4	US-09-815-048-3	Sequence 3, Appli	C 469	81.5	6.1	1362	4	US-09-252-991A-8259	Sequence 8259, Ap
397	83	6.2	42450	4	US-08-804-227C-1	Sequence 1, Appli	C 470	81.5	6.1	1503	4	US-09-252-991A-13684	Sequence 13684, A
398	82.5	6.1	651	4	US-09-252-991A-2095	Sequence 2095, Ap	C 471	81.5	6.1	1584	4	US-09-252-991A-625	Sequence 625, App
399	82.5	6.1	816	4	US-09-252-991A-507	Sequence 507, App	C 472	81.5	6.1	1674	4	US-09-252-991A-3990	Sequence 3990, Ap
400	82.5	6.1	957	4	US-09-252-991A-6278	Sequence 6278, Ap	C 473	81.5	6.1	1746	4	US-09-252-991A-13461	Sequence 13461, A
401	82.5	6.1	1209	4	US-09-252-991A-572	Sequence 572, App	C 474	81.5	6.1	1983	4	US-09-252-991A-15635	Sequence 15635, A
402	82.5	6.1	1245	4	US-09-252-991A-594	Sequence 594, App	C 475	81.5	6.1	2190	4	US-09-252-991A-10256	Sequence 10256, A
403	82.5	6.1	1623	4	US-09-613-303-3	Sequence 3, Appli	C 476	81.5	6.1	2211	4	US-09-252-991A-15685	Sequence 15685, A
404	82.5	6.1	1623	4	US-10-267-311-3	Sequence 3, Appli	C 477	81.5	6.1	2325	4	US-09-252-991A-8064	Sequence 8064, Ap
405	82.5	6.1	1764	4	US-09-252-991A-6133	Sequence 6133, Ap	C 478	81.5	6.1	2403	4	US-09-252-991A-7056	Sequence 7056, Ap
406	82.5	6.1	1785	4	US-09-252-991A-4278	Sequence 4278, Ap	C 479	81.5	6.1	4242	4	US-09-919-039-112	Sequence 112, App
407	82.5	6.1	1879	4	US-09-614-748A-10	Sequence 10, Appli	C 480	81.5	6.1	4346	4	US-09-252-991A-6997	Sequence 6997, Ap
408	82.5	6.1	1886	1	US-07-980-526-1	Sequence 1, Appli	C 481	81.5	6.1	10023	4	US-09-489-039A-2253	Sequence 2253, Ap
409	82.5	6.1	1920	4	US-09-613-303-16	Sequence 16, Appli	C 482	81	6.0	915	4	US-08-360-756-3	Sequence 3, Appli
410	82.5	6.1	1920	4	US-10-267-311-16	Sequence 16, Appli	C 483	81	6.0	999	2	US-09-266-965-45	Sequence 45, Appli
411	82.5	6.1	1947	4	US-09-613-303-28	Sequence 28, Appli	C 484	81	6.0	1152	4	US-08-960-022-17	Sequence 17, Appli
412	82.5	6.1	1947	4	US-10-267-311-28	Sequence 28, Appli	C 485	81	6.0	1307	2	US-08-960-022-17	Sequence 17, Appli
413	82.5	6.1	1956	4	US-09-252-991A-12032	Sequence 12032, A	C 486	81	6.0	1470	4	US-09-252-991A-3389	Sequence 3389, Ap
414	82.5	6.1	2017	4	US-09-614-748A-8	Sequence 8, Appli	C 487	81	6.0	1584	4	US-09-489-039A-2524	Sequence 2524, Ap
415	82.5	6.1	2067	4	US-09-252-991A-527	Sequence 527, App	C 488	81	6.0	1682	3	US-09-096-399-1	Sequence 1, Appli
416	82.5	6.1	2499	4	US-09-758-282B-96	Sequence 96, Appli	C 489	81	6.0	1696	3	US-09-096-399-3	Sequence 3, Appli
417	82.5	6.1	2499	4	US-09-577-304A-96	Sequence 96, Appli	C 490	81	6.0	1899	4	US-09-640-958-9	Sequence 9, Appli
418	82.5	6.1	2517	4	US-09-758-282B-78	Sequence 78, Appli	C 491	81	6.0	1904	4	US-09-640-958-9	Sequence 9, Appli
419	82.5	6.1	2517	4	US-09-758-282B-86	Sequence 86, Appli	C 492	81	6.0	1944	4	US-09-252-991A-16245	Sequence 16245, A
420	82.5	6.1	2517	4	US-09-758-282B-86	Sequence 86, Appli	C 493	81	6.0	1965	4	US-09-640-958-11	Sequence 11, Appli
421	82.5	6.1	2517	4	US-09-758-282B-102	Sequence 102, App	C 494	81	6.0	2499	1	US-07-977-434-1	Sequence 1, Appli
422	82.5	6.1	2517	4	US-09-758-282B-105	Sequence 105, App	C 495	81	6.0	2499	1	US-08-458-819-1	Sequence 1, Appli
423	82.5	6.1	2517	4	US-09-758-282B-108	Sequence 108, App	C 496	81	6.0	2499	3	US-07-602-848E-1	Sequence 1, Appli
424	82.5	6.1	2517	4	US-09-758-282B-111	Sequence 111, App	C 497	81	6.0	2499	3	US-09-587-856-1	Sequence 1, Appli
425	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App	C 498	81	6.0	2499	3	US-09-777-537-1	Sequence 1, Appli
426	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App	C 499	81	6.0	2499	3	US-09-777-538-1	Sequence 1, Appli
427	82.5	6.1	2517	4	US-09-577-304A-78	Sequence 78, Appli	C 500	81	6.0	2499	4	US-09-758-282B-100	Sequence 100, App
428	82.5	6.1	2517	4	US-09-577-304A-84	Sequence 84, Appli	C 501	81	6.0	2499	4	US-09-577-304A-100	Sequence 100, App
429	82.5	6.1	2517	4	US-09-577-304A-86	Sequence 86, Appli	C 502	81	6.0	2499	5	PCT-US91-07035-1	Sequence 1, Appli
430	82.5	6.1	2517	4	US-09-577-304A-102	Sequence 102, App	C 503	81	6.0	2505	2	US-08-757-653-167	Sequence 65, Appli
431	82.5	6.1	2517	4	US-09-577-304A-105	Sequence 105, App	C 504	81	6.0	2505	2	US-08-823-516-65	Sequence 106, App
432	82.5	6.1	2517	4	US-09-577-304A-108	Sequence 108, App	C 505	81	6.0	2505	3	US-08-759-038-106	Sequence 106, App
433	82.5	6.1	2517	4	US-09-577-304A-111	Sequence 111, App	C 506	81	6.0	2505	3	US-08-758-314-106	Sequence 106, App
434	82.5	6.1	2526	4	US-09-758-282B-90	Sequence 90, Appli	C 507	81	6.0	2505	4	US-09-684-938-106	Sequence 106, App
435	82.5	6.1	2526	4	US-09-577-304A-90	Sequence 90, Appli	C 508	81	6.0	2505	4	US-09-308-825A-106	Sequence 55, Appli
436	82.5	6.1	2766	4	US-09-252-991A-3756	Sequence 3756, Ap	C 509	81	6.0	2505	4	US-09-758-282B-55	Sequence 55, Appli
437	82.5	6.1	2847	4	US-09-613-303-20	Sequence 20, Appli	C 510	81	6.0	2505	4	US-09-940-244-65	Sequence 55, Appli
438	82.5	6.1	2847	4	US-10-267-311-20	Sequence 20, Appli	C 511	81	6.0	2505	4	US-09-577-304A-55	Sequence 1, Appli
439	82.5	6.1	2874	4	US-09-252-991A-3637	Sequence 3637, Ap	C 512	81	6.0	2506	1	US-08-073-384C-1	Sequence 1, Appli
440	82.5	6.1	3390	3	US-09-252-991A-11981	Sequence 11981, A	C 513	81	6.0	2506	1	US-08-254-359A-1	Sequence 1, Appli
441	82.5	6.1	4380	3	US-08-955-565A-3	Sequence 3, Appli	C 514	81	6.0	2506	1	US-08-483-043-1	Sequence 1, Appli
442	82.5	6.1	28804	2	US-08-592-874-1	Sequence 2, Appli	C 515	81	6.0	2506	1	US-08-481-238-1	Sequence 1, Appli
443	82.5	6.1	28804	3	US-09-096-867-2	Sequence 2, Appli	C 516	81	6.0	2506	2	US-08-484-956-1	Sequence 1, Appli
444	82.5	6.1	28804	3	US-09-096-867-2	Sequence 2, Appli	C 517	81	6.0	2506	2	US-08-757-653-1	Sequence 1, Appli
445	82	6.1	789	1	US-08-181-335B-3	Sequence 3, Appli	C 518	81	6.0	2506	2	US-08-599-491-1	Sequence 1, Appli
446	82	6.1	789	1	US-08-181-335B-5	Sequence 5, Appli	C 519	81	6.0	2506	2	US-08-756-386-1	Sequence 1, Appli
447	82	6.1	789	1	US-08-181-335B-6	Sequence 6, Appli	C 520	81	6.0	2506	3	US-08-823-516-1	Sequence 1, Appli
448	82	6.1	789	5	PCT-US95-00129-3	Sequence 3, Appli	C 521	81	6.0	2506	3	US-08-682-853A-1	Sequence 1, Appli
449	82	6.1	789	5	PCT-US95-00129-5	Sequence 5, Appli	C 522	81	6.0	2506	3	US-08-759-038-1	Sequence 1, Appli
450	82	6.1	789	5	PCT-US95-00129-6	Sequence 6, Appli	C 523	81	6.0	2506	3	US-08-758-314-1	Sequence 1, Appli
451	82	6.1	852	4	US-09-252-991A-6125	Sequence 6125, Ap	C 524	81	6.0	2506	3	US-09-350-309-1	Sequence 1, Appli



C 525	81	6.0	2506	3	US-08-520-946-1	Sequence 1, Appli	C 598	81	6.0	2517	4	US-09-577-304A-233	Sequence 233, App
C 526	81	6.0	2506	4	US-09-684-938-1	Sequence 1, Appli	C 599	81	6.0	2526	4	US-09-758-282B-76	Sequence 76, Appl
C 527	81	6.0	2506	4	US-09-308-822A-1	Sequence 1, Appli	C 600	81	6.0	2526	4	US-09-758-282B-240	Sequence 240, App
C 528	81	6.0	2506	4	US-09-758-282B-1	Sequence 1, Appli	C 601	81	6.0	2526	4	US-09-758-282B-362	Sequence 362, App
C 529	81	6.0	2506	4	US-09-655-378A-1	Sequence 1, Appli	C 602	81	6.0	2526	4	US-09-577-304A-76	Sequence 76, Appl
C 530	81	6.0	2506	4	US-09-940-244-1	Sequence 1, Appli	C 603	81	6.0	2526	4	US-09-577-304A-240	Sequence 240, App
C 531	81	6.0	2506	4	US-09-333-145-1	Sequence 1, Appli	C 604	81	6.0	2526	4	US-09-577-304A-262	Sequence 262, App
C 532	81	6.0	2506	4	US-09-577-304A-1	Sequence 1, Appli	C 605	81	6.0	2626	1	US-08-156-020-1	Sequence 1, Appli
C 533	81	6.0	2514	4	US-09-758-282B-164	Sequence 264, App	C 606	81	6.0	2626	1	US-08-156-020-3	Sequence 3, Appli
C 534	81	6.0	2514	4	US-09-577-304A-264	Sequence 264, App	C 607	81	6.0	2626	1	US-08-156-020-5	Sequence 5, Appli
C 535	81	6.0	2517	4	US-09-758-282B-62	Sequence 62, Appl	C 608	81	6.0	2626	1	US-08-156-020-7	Sequence 7, Appli
C 536	81	6.0	2517	4	US-09-758-282B-71	Sequence 71, Appl	C 609	81	6.0	2626	1	US-08-156-020-9	Sequence 9, Appli
C 537	81	6.0	2517	4	US-09-758-282B-82	Sequence 82, Appl	C 610	81	6.0	2626	3	US-08-978-806-1	Sequence 1, Appli
C 538	81	6.0	2517	4	US-09-758-282B-88	Sequence 88, Appl	C 611	81	6.0	2727	4	US-09-623-326-3	Sequence 3, Appli
C 539	81	6.0	2517	4	US-09-758-282B-114	Sequence 114, App	C 612	81	6.0	2727	4	US-09-623-326-4	Sequence 4, Appli
C 540	81	6.0	2517	4	US-09-758-282B-117	Sequence 117, App	C 613	81	6.0	2733	4	US-09-623-326-1	Sequence 1, Appli
C 541	81	6.0	2517	4	US-09-758-282B-120	Sequence 120, App	C 614	81	6.0	2733	4	US-09-623-326-2	Sequence 2, Appli
C 542	81	6.0	2517	4	US-09-758-282B-123	Sequence 123, App	C 615	81	6.0	2763	4	US-09-640-958-5	Sequence 5, Appli
C 543	81	6.0	2517	4	US-09-758-282B-126	Sequence 126, App	C 616	81	6.0	2850	4	US-09-623-326-5	Sequence 5, Appli
C 544	81	6.0	2517	4	US-09-758-282B-129	Sequence 129, App	C 617	81	6.0	2949	4	US-09-623-326-6	Sequence 6, Appli
C 545	81	6.0	2517	4	US-09-758-282B-132	Sequence 132, App	C 618	81	6.0	3114	4	US-09-252-991A-225	Sequence 225, App
C 546	81	6.0	2517	4	US-09-758-282B-141	Sequence 141, App	C 619	81	6.0	3261	4	US-09-252-991A-8480	Sequence 8480, App
C 547	81	6.0	2517	4	US-09-758-282B-147	Sequence 147, App	C 620	81	6.0	3345	4	US-09-252-991A-8394	Sequence 8394, App
C 548	81	6.0	2517	4	US-09-758-282B-149	Sequence 149, App	C 621	81	6.0	3402	4	US-09-252-991A-1374	Sequence 1374, App
C 549	81	6.0	2517	4	US-09-758-282B-152	Sequence 152, App	C 622	81	6.0	3687	4	US-09-252-991A-1193	Sequence 1193, App
C 550	81	6.0	2517	4	US-09-758-282B-168	Sequence 168, App	C 623	81	6.0	3864	4	US-09-252-991A-13035	Sequence 13035, A
C 551	81	6.0	2517	4	US-09-758-282B-177	Sequence 177, App	C 624	81	6.0	3876	4	US-09-252-991A-2933	Sequence 2933, A
C 552	81	6.0	2517	4	US-09-758-282B-180	Sequence 180, App	C 625	81	6.0	4266	4	US-09-252-991A-1234	Sequence 1234, App
C 553	81	6.0	2517	4	US-09-758-282B-183	Sequence 183, App	C 626	81	6.0	5849	3	US-09-134-246-6	Sequence 6, Appli
C 554	81	6.0	2517	4	US-09-758-282B-186	Sequence 186, App	C 627	81	6.0	6714	1	US-08-021-623C-5	Sequence 5, Appli
C 555	81	6.0	2517	4	US-09-758-282B-189	Sequence 189, App	C 628	81	6.0	6732	4	US-09-976-594-99	Sequence 99, Appli
C 556	81	6.0	2517	4	US-09-758-282B-199	Sequence 199, App	C 629	81	6.0	7119	3	US-09-453-702B-111	Sequence 111, App
C 557	81	6.0	2517	4	US-09-758-282B-201	Sequence 201, App	C 630	81	6.0	38494	4	US-08-311-731A-24	Sequence 24, Appl
C 558	81	6.0	2517	4	US-09-758-282B-203	Sequence 203, App	C 631	81	6.0	38675	4	US-08-311-731A-135	Sequence 135, App
C 559	81	6.0	2517	4	US-09-758-282B-205	Sequence 205, App	C 632	81	6.0	50937	3	US-09-428-517-1	Sequence 1, Appli
C 560	81	6.0	2517	4	US-09-758-282B-217	Sequence 217, App	C 633	81	6.0	53500	4	US-09-266-965-76	Sequence 76, Appl
C 561	81	6.0	2517	4	US-09-758-282B-220	Sequence 220, App	C 634	80.5	6.0	672	4	US-09-252-991A-9638	Sequence 9638, App
C 562	81	6.0	2517	4	US-09-758-282B-225	Sequence 225, App	C 635	80.5	6.0	807	4	US-09-489-039A-139	Sequence 139, App
C 563	81	6.0	2517	4	US-09-758-282B-227	Sequence 227, App	C 636	80.5	6.0	936	4	US-09-489-039A-2270	Sequence 2270, App
C 564	81	6.0	2517	4	US-09-758-282B-229	Sequence 229, App	C 637	80.5	6.0	957	4	US-09-252-991A-3959	Sequence 3959, App
C 565	81	6.0	2517	4	US-09-758-282B-231	Sequence 231, App	C 638	80.5	6.0	1362	4	US-09-252-991A-3943	Sequence 3943, App
C 566	81	6.0	2517	4	US-09-758-282B-233	Sequence 233, App	C 639	80.5	6.0	1449	4	US-09-252-991A-1976	Sequence 1976, App
C 567	81	6.0	2517	4	US-09-577-304A-62	Sequence 62, Appl	C 640	80.5	6.0	1524	4	US-09-807-897-3	Sequence 3, Appli
C 568	81	6.0	2517	4	US-09-577-304A-71	Sequence 71, Appl	C 641	80.5	6.0	1596	4	US-09-252-991A-10119	Sequence 10119, A
C 569	81	6.0	2517	4	US-09-577-304A-82	Sequence 82, Appl	C 642	80.5	6.0	1605	4	US-09-252-991A-10729	Sequence 10729, A
C 570	81	6.0	2517	4	US-09-577-304A-88	Sequence 88, Appl	C 643	80.5	6.0	1686	2	US-08-648-657-14	Sequence 14, Appl
C 571	81	6.0	2517	4	US-09-577-304A-114	Sequence 114, App	C 644	80.5	6.0	2155	4	US-09-620-312D-65	Sequence 65, Appl
C 572	81	6.0	2517	4	US-09-577-304A-117	Sequence 117, App	C 645	80.5	6.0	2220	2	US-08-864-224-1	Sequence 1, Appli
C 573	81	6.0	2517	4	US-09-577-304A-120	Sequence 120, App	C 646	80.5	6.0	2325	4	US-09-252-991A-218	Sequence 218, App
C 574	81	6.0	2517	4	US-09-577-304A-123	Sequence 123, App	C 647	80.5	6.0	2493	4	US-09-252-991A-5433	Sequence 5433, App
C 575	81	6.0	2517	4	US-09-577-304A-126	Sequence 126, App	C 648	80.5	6.0	2505	4	US-09-334-818A-1	Sequence 1, Appli
C 576	81	6.0	2517	4	US-09-577-304A-129	Sequence 129, App	C 649	80.5	6.0	2538	4	US-09-252-991A-1285	Sequence 1285, App
C 577	81	6.0	2517	4	US-09-577-304A-132	Sequence 132, App	C 650	80.5	6.0	2571	4	US-09-252-991A-1279	Sequence 1279, App
C 578	81	6.0	2517	4	US-09-577-304A-141	Sequence 141, App	C 651	80.5	6.0	2610	4	US-09-252-991A-8489	Sequence 8489, App
C 579	81	6.0	2517	4	US-09-577-304A-147	Sequence 147, App	C 652	80.5	6.0	2794	4	US-09-252-991A-194	Sequence 194, App
C 580	81	6.0	2517	4	US-09-577-304A-149	Sequence 149, App	C 653	80.5	6.0	2946	4	US-09-252-991A-227	Sequence 227, App
C 581	81	6.0	2517	4	US-09-577-304A-152	Sequence 152, App	C 654	80.5	6.0	4283	4	US-09-252-991A-10434	Sequence 10434, A
C 582	81	6.0	2517	4	US-09-577-304A-168	Sequence 168, App	C 655	80.5	6.0	4564	4	US-09-252-991A-4765	Sequence 4765, App
C 583	81	6.0	2517	4	US-09-577-304A-177	Sequence 177, App	C 656	80.5	6.0	7266	3	US-08-713-118-1	Sequence 1, Appli
C 584	81	6.0	2517	4	US-09-577-304A-180	Sequence 180, App	C 657	80.5	6.0	7266	3	US-09-452-007-1	Sequence 1, Appli
C 585	81	6.0	2517	4	US-09-577-304A-183	Sequence 183, App	C 658	80.5	6.0	11613	1	US-08-484-044-10	Sequence 10, Appl
C 586	81	6.0	2517	4	US-09-577-304A-186	Sequence 186, App	C 659	80.5	6.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 587	81	6.0	2517	4	US-09-577-304A-189	Sequence 189, App	C 660	80.5	6.0	50341	1	US-08-247-901C-1	Sequence 1, Appli
C 588	81	6.0	2517	4	US-09-577-304A-199	Sequence 199, App	C 661	80.5	6.0	50341	2	US-09-075-904-1	Sequence 1, Appli
C 589	81	6.0	2517	4	US-09-577-304A-201	Sequence 201, App	C 662	80.5	6.0	52297	3	US-09-426-436-1	Sequence 1, Appli
C 590	81	6.0	2517	4	US-09-577-304A-203	Sequence 203, App	C 663	80.5	6.0	52297	3	US-08-705-557-1	Sequence 1, Appli
C 591	81	6.0	2517	4	US-09-577-304A-205	Sequence 205, App	C 664	80	6.0	618	4	US-09-489-039A-1035	Sequence 1035, App
C 592	81	6.0	2517	4	US-09-577-304A-217	Sequence 217, App	C 665	80	6.0	855	4	US-09-252-991A-9422	Sequence 9422, App
C 593	81	6.0	2517	4	US-09-577-304A-220	Sequence 220, App	C 666	80	6.0	1008	1	US-08-347-826A-3	Sequence 3, Appli
C 594	81	6.0	2517	4	US-09-577-304A-225	Sequence 225, App	C 667	80	6.0	1101	4	US-09-252-991A-9455	Sequence 9455, App
C 595	81	6.0	2517	4	US-09-577-304A-227	Sequence 227, App	C 668	80	6.0	1122	4	US-09-252-991A-8798	Sequence 8798, App
C 596	81	6.0	2517	4	US-09-577-304A-229	Sequence 229, App	C 669	80	6.0	1417	4	US-09-904-615-31	Sequence 31, Appl
C 597	81	6.0	2517	4	US-09-577-304A-231	Sequence 231, App	C 670	80	6.0	1524	4	US-09-489-039A-3444	Sequence 3444, App



671	80	1791	4	US-09-252-991A-9892	Sequence 9892, Ap	744	79	5.9	1650	4	US-09-344-510B-9	Sequence 9, Appli
672	80	2037	4	US-09-489-039A-4049	Sequence 4049, Ap	745	79	5.9	1692	4	US-09-252-991A-7872	Sequence 7872, Ap
673	80	2083	4	US-09-774-528-344	Sequence 344, App	746	79	5.9	1800	4	US-09-252-991A-679	Sequence 679, App
674	80	2379	4	US-09-252-991A-9252	Sequence 9252, Ap	747	79	5.9	1816	1	US-07-865-662F-5	Sequence 5, Appli
675	80	3033	4	US-09-724-797-81	Sequence 81, Appl	748	79	5.9	1816	3	US-08-374-219B-5	Sequence 5, Appli
676	80	6401	4	US-09-221-017B-804	Sequence 804, App	749	79	5.9	1822	3	US-07-865-662F-6	Sequence 6, Appli
677	79.5	828	4	US-09-252-991A-11099	Sequence 11099, A	750	79	5.9	1822	3	US-08-374-219B-6	Sequence 6, Appli
678	79.5	850	1	US-08-114-461-2	Sequence 2, Appli	751	79	5.9	1938	4	US-09-543-681A-3585	Sequence 3585, Ap
679	79.5	850	1	US-08-192-156-2	Sequence 2, Appli	752	79	5.9	2244	5	US-08-476-519-10	Sequence 10, Appl
680	79.5	850	1	US-08-370-789-2	Sequence 2, Appli	753	79	5.9	2244	5	PCT-US95-09323-10	Sequence 10, Appl
681	79.5	852	4	US-09-252-991A-10276	Sequence 10276, A	754	79	5.9	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
682	79.5	882	4	US-09-252-991A-16022	Sequence 16022, A	755	79	5.9	2334	1	US-08-476-519-1	Sequence 1, Appli
683	79.5	1065	4	US-09-270-767-12932	Sequence 12932, A	756	79	5.9	2334	5	PCT-US95-09323-1	Sequence 1, Appli
684	79.5	1317	4	US-09-270-767-12932	Sequence 12932, A	757	79	5.9	2418	4	US-09-252-991A-2294	Sequence 2294, Ap
685	79.5	1359	4	US-09-252-991A-10889	Sequence 10889, A	758	79	5.9	2610	4	US-09-252-991A-175	Sequence 175, App
686	79.5	1377	4	US-09-252-991A-2528	Sequence 2528, Ap	759	79	5.9	2610	4	US-09-252-991A-7311	Sequence 7311, Ap
687	79.5	1473	4	US-09-489-039A-6783	Sequence 6783, Ap	760	79	5.9	2817	4	US-09-252-991A-7187	Sequence 7187, Ap
688	79.5	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	761	79	5.9	2880	4	US-09-252-991A-7187	Sequence 3, Appli
689	79.5	1715	1	US-07-847-743B-24	Sequence 24, Appl	762	79	5.9	2943	4	US-09-379-530B-3	Sequence 7, Appli
690	79.5	1715	1	US-08-456-201-24	Sequence 24, Appl	763	79	5.9	3134	1	US-07-865-662F-7	Sequence 7, Appli
691	79.5	1715	2	US-08-456-241-24	Sequence 24, Appl	764	79	5.9	3134	3	US-08-374-219B-7	Sequence 2, Appli
692	79.5	1715	5	PCT-US92-04295A-24	Sequence 24, Appl	765	79	5.9	3373	1	US-08-273-411-2	Sequence 10, Appl
693	79.5	1731	4	US-09-252-991A-15928	Sequence 15928, A	766	79	5.9	3373	1	US-09-898-361-10	Sequence 5711, Ap
694	79.5	1872	4	US-09-252-991A-13815	Sequence 13815, A	767	79	5.9	4230	4	US-09-252-991A-5741	Sequence 5741, Ap
695	79.5	1964	4	US-09-774-528-308	Sequence 308, App	768	79	5.9	4941	4	US-09-344-510B-8	Sequence 8, Appli
696	79.5	2077	4	US-09-921-039A-16	Sequence 16, Appl	769	79	5.9	5032	4	US-09-230-652-1	Sequence 5, Appli
697	79.5	2232	4	US-09-489-039A-3902	Sequence 3902, Ap	770	79	5.9	8091	4	US-07-914-281-5	Sequence 5, Appli
698	79.5	2431	1	US-07-847-743B-25	Sequence 25, Appl	771	79	5.9	8174	1	US-08-393-246-5	Sequence 5, Appli
699	79.5	2431	1	US-08-456-201-25	Sequence 25, Appl	772	79	5.9	8174	1	US-08-525-058A-5	Sequence 5, Appli
700	79.5	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	773	79	5.9	8174	2	US-08-696-731-5	Sequence 5, Appli
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702	79.5	2469	4	US-10-274-878-1	Sequence 1, Appli	775	79	5.9	8257	4	PCT-US91-00899-3	Sequence 3, Appli
703	79.5	2472	3	US-08-743-168B-35	Sequence 35, Appl	776	79	5.9	16080	4	US-09-484-970B-65	Sequence 65, Appl
704	79.5	2472	3	US-08-743-168B-37	Sequence 37, Appl	777	79	5.9	34446	4	US-09-724-566A-48	Sequence 48, Appl
705	79.5	2478	4	US-09-252-991A-592	Sequence 592, App	778	79	5.9	137000	4	US-09-103-330-35	Sequence 35, Appl
706	79.5	2490	1	US-07-847-743B-23	Sequence 23, Appl	779	79	5.9	137000	4	US-10-172-911-11	Sequence 11, Appl
707	79.5	2490	1	US-08-456-201-23	Sequence 23, Appl	780	79	5.9	137000	4	US-09-557-88A-1	Sequence 1, Appli
708	79.5	2490	2	US-08-456-241-23	Sequence 23, Appl	781	79	5.9	137000	4	US-09-557-88A-1	Sequence 1, Appli
709	79.5	2490	5	PCT-US92-04295A-23	Sequence 23, Appl	782	79	5.9	137000	4	US-09-557-88A-1	Sequence 1, Appli
710	79.5	2502	4	US-09-252-991A-15767	Sequence 15767, A	783	78.5	5.8	681	4	US-10-329-960-1	Sequence 1, Appli
711	79.5	2517	4	US-09-758-282B-144	Sequence 144, App	784	78.5	5.8	681	4	US-09-252-991A-3852	Sequence 3852, Ap
712	79.5	2517	4	US-09-577-304A-144	Sequence 144, App	785	78.5	5.8	791	3	US-08-858-207A-219	Sequence 219, App
713	79.5	2742	4	US-09-252-991A-5556	Sequence 5556, Ap	786	78.5	5.8	801	4	US-09-489-039A-5911	Sequence 5911, Ap
714	79.5	2742	4	US-09-252-991A-10486	Sequence 10486, A	787	78.5	5.8	831	4	US-09-252-991A-5052	Sequence 5052, Ap
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716	79.5	3231	4	US-09-252-991A-5668	Sequence 5668, Ap	789	78.5	5.8	1014	4	US-09-252-991A-195	Sequence 195, App
717	79.5	3339	4	US-09-252-991A-10685	Sequence 10685, A	790	78.5	5.8	1245	4	US-09-252-991A-5535	Sequence 5535, Ap
718	79.5	6575	3	US-08-949-386-3	Sequence 3, Appli	791	78.5	5.8	1488	4	US-09-023-655-880	Sequence 880, App
719	79.5	6575	3	US-08-450-562-3	Sequence 3, Appli	792	78.5	5.8	1527	4	US-09-244-111-7	Sequence 7, Appli
720	79.5	6575	3	US-08-984-709A-3	Sequence 3, Appli	793	78.5	5.8	1546	3	US-09-383-318A-1	Sequence 1, Appli
721	79.5	6575	3	US-08-450-272-3	Sequence 3, Appli	794	78.5	5.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap
722	79.5	6575	4	US-08-450-273-3	Sequence 36, Appl	795	78.5	5.8	1695	4	US-09-252-991A-1686	Sequence 1686, Ap
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724	79.5	6725	3	US-08-450-562-36	Sequence 36, Appl	797	78.5	5.8	1831	4	US-09-799-451-646	Sequence 646, App
725	79.5	6725	3	US-08-984-709A-36	Sequence 36, Appl	798	78.5	5.8	1869	4	US-09-451-646	Sequence 3231, Ap
726	79.5	6725	3	US-08-450-272-36	Sequence 36, Appl	799	78.5	5.8	2166	2	US-09-252-991A-1654	Sequence 1654, Ap
727	79.5	6725	3	US-08-450-273-36	Sequence 36, Appl	800	78.5	5.8	2283	4	US-09-252-991A-3231	Sequence 30, Appl
728	79.5	15872	3	US-09-105-537-1	Sequence 1, Appli	801	78.5	5.8	2499	4	US-08-408-095-30	Sequence 3298, Ap
729	79.5	15872	4	US-09-091-609-1	Sequence 1, Appli	802	78.5	5.8	2499	4	US-09-252-991A-3298	Sequence 51, Appl
730	79.5	15872	4	US-09-091-609-3	Sequence 3, Appli	803	78.5	5.8	2499	4	US-09-758-282B-250	Sequence 250, App
731	79.5	193303	4	US-09-497-855A-37	Sequence 37, Appli	804	78.5	5.8	2499	4	US-09-577-304A-51	Sequence 51, Appl
732	79.5	193303	4	US-09-497-855A-44	Sequence 44, Appl	805	78.5	5.8	2514	4	US-09-577-304A-250	Sequence 9494, Ap
733	79	939	4	US-09-252-991A-1305	Sequence 1305, Ap	806	78.5	5.8	2514	4	US-09-252-991A-9494	Sequence 260, App
734	79	1122	4	US-09-252-991A-11607	Sequence 11607, A	807	78.5	5.8	2514	4	US-09-758-282B-260	Sequence 264, App
735	79	1161	4	PCT-US95-07554-3	Sequence 3, Appli	808	78.5	5.8	2514	4	US-09-577-304A-264	Sequence 264, App
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737	79	1194	4	US-09-252-991A-7020	Sequence 7020, Ap	810	78.5	5.8	2583	3	US-09-171-710-1	Sequence 7, Appli
738	79	1221	4	US-09-252-991A-7692	Sequence 7692, Ap	811	78.5	5.8	3024	1	US-07-923-976-7	Sequence 1, Appli
739	79	1263	4	US-09-252-991A-11762	Sequence 11762, A	812	78.5	5.8	3024	1	US-09-252-991A-12013	Sequence 12013, A
740	79	1305	4	US-09-252-991A-11762	Sequence 11762, A	813	78.5	5.8	3264	4	US-09-252-991A-11905	Sequence 11905, A
741	79	1350	4	US-09-252-991A-1330	Sequence 1330, Ap	814	78.5	5.8	3279	4	US-09-023-655-1180	Sequence 1180, Ap
742	79	1488	4	US-09-252-991A-197	Sequence 197, App	815	78.5	5.8	3625	4	US-09-023-655-1180	Sequence 6666, Ap
743	79	1560	4	US-09-252-991A-166	Sequence 166, App	816	78.5	5.8	3702	4	US-09-252-991A-6666	Sequence 6666, Ap







968	76.5	5.7	1215	4	US-09-252-991A-2595	Sequence 2595, Ap	1046	76.5	5.7	22108	3	US-09-085-761A-3	Sequence 3, Appli
969	76.5	5.7	1227	4	US-09-252-991A-9232	Sequence 9232, Ap	c1047	76.5	5.7	44453	3	US-09-146-053-5	Sequence 5, Appli
c 970	76.5	5.7	1239	4	US-09-252-991A-13781	Sequence 13781, A	1048	76	5.7	398	4	US-09-513-9990-2203	Sequence 2203, Ap
971	76.5	5.7	1245	4	US-09-252-991A-4611	Sequence 4611, Ap	c1049	76	5.7	720	4	US-09-252-991A-12414	Sequence 12414, A
972	76.5	5.7	1251	4	US-09-252-991A-16089	Sequence 16089, A	c1050	76	5.7	990	4	US-09-252-991A-1849	Sequence 1849, Ap
973	76.5	5.7	1443	4	US-09-252-991A-10295	Sequence 10295, A	1051	76	5.7	1002	4	US-09-252-991A-58	Sequence 58, Appl
974	76.5	5.7	1503	3	US-09-463-702A-33	Sequence 33, Appl	1052	76	5.7	1011	4	US-09-252-991A-12242	Sequence 12242, A
975	76.5	5.7	1503	4	US-09-699-135-33	Sequence 33, Appl	1053	76	5.7	1101	3	US-08-987-904A-1	Sequence 1, Appli
976	76.5	5.7	1527	4	US-09-252-991A-16194	Sequence 16194, A	1054	76	5.7	1101	4	US-09-438-623A-1	Sequence 1, Appli
977	76.5	5.7	1557	1	US-08-481-130-26	Sequence 26, Appl	1055	76	5.7	1128	4	US-09-489-039A-2636	Sequence 56, Appl
978	76.5	5.7	1557	1	US-08-656-984A-26	Sequence 26, Appl	c1056	76	5.7	1146	4	US-09-252-991A-56	Sequence 1940, Ap
979	76.5	5.7	1557	1	US-08-485-604-26	Sequence 26, Appl	1057	76	5.7	1188	4	US-09-252-991A-1340	Sequence 3685, Ap
980	76.5	5.7	1557	2	US-08-487-595-26	Sequence 26, Appl	c1058	76	5.7	1311	4	US-09-252-991A-3685	Sequence 12317, A
981	76.5	5.7	1566	4	US-09-252-991A-14361	Sequence 14361, A	c1059	76	5.7	1311	4	US-09-489-039A-3192	Sequence 3192, Ap
982	76.5	5.7	1569	4	US-09-252-991A-15857	Sequence 15857, A	1060	76	5.7	1371	4	US-09-489-039A-3192	Patent No. 5270178
c 983	76.5	5.7	1662	4	US-09-252-991A-16399	Sequence 16399, A	1061	76	5.7	1387	6	5270178-1	Sequence 84, Appl
984	76.5	5.7	1686	4	US-09-252-991A-10406	Sequence 10406, A	c1062	76	5.7	1461	4	US-09-252-991A-1413	Sequence 1413, Ap
985	76.5	5.7	1824	4	US-09-252-991A-4025	Sequence 4025, Ap	c1068	76	5.7	1662	4	US-08-910-856-1	Sequence 1, Appli
986	76.5	5.7	1854	4	US-09-252-991A-4542	Sequence 4542, Ap	c1069	76	5.7	1785	2	US-09-252-991A-3694	Sequence 3694, Ap
c 992	76.5	5.7	1875	4	US-09-252-991A-3919	Sequence 3919, Ap	c1070	76	5.7	1869	4	US-09-252-991A-3492	Sequence 3492, Ap
c 993	76.5	5.7	1875	4	US-09-252-991A-8812	Sequence 8812, Ap	c1071	76	5.7	1896	4	US-09-252-991A-2359	Sequence 2359, Ap
994	76.5	5.7	1928	3	US-09-352-159-43	Sequence 43, Appl	1072	76	5.7	2019	4	US-09-252-991A-12103	Sequence 12103, A
995	76.5	5.7	1928	4	US-09-771-045B-43	Sequence 43, Appl	1073	76	5.7	2052	4	US-09-252-991A-3938	Sequence 3938, Ap
996	76.5	5.7	2028	4	US-09-252-991A-12590	Sequence 12590, A	1074	76	5.7	2061	4	US-09-252-991A-3938	Sequence 821, App
c 997	76.5	5.7	2040	4	US-09-252-991A-10540	Sequence 10540, A	1075	76	5.7	2077	4	US-09-221-017B-821	Sequence 373, Appl
c 998	76.5	5.7	2046	4	US-09-490-291-3	Sequence 3, Appli	c1076	76	5.7	2141	4	US-09-774-528-373	Sequence 1, Appli
c 999	76.5	5.7	2076	4	US-09-490-291-5	Sequence 5, Appli	1077	76	5.7	2163	1	US-07-731-157A-1	Sequence 1, Appli
1000	76.5	5.7	2116	4	US-09-023-655-1256	Sequence 1256, Ap	1078	76	5.7	2163	2	US-08-541-780-1	Sequence 2198, Ap
1001	76.5	5.7	2176	6	5320958-1	Patent No. 5320958	1079	76	5.7	2196	4	US-09-252-991A-2198	Sequence 3884, Ap
1002	76.5	5.7	2196	4	US-09-252-991A-9319	Sequence 9319, Ap	1080	76	5.7	2316	4	US-09-252-991A-3884	Sequence 3965, Ap
1003	76.5	5.7	2517	4	US-09-252-991A-9238	Sequence 9238, Ap	c1081	76	5.7	2328	4	US-09-252-991A-3965	Sequence 3, Appli
c1004	76.5	5.7	2541	4	US-09-252-991A-7209	Sequence 7209, Ap	1082	76	5.7	2406	4	US-09-816-760-3	Sequence 3, Appli
1005	76.5	5.7	2826	1	US-08-156-020-9	Sequence 9, Appli	1083	76	5.7	2406	4	US-09-838-561-3	Sequence 5, Appli
c1006	76.5	5.7	2715	4	US-09-252-991A-8715	Sequence 8715, Ap	1084	76	5.7	2406	4	US-07-977-434-5	Sequence 5, Appli
c1007	76.5	5.7	2775	1	US-08-481-130-25	Sequence 25, Appl	c1085	76	5.7	2493	1	US-08-458-819-5	Sequence 5, Appli
1008	76.5	5.7	2775	1	US-08-656-984A-25	Sequence 25, Appl	c1086	76	5.7	2493	5	PCT-US91-07035-5	Sequence 1, Appli
1009	76.5	5.7	2775	1	US-08-485-604-25	Sequence 25, Appl	c1087	76	5.7	2660	4	US-09-634-955B-1	Sequence 1, Appli
1010	76.5	5.7	2775	2	US-08-487-595-25	Sequence 25, Appl	1088	76	5.7	2660	4	US-09-816-760-1	Sequence 1, Appli
c1011	76.5	5.7	2850	2	US-08-224-482-7	Sequence 7, Appli	1089	76	5.7	2660	4	US-09-838-561-1	Sequence 1, Appli
c1012	76.5	5.7	2896	4	US-09-266-228D-9	Sequence 9, Appli	1090	76	5.7	2754	4	US-09-252-991A-1147	Sequence 1, Appli
1013	76.5	5.7	2927	1	US-08-481-130-27	Sequence 27, Appl	1091	76	5.7	2754	4	US-07-928-464-1	Sequence 1, Appli
1014	76.5	5.7	2927	1	US-08-656-984A-27	Sequence 27, Appl	1092	76	5.7	2890	5	PCT-US93-07347-1	Sequence 1, Appli
1015	76.5	5.7	2927	1	US-08-485-604-27	Sequence 27, Appl	1093	76	5.7	2890	5	US-08-003-311B-1	Sequence 1, Appli
1016	76.5	5.7	2927	2	US-08-487-595-27	Sequence 27, Appl	1094	76	5.7	3033	1	US-08-261-432-1	Sequence 1, Appli
c1017	76.5	5.7	3000	3	US-08-460-269C-5	Sequence 5, Appli	1095	76	5.7	3033	2	US-08-813-940-3	Sequence 3, Appli
1018	76.5	5.7	3059	4	US-09-620-312D-213	Sequence 213, App	c1096	76	5.7	3107	2	US-08-910-856-9	Sequence 9, Appli
1019	76.5	5.7	3059	4	US-09-620-312D-214	Sequence 214, App	c1097	76	5.7	3187	2	US-08-910-856-10	Sequence 10, Appl
1020	76.5	5.7	3134	4	US-09-252-991A-7487	Sequence 7487, Ap	c1098	76	5.7	3187	4	US-09-672-749-16	Sequence 16, Appl
1021	76.5	5.7	3134	4	US-09-620-312D-212	Sequence 212, App	c1099	76	5.7	3187	4	US-10-014-882-3	Sequence 3, Appli
1022	76.5	5.7	3175	4	US-09-799-451-793	Sequence 4, Appli	1100	76	5.7	3518	4	US-09-252-991A-12708	Sequence 12708, A
c1023	76.5	5.7	3196	2	US-09-096-982-4	Sequence 4, Appli	1101	76	5.7	3525	4	US-09-252-991A-1324	Sequence 1324, Ap
c1024	76.5	5.7	3196	2	US-08-653-650A-4	Sequence 4, Appli	c1102	76	5.7	3525	4	US-09-252-991A-1324	Sequence 1, Appli
1025	76.5	5.7	3199	4	US-09-023-655-947	Sequence 947, App	1103	76	5.7	3651	2	US-08-790-374-1	Sequence 13251, A
1026	76.5	5.7	3223	2	US-08-620-694A-9	Sequence 9, Appli	c1104	76	5.7	3906	4	US-09-252-991A-13251	Sequence 1, Appli
1027	76.5	5.7	3223	2	US-09-022-255-9	Sequence 9, Appli	1105	76	5.7	3906	4	US-09-252-991A-14037	Sequence 14037, Ap
1028	76.5	5.7	3223	3	US-09-022-696-9	Sequence 9, Appli	1106	76	5.7	3906	4	US-09-252-991A-14310	Sequence 14310, A
1029	76.5	5.7	3223	3	US-08-978-773-3	Sequence 3, Appli	c1107	76	5.7	34094	4	US-09-252-991A-14547	Sequence 14547, A
1030	76.5	5.7	3223	3	US-09-022-253-9	Sequence 9, Appli	1108	76	5.7	41684	4	US-09-252-991A-15677	Sequence 15677, A
1031	76.5	5.7	3223	3	US-09-022-260-9	Sequence 9, Appli	c1109	76	5.7	70559	4	US-09-409-800B-1	Sequence 8, Appli
1032	76.5	5.7	3223	3	US-09-022-259-9	Sequence 9, Appli	1110	75.5	5.6	699	4	US-09-252-991A-7077	Sequence 7077, Ap
1033	76.5	5.7	3223	3	US-09-022-257-9	Sequence 9, Appli	1111	75.5	5.6	858	4	US-09-252-991A-10979	Sequence 10979, A
1034	76.5	5.7	3223	4	US-09-549-679-9	Sequence 9, Appli	1112	75.5	5.6	867	4	US-09-252-991A-14037	Sequence 14037, Ap
1035	76.5	5.7	3540	4	US-09-252-991A-1324	Sequence 1324, Ap	1113	75.5	5.6	951	4	US-09-252-991A-14310	Sequence 14310, A
1036	76.5	5.7	3627	4	US-09-792-594-3	Sequence 3, Appli	1114	75.5	5.6	1035	4	US-09-252-991A-14547	Sequence 14547, A
1037	76.5	5.7	3850	3	US-09-463-702A-1	Sequence 1, Appli	1115	75.5	5.6	1116	3	US-09-252-991A-15677	Sequence 15677, A
1038	76.5	5.7	3850	3	US-09-699-135-1	Sequence 1, Appli	1116	75.5	5.6	1149	3	US-08-660-645A-8	Sequence 8, Appli
1039	76.5	5.7	3981	4	US-09-252-991A-1361	Sequence 1361, Ap	1117	75.5	5.6	1149	3	US-09-298-718-8	Sequence 8, Appli
c1040	76.5	5.7	4179	4	US-09-252-991A-1244	Sequence 1244, Ap	1118	75.5	5.6	1149	3	US-09-548-969-8	Sequence 8, Appli
c1041	76.5	5.7	4408	4	US-09-321-017B-830	Sequence 830, App	c1119	75.5	5.6	1149	4	US-09-547-927-8	Sequence 8, Appli
c1042	76.5	5.7	5215	4	US-09-231-899-71	Sequence 71, Appl	1120	75.5	5.6	1179	4	US-09-252-991A-9487	Sequence 9487, Ap
1043	76.5	5.7	5581	4	US-09-023-655-966	Sequence 966, App	c1121	75.5	5.6	1179	4	US-09-252-991A-14720	Sequence 14720, A
1044	76.5	5.7	6200	4	US-09-795-061-3	Sequence 3, Appli	1122	75.5	5.6	1197	4	US-09-252-991A-14720	Sequence 421, App
1045	76.5	5.7	22108	3	US-09-053-197A-3	Sequence 3, Appli	1123	75.5	5.6	1197	4	US-09-774-528-421	Sequence 421, App



c1124	75.5	5.6	1209	4	US-09-252-991A-9346	Sequence 9346, Ap	c1197	75.5	5.6	3425	4	US-09-800-971-1	Sequence 1, Appli
c1125	75.5	5.6	1212	4	US-09-252-991A-807	Sequence 807, App	c1198	75.5	5.6	3456	4	US-09-854-845-9	Sequence 9, Appli
c1126	75.5	5.6	1215	4	US-09-252-991A-847	Sequence 847, App	c1199	75.5	5.6	3685	4	US-09-919-039-239	Sequence 239, App
c1127	75.5	5.6	1236	4	US-09-252-991A-3079	Sequence 3079, Ap	1200	75.5	5.6	3801	4	US-09-252-991A-14280	Sequence 14280, A
c1128	75.5	5.6	1234	4	US-09-252-991A-415	Sequence 415, App	c1201	75.5	5.6	3883	4	US-09-620-312D-780	Sequence 780, App
c1129	75.5	5.6	1293	4	US-09-252-991A-14817	Sequence 14817, A	c1202	75.5	5.6	4074	4	US-09-854-845-17	Sequence 17, Appl
c1130	75.5	5.6	1309	4	US-09-544-618-5	Sequence 5, Appli	c1203	75.5	5.6	4389	4	US-09-023-655-991	Sequence 991, App
c1131	75.5	5.6	1344	4	US-09-252-991A-6450	Sequence 6450, Ap	1204	75.5	5.6	6039	1	US-08-324-977-11	Sequence 11, Appl
c1132	75.5	5.6	1401	2	US-08-812-412-1	Sequence 4, Appli	1205	75.5	5.6	6039	2	US-08-384-616-11	Sequence 11, Appl
c1133	75.5	5.6	1401	3	US-09-180-271-4	Sequence 1, Appli	1206	75.5	5.6	6039	2	US-08-904-686A-11	Sequence 11, Appl
c1134	75.5	5.6	1446	4	US-09-252-991A-6746	Sequence 6746, Ap	1207	75.5	5.6	6039	3	US-09-315-850-11	Sequence 11, Appl
c1135	75.5	5.6	1500	4	US-09-489-039A-2856	Sequence 2856, Ap	1208	75.5	5.6	7863	1	US-08-324-977-35	Sequence 35, Appl
c1136	75.5	5.6	1506	4	US-09-252-991A-6098	Sequence 6098, Ap	1209	75.5	5.6	7863	2	US-08-384-616-35	Sequence 35, Appl
c1137	75.5	5.6	1506	4	US-09-252-991A-10637	Sequence 10637, A	1210	75.5	5.6	7863	2	US-08-904-686A-35	Sequence 35, Appl
c1138	75.5	5.6	1521	4	US-09-252-991A-6686	Sequence 6686, Ap	1211	75.5	5.6	7863	3	US-09-315-850-35	Sequence 35, Appl
c1139	75.5	5.6	1569	4	US-09-252-991A-423	Sequence 423, App	1212	75.5	5.6	7917	1	US-08-324-977-31	Sequence 31, Appl
c1140	75.5	5.6	1590	4	US-09-252-991A-14397	Sequence 14397, A	1213	75.5	5.6	7917	2	US-08-384-616-31	Sequence 31, Appl
c1141	75.5	5.6	1617	4	US-09-252-991A-381	Sequence 381, App	1214	75.5	5.6	7917	2	US-08-904-686A-31	Sequence 31, Appl
c1142	75.5	5.6	1629	4	US-09-252-991A-2042	Sequence 2042, Ap	1215	75.5	5.6	7917	3	US-09-315-850-31	Sequence 31, Appl
c1143	75.5	5.6	1818	4	US-09-252-991A-2891	Sequence 2891, Ap	1216	75.5	5.6	8625	3	US-08-980-832-1	Sequence 1, Appli
c1144	75.5	5.6	1827	4	US-09-252-991A-1375	Sequence 1375, Ap	c1217	75.5	5.6	8625	4	US-09-920-923B-1	Sequence 1, Appli
c1145	75.5	5.6	1839	4	US-09-489-039A-2969	Sequence 2969, Ap	1218	75.5	5.6	9030	1	US-08-324-977-13	Sequence 13, Appl
c1146	75.5	5.6	1866	4	US-09-252-991A-11804	Sequence 11804, A	1219	75.5	5.6	9030	2	US-08-384-616-13	Sequence 13, Appl
c1147	75.5	5.6	1908	4	US-09-252-991A-1914	Sequence 1914, Ap	1220	75.5	5.6	9030	2	US-08-904-686A-13	Sequence 13, Appl
c1148	75.5	5.6	1908	4	US-09-252-991A-15513	Sequence 15513, A	1221	75.5	5.6	9030	3	US-09-315-850-13	Sequence 13, Appl
c1149	75.5	5.6	1941	4	US-09-252-991A-11635	Sequence 11635, A	1222	75.5	5.6	9416	1	US-08-324-977-1	Sequence 1, Appli
c1150	75.5	5.6	1986	4	US-09-107-532A-23	Sequence 23, Appl	1223	75.5	5.6	9416	2	US-08-384-616-1	Sequence 1, Appli
c1151	75.5	5.6	2103	4	US-09-252-991A-2813	Sequence 2813, Ap	1224	75.5	5.6	9416	3	US-08-904-686A-1	Sequence 1, Appli
c1152	75.5	5.6	2169	4	US-09-252-991A-10268	Sequence 10268, A	1225	75.5	5.6	9416	3	US-09-315-850-1	Sequence 1, Appli
c1153	75.5	5.6	2181	4	US-09-252-991A-14909	Sequence 14909, A	1226	75.5	5.6	9416	4	US-08-823-895A-27	Sequence 27, Appl
c1154	75.5	5.6	2211	4	US-09-800-971-3	Sequence 3, Appli	1227	75.5	5.6	11220	3	US-09-105-537-2	Sequence 27, Appl
c1155	75.5	5.6	2262	4	US-09-252-991A-1416	Sequence 1416, Ap	c1228	75.5	5.6	11233	3	US-08-980-832-27	Sequence 27, Appl
c1156	75.5	5.6	2316	4	US-09-252-991A-13835	Sequence 13835, A	c1229	75.5	5.6	11233	4	US-09-920-923B-27	Sequence 27, Appl
c1157	75.5	5.6	2363	3	US-09-721-383-1	Sequence 1, Appli	c1230	75.5	5.6	11558	5	PCT-US93-06251-23	Sequence 23, Appl
c1158	75.5	5.6	2363	3	US-09-721-137-1	Sequence 1, Appli	1231	75.5	5.6	33529	3	US-09-144-085-3	Sequence 3, Appli
c1159	75.5	5.6	2363	4	US-09-721-251-1	Sequence 1, Appli	c1232	75.5	5.6	35524	3	US-08-923-137-1	Sequence 1, Appli
c1160	75.5	5.6	2363	4	US-10-114-764-1	Sequence 1, Appli	1233	75.5	5.6	36778	3	US-09-105-537-5	Sequence 5, Appli
c1161	75.5	5.6	2391	4	US-09-252-991A-1192	Sequence 1192, Ap	1234	75.5	5.6	38506	3	US-09-320-878-19	Sequence 19, Appl
c1162	75.5	5.6	2433	4	US-09-489-039A-2577	Sequence 2577, Ap	1235	75.5	5.6	38506	4	US-09-141-908-1	Sequence 1, Appli
c1163	75.5	5.6	2504	1	US-08-073-384C-3	Sequence 3, Appli	1236	75.5	5.6	38506	4	US-09-657-440-19	Sequence 19, Appl
c1164	75.5	5.6	2504	1	US-08-254-359A-3	Sequence 3, Appli	1237	75.5	5.6	70000	4	US-09-851-896-3	Sequence 3, Appli
c1165	75.5	5.6	2504	1	US-08-483-043-3	Sequence 3, Appli	1238	75.5	5.6	536165	4	US-09-214-808-1	Sequence 1, Appli
c1166	75.5	5.6	2504	1	US-08-481-238-3	Sequence 3, Appli	c1239	75.5	5.6	344	4	US-09-621-976-638	Sequence 638, App
c1167	75.5	5.6	2504	2	US-08-471-066B-3	Sequence 3, Appli	1240	75.5	5.6	591	4	US-09-583-110-31	Sequence 31, Appl
c1168	75.5	5.6	2504	2	US-08-484-956-3	Sequence 3, Appli	1241	75.5	5.6	603	4	US-09-252-991A-3222	Sequence 3222, Ap
c1169	75.5	5.6	2504	2	US-08-757-653-3	Sequence 3, Appli	c1242	75.5	5.6	603	4	US-09-252-991A-7177	Sequence 7177, Ap
c1170	75.5	5.6	2504	2	US-08-599-491-3	Sequence 3, Appli	1243	75.5	5.6	828	4	US-09-266-965-35	Sequence 35, Appl
c1171	75.5	5.6	2504	2	US-08-756-386-3	Sequence 3, Appli	1244	75.5	5.6	846	4	US-08-252-991A-3287	Sequence 3287, Ap
c1172	75.5	5.6	2504	2	US-08-823-156-3	Sequence 3, Appli	c1245	75.5	5.6	879	4	US-09-252-991A-12575	Sequence 12575, A
c1173	75.5	5.6	2504	3	US-08-682-853A-3	Sequence 3, Appli	c1246	75.5	5.6	885	4	US-09-252-991A-12721	Sequence 12721, A
c1174	75.5	5.6	2504	3	US-08-759-038-3	Sequence 3, Appli	c1247	75.5	5.6	897	4	US-09-252-991A-14531	Sequence 14531, A
c1175	75.5	5.6	2504	3	US-08-758-314-3	Sequence 3, Appli	c1248	75.5	5.6	915	4	US-09-252-991A-7455	Sequence 7455, Ap
c1176	75.5	5.6	2504	3	US-09-350-309-3	Sequence 3, Appli	c1249	75.5	5.6	954	4	US-09-252-991A-15575	Sequence 15575, A
c1177	75.5	5.6	2504	3	US-08-520-946-3	Sequence 3, Appli	1250	75.5	5.6	1014	4	US-08-252-991A-13690	Sequence 13690, A
c1178	75.5	5.6	2504	4	US-09-684-938-3	Sequence 3, Appli	1251	75.5	5.6	1230	4	US-09-489-039A-5088	Sequence 5088, Ap
c1179	75.5	5.6	2504	4	US-09-308-825A-3	Sequence 3, Appli	1252	75.5	5.6	1395	4	US-09-252-991A-3925	Sequence 3925, Ap
c1180	75.5	5.6	2504	4	US-09-655-378A-3	Sequence 3, Appli	c1253	75.5	5.6	1341	4	US-09-252-991A-8747	Sequence 8747, Ap
c1181	75.5	5.6	2504	4	US-09-940-244-3	Sequence 3, Appli	1254	75.5	5.6	1344	4	US-09-252-991A-11184	Sequence 11184, A
c1182	75.5	5.6	2504	4	US-09-333-145-3	Sequence 3, Appli	1255	75.5	5.6	1352	1	US-08-552-142A-10	Sequence 10, Appl
c1183	75.5	5.6	2811	4	US-09-252-991A-13619	Sequence 13619, A	c1256	75.5	5.6	1377	4	US-09-252-991A-11074	Sequence 11074, A
c1184	75.5	5.6	3150	4	US-09-854-845-5	Sequence 5, Appli	1257	75.5	5.6	1386	4	US-10-182-263-8	Sequence 8, Appli
c1185	75.5	5.6	3150	4	US-09-252-991A-11487	Sequence 11487, A	c1258	75.5	5.6	1404	4	US-09-252-991A-12291	Sequence 12291, A
c1186	75.5	5.6	3150	4	US-09-854-845-1	Sequence 1, Appli	c1259	75.5	5.6	1407	3	US-09-193-377B-2	Sequence 2, Appli
c1187	75.5	5.6	3153	4	US-09-922-501-13	Sequence 13, Appl	c1260	75.5	5.6	1407	4	US-09-252-991A-11004	Sequence 11004, A
c1188	75.5	5.6	3237	4	US-09-854-845-7	Sequence 7, Appli	c1261	75.5	5.6	1428	3	US-09-193-377B-1	Sequence 1, Appli
c1189	75.5	5.6	3264	2	US-08-708-541A-31	Sequence 31, Appl	c1262	75.5	5.6	1446	4	US-09-252-991A-7984	Sequence 7984, Ap
c1190	75.5	5.6	3264	2	US-08-708-541A-33	Sequence 33, Appl	1263	75.5	5.6	1475	4	US-09-252-991A-7653	Sequence 7653, Ap
c1191	75.5	5.6	3264	4	US-09-147-771-31	Sequence 31, Appl	1264	75.5	5.6	1485	4	US-09-252-991A-7738	Sequence 7738, Ap
c1192	75.5	5.6	3264	4	US-09-147-771-33	Sequence 33, Appl	c1265	75.5	5.6	1500	3	US-09-193-377B-3	Sequence 3, Appli
c1193	75.5	5.6	3282	4	US-09-854-845-3	Sequence 3, Appli	c1266	75.5	5.6	1536	4	US-09-252-991A-12037	Sequence 12037, A
c1194	75.5	5.6	3372	4	US-09-252-991A-11405	Sequence 11405, A	1267	75.5	5.6	1584	4	US-09-252-991A-5109	Sequence 5109, Ap
c1195	75.5	5.6	3481	4	US-09-252-991A-14461	Sequence 14461, A	1268	75.5	5.6	1605	4	US-09-252-991A-3897	Sequence 3897, Ap
c1196	75.5	5.6	3411	4	US-09-854-845-11	Sequence 11, Appl	c1269	75.5	5.6	1680	3	US-09-603-185-1	Sequence 1, Appli



1270	75	5.6	1686	4	US-09-252-991A-5746	Sequence 5746, Ap	1343	74.5	5.5	1602	4	US-09-252-991A-6382	Sequence 6382, Ap
1271	75	5.6	1716	4	US-09-252-991A-11978	Sequence 11978, A	1344	74.5	5.5	1638	4	US-09-252-991A-14339	Sequence 14339, A
c1272	75	5.6	1728	4	US-09-252-991A-13641	Sequence 13641, A	1345	74.5	5.5	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
1273	75	5.6	1755	6	5225537-1	Patent No. 5225537	1346	74.5	5.5	1680	4	US-09-252-991A-9536	Sequence 9536, Ap
1274	75	5.6	1761	4	US-09-252-991A-5762	Sequence 5762, Ap	c1347	74.5	5.5	1728	4	US-09-252-991A-12870	Sequence 12870, A
1275	75	5.6	1812	4	US-09-252-991A-8467	Sequence 8467, Ap	c1348	74.5	5.5	1734	4	US-09-489-039A-4357	Sequence 4357, Ap
1276	75	5.6	1843	4	US-09-328-925-49	Sequence 49, Appl	c1349	74.5	5.5	1738	4	US-09-252-991A-1949	Sequence 1949, Ap
c1277	75	5.6	1857	4	US-09-252-991A-3688	Sequence 3688, Ap	c1350	74.5	5.5	1791	4	US-09-252-991A-4684	Sequence 4684, Ap
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c1286	75	5.6	2754	4	US-09-252-991A-1147	Sequence 1147, Ap	1359	74.5	5.5	2090	3	US-08-451-9468-7	Sequence 7, Appl
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1290	75	5.6	4539	4	US-09-704-725-1	Sequence 1, Appl	1363	74.5	5.5	2090	3	US-09-183-543-7	Sequence 7, Appl
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1304	74.5	5.5	765	4	US-09-252-991A-3699	Sequence 3699, Ap	c1377	74.5	5.5	2343	4	US-09-252-991A-2549	Sequence 2549, Ap
1305	74.5	5.5	768	4	US-09-543-681A-3544	Sequence 3544, Ap	1378	74.5	5.5	2514	4	US-09-489-039A-5475	Sequence 5475, Ap
1306	74.5	5.5	855	4	US-09-252-991A-14464	Sequence 14464, A	1379	74.5	5.5	2517	4	US-09-758-282B-183	Sequence 183, App
c1307	74.5	5.5	861	4	US-09-252-991A-4760	Sequence 4760, Ap	1380	74.5	5.5	2517	4	US-09-758-282B-220	Sequence 220, App
c1308	74.5	5.5	885	4	US-09-252-991A-2618	Sequence 2618, Ap	1381	74.5	5.5	2517	4	US-09-577-304A-183	Sequence 183, App
1309	74.5	5.5	891	4	US-09-540-236-730	Sequence 730, App	1382	74.5	5.5	2517	4	US-09-577-304A-220	Sequence 220, App
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1317	74.5	5.5	1236	4	US-09-270-767-12835	Sequence 12835, A	c1389	74.5	5.5	2772	4	US-09-613-182-5	Sequence 3, Appl
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1320	74.5	5.5	1281	3	US-08-460-900C-3	Sequence 3, Appl	1392	74.5	5.5	2853	4	US-09-199-637A-272	Sequence 413, App
1321	74.5	5.5	1281	3	US-08-954-698-3	Sequence 3, Appl	1393	74.5	5.5	2970	4	US-09-252-991A-4897	Sequence 26, Appl
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c1335	74.5	5.5	1335	4	US-09-252-991A-3984	Sequence 3984, Ap	1407	74.5	5.5	21410	4	US-09-596-002-12	Sequence 12, Appl
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1341	74.5	5.5	1539	4	US-09-072-596-32	Sequence 32, Appl	1413	74	5.5	861	4	US-09-252-991A-15237	Sequence 23, Appl
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 21:39:08 ; Search time 3347 Seconds

(without alignments)  
3701.793 Million cell updates/sec

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Perfect score: 1343

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Searched: 4526729 seqs, 23644849745 residues

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Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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92	386	28.7	1026	6	BD005645 Materials	165	345	25.7	1150	8	AY279013 Zea mays
93	386	28.7	1118	8	BT009186 Triticum	166	345	25.7	1150	8	AY279030 Zea mays
94	386	28.7	1146	8	BT009186 Triticum	167	345	25.7	1150	8	AY279033 Zea mays
95	386	28.7	1146	8	AR236695 Sequence	168	345	25.7	1150	8	AY279008 Zea mays
96	385.5	28.7	931	6	AR236702 Sequence	169	343	25.5	1209	8	AY279028 Zea mays
97	385.5	28.7	931	6	AR236702 Sequence	170	343	25.5	1222	8	AY279029 Zea mays
98	385	28.7	1136	8	ZMA242980	171	343	25.5	1222	8	AR236709 Sequence
99	384.5	28.6	1033	6	AY088577 Arabidops	172	341	25.4	982	6	AR236709 Sequence
100	384	28.6	783	8	AX654528 Sequence	173	340	25.3	82746	1	AF453501 Actinosyn
101	384	28.6	1149	8	AK061157	174	338	25.2	1227	8	Z82982 Nicotina ta
102	383.5	28.6	1016	8	BT009093 Triticum	175	337.5	25.1	1182	8	AY279004 Zea mays
103	383.5	28.6	1023	8	AB061268 Solanum t	176	337	25.1	1434	8	AY279014 Zea mays
104	383.5	28.6	1057	6	AR236696 Sequence	177	336.5	25.1	1463	8	AY279015 Zea mays
105	382.5	28.5	929	6	AR236703 Sequence	178	335	24.9	1464	8	AY279006 Zea mays
106	381	28.4	1049	6	AR236715 Sequence	179	335	24.9	1464	8	AY279007 Zea mays
107	379.5	28.3	845	6	AR225248 Sequence	180	333	24.8	1172	8	AY279006 Zea mays
108	379.5	28.3	1258	6	A22706 Caffeoyl-Co	181	333	24.8	1172	8	AY279022 Zea mays
109	379	28.2	1112	6	AX660732 Sequence	182	333	24.8	1442	8	AY279017 Zea mays
110	377.5	28.1	959	8	AK108479 Triticum	183	333	24.8	1442	8	AY279018 Zea mays
111	377	28.1	875	8	AB158406 Triticum	184	333	24.8	1444	8	AY279018 Zea mays
112	377	28.1	1018	8	BT009093 Triticum	185	333	24.8	1445	8	AY279025 Zea mays
113	376	28.0	909	6	BT013139 Lycopersi	186	333	24.8	1445	8	AY279025 Zea mays
114	376	28.0	923	6	AR236697 Sequence	187	333	24.8	1445	8	AY279022 Zea mays
115	373.5	27.8	816	8	AF022775 Sequence	188	332.5	24.8	1438	8	AY279022 Zea mays
116	373.5	27.8	890	8	AR225246 Sequence	189	332.5	24.8	1451	8	AY279020 Zea mays
117	373.5	27.8	890	8	NTU38612 Sequence	190	331	24.6	908	8	AY500159 Corchorus
118	373.5	27.8	955	8	NTU62736 Sequence	191	331	24.6	1298	8	AY323254 Zea mays
119	373.5	27.8	1003	8	NTU62734 Sequence	192	331	24.6	1298	8	AY323255 Zea mays
120	373.5	27.8	1014	8	NTU62734 Sequence	193	331	24.6	1298	8	AY323258 Zea mays
121	372.5	27.7	811	6	AR225247 Sequence	194	331	24.6	1298	8	AY323259 Zea mays
122	372.5	27.7	1104	8	AF053553 Mesembrya	195	331	24.6	1298	8	AY323261 Zea mays
123	372.5	27.7	1258	6	AF122016 Sequence	196	331	24.6	1298	8	AY323261 Zea mays
124	372.5	27.7	1258	6	I92681 Sequence 1	197	331	24.6	1298	8	AY323263 Zea mays
125	369	27.5	730	8	AY056313 Arabidops	198	331	24.6	1298	8	AY323265 Zea mays
126	369	27.5	956	8	AF360317 Arabidops	199	331	24.6	1536	8	AY323241 Zea mays
127	369	27.5	1098	8	AY128822 Arabidops	200	331	24.6	1536	8	AY323243 Zea mays
128	369	27.5	1185	8	AY087981 Arabidops	201	331	24.6	1536	8	AY323245 Zea mays
129	369	27.5	1201	8	AY093172 Arabidops	202	331	24.6	1536	8	AY323247 Zea mays
130	368.5	27.4	744	8	AF327458 Populus a	203	331	24.6	1536	8	AY323248 Zea mays
131	368.5	27.4	1013	8	AF327458 Populus a	204	331	24.6	1536	8	AY323250 Zea mays
132	368.5	27.4	1018	6	AR236711 Sequence	205	331	24.6	1537	8	AY323251 Zea mays
133	367.5	27.4	835	6	AX660084 Sequence	206	330.5	24.6	772	8	FVAJ1447 Fragaria
134	366	27.3	326	6	AX407985 Sequence	207	329.5	24.5	1153	8	AY279010 Zea mays
135	365	27.2	1232	3	AC116551 Dictyoste	208	327.5	24.4	1314	8	AY323253 Zea mays
136	365	27.2	153751	3	ZEUI13151	209	327.5	24.4	1314	8	AY323258 Zea mays
137	364.5	27.1	1158	8	AY644637 Oryza sat	210	327	24.3	105815	8	AP002536 Oryza sat
138	364.5	27.1	137354	8	AF000364 Oryza sat	211	327	24.3	156054	8	AB023482 Oryza sat
139	364.5	27.1	137354	8	AF000364 Oryza sat	212	327	24.3	156054	8	AB023482 Oryza sat
140	363.5	27.1	1116	8	AF060180 Nicotiana	213	326	24.3	1311	8	AY323252 Zea mays
141	362	27.0	917	8	AY087244 Arabidops	214	326	24.3	1311	8	AY323257 Zea mays
142	360.5	26.8	730	8	AF060180 Nicotiana	215	326	24.3	1311	8	AY323264 Zea mays
143	360	26.8	729	6	AX507705 Sequence	216	326	24.3	1311	8	AY323267 Zea mays
144	354	26.4	912	6	AR236707 Sequence	217	326	24.3	1549	8	AY323249 Zea mays
145	353.5	26.3	1136	8	AY279011 Zea mays	218	324	24.1	833	8	AY088274 Arabidops
146	353.5	26.3	1152	8	AY279023 Zea mays	219	323	24.1	60090	1	U30252 Synecococc
147	353.5	26.3	1152	8	AY279032 Zea mays	220	320.5	23.9	1320	8	AY323271 Zea mays
148	353	26.3	1180	6	AX798857 Sequence	221	318.5	23.7	1309	8	AY323239 Zea mays
149	351.5	26.1	1466	8	AX065515 Oryza sat	222	318.5	23.7	1309	8	AY323256 Zea mays
150	350.5	26.1	1136	8	AY279034 Zea mays	223	318.5	23.7	1309	8	AY323266 Zea mays







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370	168.5	12.5	302325	1	AE017236	Myobactae	443	121.5	9.0	11309	6	CQ789017	Sequence
C 371	168	12.5	2233	6	AX416554	Sequence	444	121.5	9.0	11309	6	AR218376	Sequence
C 372	168	12.5	290507	1	AE017327	Listeria	445	121.5	9.0	11309	6	BD003788	Polynucle
C 373	166	12.4	4560	1	L1LVSPFPP	X99710 L. lactis OR	446	121.5	9.0	11552	1	AE008462	Streptoco
C 374	164.5	12.2	296750	1	AE003191	AE003191 Clostridi	447	121.5	9.0	11378	1	AE007401	Streptoco
C 375	164	12.2	399	6	BD224469	BD224469 Materials	448	121.5	9.0	11135	2	SPNEU1906	Sequence
C 376	164	12.2	399	6	AE216519	AE216519 Sequence	449	121.5	9.0	349980	6	AX571762	Sequence
C 377	164	12.2	330350	1	AL596168	AL596168 Listeria	450	121	9.0	518	6	CQ720861	Sequence
C 378	164	12.2	349980	6	AX4113017	AX4113017 Sequence	C 451	120	8.9	301550	1	SC093134	Staphyloc
C 379	164	12.2	349980	6	AX4117044	AX4117044 Sequence	C 452	120	8.9	303450	1	AP003362	Staphyloc
C 380	164	12.2	349980	6	AX4117045	AX4117045 Sequence	C 453	120	8.9	346300	1	AP003362	Staphyloc
C 381	162.5	12.1	702	6	AR320113	AR320113 Sequence	C 454	119.5	8.9	298050	1	AX321861	Nitrosomo
C 382	162.5	12.1	12898	1	AE006403	AE006403 Lactococ	C 455	119	8.9	12014	1	AE010732	Methanosa
C 383	162	12.1	13325	1	AE005016	AE005016 Halobacte	C 456	118.5	8.8	1262	10	BC010402	Mus muscu
C 384	161.5	12.0	349450	1	MLPRTN4	MLPRTN4 Myobactae	C 457	118	8.8	37768	3	U40414	Sequence
C 385	159.5	11.9	299550	1	AE001511	AE001511 Bacillus	C 458	118	8.8	288404	1	AE017272	Caenorhabd
C 386	158	11.8	38675	1	MLU15180	MLU15180 Mycobacteri	C 459	118	8.8	288404	1	AE017272	Bacillus
C 387	158	11.8	38675	6	AR345367	AR345367 Sequence	C 460	116.5	8.7	10763	1	AE010544	Fusobacte
C 388	158	11.8	110000	1	AE016822_09	Continuation (10 o	C 461	115	8.6	639	6	AX121324	Sequence
C 389	157	11.7	801	6	AR394036	AR394036 Sequence	C 462	115	8.6	639	6	BD163441	Novel pol
C 390	157	11.7	301278	1	AE015939	AE015939 Clostridi	C 463	115	8.6	769	6	AX771879	Sequence
C 391	157	11.7	302132	1	AE016955	AE016955 Enterococ	C 464	115	8.6	33150	1	AP005277	Coryneb
C 392	156	11.6	19024	6	BD193585	BD193585 Enterococ	C 465	115	8.6	349459	1	AX927151	Coryneb
C 393	154	11.5	8367	1	AF400582	AF400582 Acinetoba	C 466	115	8.6	349980	6	AX127146	Sequence
C 394	154	11.5	110000	1	CR543861_14	Continuation (15 o	C 467	114.5	8.5	2868	1	AB049411	Acinetoba
C 395	150.5	11.2	81866	8	NC64C2	Continuation (15 o	C 468	114.5	8.5	143109	8	OSUN00224	Oryza sat
C 396	149.5	11.1	508	6	AR236701	AR236701 Neurospor	C 469	114.5	8.5	300750	1	AP005217	Coryneb
C 397	147	10.9	1433	8	AF168779	AF168779 Eucalyptu	C 470	114	8.5	636	6	AX617408	Sequence
C 398	147	10.9	199173	1	BSUB0014	Z99117 Bacillus su	C 471	114	8.5	1255	10	AP076156	Mus muscu
C 399	146.5	10.9	110000	1	AE017180_05	Continuation (6 of	C 472	114	8.5	1605	8	PAN245505	Podospo
C 400	145	10.8	1504	8	AY267760	AY267760 Fusarium	C 473	114	8.5	110000	1	AE000516_19	Continuation (20 o
C 401	144	10.7	300550	1	AP004599	AP004599 Oceanobac	C 474	114	8.5	110000	1	EX571857_16	Continuation (17 o
C 402	141	10.5	957	5	AX930132	AX930132 Gallus ga	C 475	114	8.5	231050	1	BP248340	Myobactae
C 403	139	10.3	51454	1	AE014157	AE014157 Streptoco	C 476	114	8.5	333750	1	AP004827	Staphyloc
C 404	139	10.3	310950	1	AP005143	AP005143 Streptoco	C 477	114	8.5	347496	1	EX842577	Myobactae
C 405	137	10.2	115339	8	AP003940	AP003940 Oryza sat	C 478	113.5	8.5	5514	6	CQ587772	Sequence
C 406	137	10.2	174478	8	AP005467	AP005467 Oryza sat	C 479	112	8.3	2066	6	AX394673	Sequence
C 407	136	10.1	705	6	CQ649680	CQ649680 Sequence	C 480	112	8.3	7912	10	RNCATOMET	Z12651 R.norvegicu
C 408	136	10.1	10844	1	AE010080	AE010080 Streptoco	C 481	112	8.3	110000	1	EX571856_17	Continuation (18 o
C 409	136	10.1	11615	1	AE010060	AE010060 Streptoco	C 482	112	8.3	300052	1	AE017232	Myobactae
C 410	136	10.1	110000	1	CP000003_10	Continuation (11 o	C 483	112	8.3	300115	1	AP005076	Vibrio pa
C 411	136	10.1	110000	1	CP000003_11	Continuation (12 o	C 484	112	8.3	300750	1	AP005217	Coryneb
C 412	134	10.0	324050	1	BX251410	BX251410 Tropherym	C 485	111	8.3	495	6	AR485101	Sequence
C 413	134	10.0	324227	1	AE016852	AE016852 Tropherym	C 486	111	8.3	495	6	AX144317	Sequence
C 414	131	9.8	304282	1	AE017005	AE017005 Bacillus	C 487	111	8.3	33715	6	AR354077	Sequence
C 415	130.5	9.7	12012	1	AE011847	AE011847 Xanthomon	C 488	111	8.3	38494	6	AR354077	Sequence
C 416	130	9.7	10398	1	AE017632	AE017632 Sequence	C 489	111	8.3	38503	1	MSGB1912CS	leprae g
C 417	128	9.5	2316	6	AX207628	AX207628 Clostridi	C 490	110.5	8.2	301443	1	AE017239	Myobactae
C 418	127.5	9.5	10069	1	AE007678	AE007678 Streptoco	C 491	110	8.2	236	6	BD224451	Materials
C 419	126.5	9.4	534	6	AX433853	AX433853 Sequence	C 492	110	8.2	236	6	AR216501	Sequence
C 420	126	9.4	777	6	AX377804	AX377804 Sequence	C 493	110	8.2	236	6	AR432903	Sequence
C 421	126	9.4	777	6	AX377804	AX377804 Sequence	C 494	110	8.2	509	11	EX784390	Pinus pin
C 422	125.5	9.3	705	6	CQ649678	CQ649678 Sequence	C 495	110	8.2	247910	1	AE017307	Thermus t
C 423	125.5	9.3	20639	1	AE014228	AE014228 Streptoco	C 496	109.5	8.2	348411	1	AP003007	Mesorhizo
C 424	125.5	9.3	349980	6	CQ655069	CQ655069 Sequence	C 497	109	8.1	11847	1	AE0031918	Deinococc
C 425	125.5	9.3	349980	6	AX954529	AX954529 Sequence	C 498	109	8.1	213732	1	AE001862	Deinococc
C 426	124.5	9.3	708	6	AX607661	AX607661 Sequence	C 499	108.5	8.1	1107	6	CQ812330	Sequence
C 427	124.5	9.3	6641	6	AX602145	AX602145 Sequence	C 500	108.5	8.1	1107	9	HUMCOMTA	Me5212 Homo sapi
C 428	124.5	9.3	167050	1	SGF766847	SGF766847 Streptoco	C 501	108	8.0	920	4	BC011935	Homo sapi
C 429	124.5	9.3	292200	1	SC0939129	SC0939129 Streptoco	C 502	108	8.0	1213	9	BC011935	Homo sapi
C 430	124	9.2	1605	1	AF016233	AF016233 Enterococ	C 503	108	8.0	10288	1	AE012905	Calif fam
C 431	124	9.2	110000	1	AE017225_22	Continuation (23 o	C 504	108	8.0	120528	9	AP000812	Chlorobiu
C 432	124	9.2	110000	1	AE017334_22	Continuation (23 o	C 505	108	8.0	132544	1	AF521085	Streptomy
C 433	124	9.2	110000	1	AE017355_23	Continuation (24 o	C 506	108	8.0	155892	2	AP002513	Homo sapi
C 434	124	9.2	293264	1	AE017031	AE017031 Bacillus	C 507	107.5	8.0	1206	6	AX774876	Sequence
C 435	123	9.2	498	6	AR347999	AR347999 Sequence	C 508	107.5	8.0	1206	6	AX774876	Sequence
C 436	123	9.2	3673	6	AR269748	AR269748 Streptoco	C 509	107.5	8.0	1291	9	CQ716680	Sequence
C 437	123	9.2	3673	6	AR485702	AR485702 Staphyloc	C 510	107.5	8.0	139628	2	AC150112	Gallus ga
C 438	123	9.2	3673	6	AX145066	AX145066 Sequence	C 511	107.5	8.0	166863	2	AC150140	Gallus ga
C 439	123	9.2	30029	1	AE016748	AE016748 Staphyloc	C 512	107.5	8.0	250950	1	AP005335	Vibrio vu
C 440	122	9.1	201	11	BV202015	BV202015 sgmm20798	C 513	107.5	8.0	302174	1	AE017241	Myobactae
C 441	121.5	9.0	714	6	AX568724	AX568724 Sequence	C 514	107.5	8.0	304490	1	AE016806	Vibrio vu
C 442	121.5	9.0	714	6	AX481634	AX481634 Sequence	C 515	107	8.0	12397	1	AE010715	Methanosa



516	106.5	7.9	10113	1	AE011156	AE011156 Methanosa	c 589	100.5	7.5	1979	6	E11456	E11456 cDNA encodi
517	105.5	7.9	816	9	CR456997	CR456997 Homo sapi	c 590	100.5	7.5	1987	6	AR448000	AR448000 Sequence
518	105.5	7.9	873	9	CR456422	CR456422 Homo sapi	c 591	100.5	7.5	2014	6	BC047750	BC047750 Homo sapi
519	105.5	7.9	9463	1	SCRTCTLUS	X95596 S.griseus c	c 592	100.5	7.5	2070	9	BC074500	BC074500 Homo sapi
520	105.5	7.9	11464	1	SCRTCTLUS	AE005915 Caulobact	c 593	100.5	7.5	247151	2	AC126662	AC126662 Rattus no
521	105.5	7.9	347625	1	BX248356	BX248356 Corynebac	c 594	100	7.4	2734	8	AK067366	AK067366 Oryza sat
522	105.5	7.9	349354	1	BX640416	BX640416 Bordetell	c 595	100	7.4	6806	1	SMWTN4556	M29297 S.fradiae c
523	105	7.8	457	6	AX394671	AX394671 Sequence	c 596	100	7.4	8460	6	I64893	I64893 Sequence 9
524	105	7.8	110000	2	AP006502_14	Continuation (15 o	c 597	100	7.4	8460	6	HSU29344	U9344 Human bres
525	105	7.8	308050	1	SC0939124	AL93124 Streptomy	c 598	100	7.4	10677	1	AE005967	AE005967 Caulobact
526	104.5	7.8	1895	8	AK108846	AK108846 Oryza sat	c 599	100	7.4	110000	1	AY316747_1	Continuation (2 of
527	104.5	7.8	10878	1	AF272737	AF272737 Streptomy	c 600	100	7.4	126845	8	AP005244	AP005244 Oryza sat
528	104.5	7.8	148762	8	AP002843	AP002843 Oryza sat	c 601	100	7.4	145911	1	AP003014	AP003014 Mesorhizo
529	104.5	7.8	278289	1	AE017306	AE017306 Thermus t	c 602	100	7.4	164628	2	AC073646	AC073646 Homo sapi
530	104	7.7	1628	10	AB010089S1	AB010089 Mus muscu	c 603	100	7.4	179937	2	AF546190	AF546190 Zea mays
531	104	7.7	158344	10	AL133401	AL133401 Mouse DNA	c 604	100	7.4	230146	2	AC134057	AC134057 Rattus no
532	104	7.7	180000	1	AF322012S1	AF322012 Bradyrhiz	c 605	100	7.4	299991	1	AE016776	AE016776 Pseudomon
533	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 606	100	7.4	300350	1	AP006574	AP006574 Gloebact
534	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 607	99.5	7.4	300450	1	AP005960	AP005960 Bradyrhiz
535	104	7.7	299850	1	AP005949	AP005949 Bradyrhiz	c 608	99.5	7.4	3079	1	PDEMXXYZ	M2421 Paracoccus
536	103.5	7.7	1491	10	RATCATAB	M60753 R.norvegicu	c 609	99.5	7.4	3949	1	AB015725	AB015725 Aeromonas
537	103.5	7.7	1540	10	RATCATAB	M60754 R.norvegicu	c 610	99.5	7.4	9088	5	AF327372	AF327372 Gallus ga
538	103.5	7.7	2138	1	STWSIGMA	L11648 Streptomyce	c 611	99.5	7.4	295500	1	AP005954	AP005954 Bradyrhiz
539	103.5	7.7	66669	1	AME16952	Y16952 Amycolatops	c 612	99.5	7.4	303350	1	AP006574	AP006574 Gloebact
540	103.5	7.7	110000	2	IMFLCHR32_17	Continuation (18 o	c 613	99.5	7.4	339681	1	AP003009	AP003009 Mesorhizo
541	103.5	7.7	233050	1	AL627271	AL627271 Salmonell	c 614	99	7.4	348171	1	EX640412	EX640412 Bordetell
542	103.5	7.7	30247	1	AE016837	AE016837 Salmonell	c 615	99	7.4	2010	6	CQ785960	CQ785960 Sequence
543	103	7.7	3307	8	AK110307	AK110307 Oryza sat	c 616	99	7.4	2030	6	I70211	I70211 Sequence 1
544	103	7.7	10732	1	AE013407	AE013407 Methanosa	c 617	99	7.4	2030	6	AE023937	AE023937 Sequence 7
545	103	7.7	11877	1	AE011683	AE011683 Xanthomon	c 618	99	7.4	2505	6	115438	115438 Sequence 7
546	103	7.7	64492	1	AB086653	AB086653 Streptomy	c 619	99	7.4	2505	6	AX924362	AX924362 Sequence
547	103	7.7	109192	8	CNS08CCR	AL954153 Oryza sat	c 620	99	7.4	2685	6	AX924386	AX924386 Sequence
548	102.5	7.6	1525	8	TAU62951	U62584 Thermus aqu	c 621	99	7.4	7528	6	CQ729217	CQ729217 Sequence
549	102.5	7.6	2760	1	TAU62951	U62584 Thermus aqu	c 622	99	7.4	7528	6	CQ729217	CQ729217 Sequence
550	102.5	7.6	3003	6	CQ845922	CQ845922 Sequence	c 623	99	7.4	7536	9	AY451392	AY451392 Homo sapi
551	102.5	7.6	3003	9	AK131436	AK131436 Homo sapi	c 624	99	7.4	8461	6	CQ785963	CQ785963 Sequence
552	102.5	7.6	2978	6	CQ735548	CQ735548 Sequence	c 625	99	7.4	8472	9	BC063242	BC063242 Homo sapi
553	102.5	7.6	5502	9	HS0808450	BX648302 Homo sapi	c 626	99	7.4	10029	1	AE010416	AE010416 Methanopy
554	102.5	7.6	10245	1	AE004569	AE004569 Pseudomon	c 627	99	7.4	10202	1	AE004483	AE004483 Pseudomon
555	102.5	7.6	119115	8	AP003358	AP003358 Oryza sat	c 628	99	7.4	18843	9	AY148100	AY148100 Homo sapi
556	102.5	7.6	298550	1	AP005961	AP005961 Bradyrhiz	c 629	99	7.4	110000	2	AP006484	AP006484 Cyanidios
557	102.5	7.6	300129	1	AE017309	AE017309 Desulfovi	c 630	99	7.4	138939	9	AC119675	AC119675 Homo sapi
558	102.5	7.6	300531	1	AE016932	AE016932 Bacteroid	c 631	99	7.4	163978	10	AC140411	AC140411 Mus muscu
559	102	7.6	1746	9	HSU14534	UI4534 Human orpha	c 632	99	7.4	193057	10	AL663067	AL663067 Mouse DNA
560	102	7.6	1898	6	I46765	I46765 Sequence 1	c 633	99	7.4	299450	1	AP005938	AP005938 Bradyrhiz
561	102	7.6	2084	11	BV177077	BV177077 sqm92606	c 634	99	7.4	300181	1	AE017318	AE017318 Desulfovi
562	102	7.6	14138	1	AE004766	AE004766 Pseudomon	c 635	99	7.4	346294	1	AP002999	AP002999 Mesorhizo
563	102	7.6	14469	1	AE011498	AE011498 Leptospir	c 636	99	7.4	346294	1	AP002999	AP002999 Mesorhizo
564	102	7.6	21394	2	AC115937	AC115937 Mus muscu	c 637	98.5	7.3	1217	9	BC000419	BC000419 Homo sapi
565	102	7.6	301250	1	AP005950	AP005950 Bradyrhiz	c 638	98.5	7.3	1695	8	AK072292	AK072292 Oryza sat
566	102	7.6	303550	1	SC0939118	AL939118 Streptomy	c 639	98.5	7.3	2384	6	AX747042	AX747042 Sequence
567	102	7.6	305541	1	AE017290	AE017290 Leptospir	c 640	98.5	7.3	2384	9	AK091535	AK091535 Homo sapi
568	102	7.6	348068	1	BX572604	BX572604 Rhodopseu	c 641	98.5	7.3	3147	6	AR232445	AR232445 Sequence
569	101.5	7.6	601	11	BV167609	BV167609 sqm96022	c 642	98.5	7.3	3147	6	AR256497	AR256497 Sequence
570	101.5	7.6	2039	9	AK130031	AK130031 Homo sapi	c 643	98.5	7.3	3147	6	AX189015	AX189015 Sequence
571	101.5	7.6	2084	11	BV177509	BV177509 sqm95100	c 644	98.5	7.3	3147	6	BD132995	BD132995 Anti-bact
572	101.5	7.6	2084	11	BV179316	BV179316 sqm10484	c 645	98.5	7.3	4355	1	ECORAJ	M4787 E.coli sbcc
573	101.5	7.6	153875	9	AC003682	AC003682 Homo sapi	c 646	98.5	7.3	4355	1	ECORAJ	M4787 E.coli sbcc
574	101.5	7.6	188324	2	BX530094	BX530094 Homo sapi	c 647	98.5	7.3	8008	1	PAU93274	PAU93274 Pseudomonas
575	101.5	7.6	189326	9	AC018462	AC018462 Homo sapi	c 648	98.5	7.3	11015	1	AE004736	AE004736 Pseudomon
576	101	7.5	1543	8	AK120652	AK120652 Oryza sat	c 649	98.5	7.3	16675	1	AE011814	AE011814 Xanthomon
577	101	7.5	1820	9	BC035516	BC035516 Homo sapi	c 650	98.5	7.3	16675	1	AE011814	AE011814 Xanthomon
578	101	7.5	129778	8	AC091123	AC091123 Oryza sat	c 651	98.5	7.3	77534	1	AF235504	AF235504 Streptomy
579	101	7.5	154620	2	BX323047	BX323047 Danio rer	c 652	98.5	7.3	77536	6	BD235937	BD235937 Polyketid
580	101	7.5	163962	9	BS000233	BS000233 Pan trogl	c 653	98.5	7.3	110000	1	U00096	Continuation (5 of
581	101	7.5	178158	8	AC084320	AC084320 Oryza sat	c 654	98.5	7.3	128824	1	ECU73857	U73857 Escherichia
582	101	7.5	349771	1	BX572594	BX572594 Rhodopseu	c 655	98.5	7.3	199439	2	AC104882	AC104882 Mus muscu
583	100.5	7.5	1447	5	BC049292	BC049292 Xenopus 1	c 656	98.5	7.3	202000	1	AP000058	AP000058 Aeropyrum
584	100.5	7.5	1688	6	AR035537	AR035537 Sequence	c 657	98.5	7.3	296300	1	AP005035	AP005035 Streptomy
585	100.5	7.5	1688	6	E11457	E11457 cDNA encodi	c 658	98.5	7.3	300271	8	AE016901	AE016901 Eremothec
586	100.5	7.5	1815	6	AB477499	AB477499 Sequence	c 659	98.5	7.3	302300	1	AP005034	AP005034 Streptomy
587	100.5	7.5	1934	9	BC007790	BC007790 Homo sapi	c 660	98.5	7.3	302550	1	AP006581	AP006581 Gloebact
588	100.5	7.5	1979	6	AR035536	AR035536 Sequence	c 661	98	7.3	1782	6	AX879871	AX879871 Sequence



C 662	98	7.3	1782	6	BD158070	BD158070 Primer fo	C 735	95.5	7.1	300810	8	AE016896	AE016896	Eremothec
C 663	98	7.3	1782	9	AK022862	AK022862 Homo sapi	736	95.5	7.1	300861	1	AE016777	AE016777 Pseudomon	
C 664	98	7.3	12772	1	AE004727	AE004727 Pseudomon	737	95.5	7.1	303550	1	SC0939131	SC0939131 Streptomy	
C 665	98	7.3	76196	1	AY354515	AY354515 Streptomy	C 738	95.5	7.1	349672	1	BX640419	BX640419 Bordetell	
C 666	98	7.3	174363	9	AC135506	AC135506 Homo sapi	739	95.5	7.1	349726	1	BX640421	BX640421 Bordetell	
C 667	98	7.3	185146	2	AC104311	AC104311 Homo sapi	C 740	95	7.1	1416	6	BD155975	BD155975 Sequence	
C 668	98	7.3	215342	9	AC109322	AC109322 Homo sapi	C 741	95	7.1	1416	6	BD155975	BD155975 Sequence	
C 669	98	7.3	279912	2	AC126572	AC126572 Rattus no	C 742	95	7.1	1416	6	BD155975	BD155975 Sequence	
C 670	98	7.3	310581	1	AE016863	AE016863 Pseudomon	C 743	95	7.1	2597	9	AK001168	AK001168 Homo sapi	
C 671	98	7.3	348971	1	BX572594	BX572594 Rhodospheu	C 744	95	7.1	2597	9	AK001168	AK001168 Homo sapi	
C 672	97.5	7.3	861	12	AY658649	AY658649 Synthetic	C 745	95	7.1	3009	9	HSN800570	HSN800570 Pseudomon	
C 673	97.5	7.3	1632	6	AR301781	AR301781 Sequence	C 746	95	7.1	3346	1	PSU81032	PSU81032 Sequence	
C 674	97.5	7.3	10130	1	AE002085	AE002085 Deinococc	C 747	95	7.1	4941	6	CQ730770	CQ730770 Sequence	
C 675	97.5	7.3	20235	1	SERERYAB	SERERYAB S. erythraea	C 748	95	7.1	4962	9	BC035577	BC035577 Homo sapi	
C 676	97.5	7.3	20235	6	AR049368	AR049368 Sequence	C 749	95	7.1	4966	9	BC035577	BC035577 Homo sapi	
C 677	97.5	7.3	20235	6	AR095529	AR095529 Sequence	C 750	95	7.1	4976	8	AK110228	AK110228 Oryza sat	
C 678	97.5	7.3	20444	1	SERERAB	SERERAB S. erythraea	C 751	95	7.1	4976	8	AK110228	AK110228 Oryza sat	
C 679	97.5	7.3	24494	6	AK301774	AK301774 Sequence	C 752	95	7.1	14568	1	AE004453	AE004453 Pseudomon	
C 680	97.5	7.3	42805	9	AC004221	AC004221 Homo sapi	C 753	95	7.1	147706	8	AC083945	AC083945 Oryza sat	
C 681	97.5	7.3	188108	2	AC118207	AC118207 Mus muscu	C 754	95	7.1	189458	10	AC134908	AC134908 Mus muscu	
C 682	97.5	7.3	302650	1	AP005958	AP005958 Bradyrhiz	C 755	95	7.1	213817	2	AC123649	AC123649 Mus muscu	
C 683	97.5	7.3	310550	1	SC0939113	SC0939113 Streptomy	C 756	95	7.1	220577	2	AC068497	AC068497 Oryza sat	
C 684	97	7.2	1192	5	BX932533	BX932533 Gallus ga	C 757	95	7.1	300029	8	AE017083	AE017083 Desulfovi	
C 685	97	7.2	2585	1	CEPCEX	CEPCEX Cellulomona	C 758	95	7.1	300181	1	AP005038	AP005038 Streptomy	
C 686	97	7.2	12541	1	AE001956	AE001956 Deinococc	C 759	95	7.1	300425	1	AP006578	AP006578 Gloeobact	
C 687	97	7.2	13026	1	AE002510	AE002510 Neisseria	C 760	95	7.1	304681	2	ACU16483	ACU16483 Pyrococcu	
C 688	97	7.2	25184	1	AE008779	AE008779 Salmonell	C 761	95	7.1	307150	1	CNSPAX01	CNSPAX01 Streptomy	
C 689	97	7.2	241178	2	AC130508	AC130508 Rattus no	C 762	95	7.1	339650	6	AX041106	AX041106 Sequence	
C 690	97	7.2	280558	1	AE017301	AE017301 Thermus t	C 763	95	7.1	349980	6	QY35395	QY35395 Sequence	
C 691	97	7.2	296282	2	AC111857	AC111857 Rattus no	C 764	94.5	7.0	534	6	BD179645	BD179645 Highly th	
C 692	97	7.2	299175	1	AP005023	AP005023 Streptomy	C 765	94.5	7.0	975	6	DMHREC2C	DMHREC2C Drosophi	
C 693	97	7.2	300704	1	AE017316	AE017316 Desulfovi	C 766	94.5	7.0	2184	3	AF324956	AF324956 Drosophi	
C 694	97	7.2	310029	1	AE016868	AE016868 Pseudomon	C 767	94.5	7.0	2239	3	AF324956	AF324956 Drosophi	
C 695	97	7.2	348074	1	BX640449	BX640449 Bordetell	C 768	94.5	7.0	2304	6	AF166541	AF166541 Sequence	
C 696	97	7.2	349980	6	AX044033	AX044033 Sequence	C 769	94.5	7.0	2304	6	I49731	I49731 Sequence 1	
C 697	96.5	7.2	11426	1	AE004590	AE004590 Pseudomon	C 770	94.5	7.0	2304	6	I49731	I49731 Sequence 1	
C 698	96.5	7.2	22233	1	SPDBFB	SPDBFB Spingomona	C 771	94.5	7.0	2311	3	DMXR2C	DMXR2C Drosophi	
C 699	96.5	7.2	106707	2	AC019314	AC019314 Homo sapi	C 772	94.5	7.0	2483	6	QY35395	QY35395 Sequence	
C 700	96.5	7.2	110000	1	AE016822_04	AE016822_04 Continuation (5 of	C 773	94.5	7.0	2506	3	AY069393	AY069393 Drosophi	
C 701	96.5	7.2	128342	9	AL627313	AL627313 Human DNA	C 774	94.5	7.0	3412	9	HSN806839	HSN806839 Sequence	
C 702	96.5	7.2	152583	2	AC131998	AC131998 Mus muscu	C 775	94.5	7.0	4483	6	CQ580820	CQ580820 Sequence	
C 703	96.5	7.2	171525	2	AC145473	AC145473 Rattus no	C 776	94.5	7.0	14343	9	AY149894	AY149894 Homo sapi	
C 704	96.5	7.2	182061	10	AF107869	AF107869 Mus muscu	C 777	94.5	7.0	14790	1	AE001885	AE001885 Deinococc	
C 705	96.5	7.2	195859	14	AF281817	AF281817 Tupaiia he	C 778	94.5	7.0	18737	6	CQ580778	CQ580778 Sequence	
C 706	96.5	7.2	219252	2	AC026760	AC026760 Mus muscu	C 779	94.5	7.0	18737	6	CQ580778	CQ580778 Sequence	
C 707	96.5	7.2	242203	2	AC097860	AC097860 Rattus no	C 780	94.5	7.0	45672	2	DMC22E5	DMC22E5 Drosophi	
C 708	96.5	7.2	258888	2	AC109677	AC109677 Thermus t	C 781	94.5	7.0	77656	2	AC017522	AC017522 Drosophi	
C 709	96.5	7.2	272101	1	AE017302	AE017302 Thermus t	C 782	94.5	7.0	110000	1	AE017180_16	AE017180_16 Continuation (17 o	
C 710	96.5	7.2	299750	1	AP005964	AP005964 Bradyrhiz	C 783	94.5	7.0	165725	2	AC024027	AC024027 Homo sapi	
C 711	96	7.1	1657	9	AK098658	AK098658 Homo sapi	C 784	94.5	7.0	165725	2	AC024027	AC024027 Homo sapi	
C 712	96	7.1	2004	6	BD180143	BD180143 Highly th	C 785	94.5	7.0	169618	3	AC105055	AC105055 Drosophi	
C 713	96	7.1	2588	1	CEPCEX	CEPCEX Cellulomona	C 786	94.5	7.0	177724	3	AC104146	AC104146 Drosophi	
C 714	96	7.1	10066	14	BHV12US	BHV12US Bovine herp	C 787	94.5	7.0	237619	2	AC073765	AC073765 Mus muscu	
C 715	96	7.1	15534	6	CQ776613	CQ776613 Sequence	C 788	94.5	7.0	240264	2	AC107434	AC107434 Rattus no	
C 716	96	7.1	15534	9	AB051895	AB051895 Homo sapi	C 789	94.5	7.0	245134	2	AC126639	AC126639 Rattus no	
C 717	96	7.1	110000	2	AP006497_2	AP006497_2 Continuation (3 of	C 790	94.5	7.0	297800	1	AP006579	AP006579 Gloebact	
C 718	96	7.1	160714	2	AC150149	AC150149 Gallus ga	C 791	94.5	7.0	300100	1	SC0939123	SC0939123 Streptomy	
C 719	96	7.1	202432	2	AC143119	AC143119 Macaca mu	C 792	94.5	7.0	300143	3	AE003422	AE003422 Prochloro	
C 720	96	7.1	210472	9	AC035139	AC035139 Homo sapi	C 793	94.5	7.0	300933	3	AE003422	AE003422 Drosophi	
C 721	96	7.1	233568	2	AC150275	AC150275 Mus muscu	C 794	94	7.0	3058	8	AK110497	AK110497 Oryza sat	
C 722	96	7.1	301191	1	AE017152	AE017152 Haemophil	C 795	94	7.0	3263	8	AK111218	AK111218 Oryza sat	
C 723	96	7.1	302134	8	AE016906	AE016906 Eremothec	C 796	94	7.0	4382	14	MMSAAX	MMSAAX Moloney mur	
C 724	96	7.1	308015	1	AE016783	AE016783 Pseudomon	C 797	94	7.0	7207	1	AF533147	AF533147 Bacillus	
C 725	95.5	7.1	666	12	AY657499	AY657499 Synthetic	C 798	94	7.0	12732	1	AE011982	AE011982 Xanthomon	
C 726	95.5	7.1	2696	8	AK121206	AK121206 Oryza sat	C 799	94	7.0	15542	1	AE004504	AE004504 Pseudomon	
C 727	95.5	7.1	2926	1	AE667481	AE667481 Lysobacte	C 800	94	7.0	17400	9	AE03925	AE03925 Homo sapi	
C 728	95.5	7.1	3173	6	E05949	E05949 DNA encodin	C 801	94	7.0	18996	1	AB034704	AB034704 Rhoactiva	
C 729	95.5	7.1	159119	1	AP006583	AP006583 Gloebact	C 802	94	7.0	82144	9	AC099660	AC099660 Homo sapi	
C 730	95.5	7.1	192202	2	AC134315	AC134315 Lemur cat	C 803	94	7.0	86896	1	RCU597682	RCU597682 Rhodobact	
C 731	95.5	7.1	277000	1	SC0939109	SC0939109 Streptomy	C 804	94	7.0	97995	9	AC067718	AC067718 Homo sapi	
C 732	95.5	7.1	298550	1	AP005029	AP005029 Streptomy	C 805	94	7.0	110000	2	CR522870_10	CR522870_10 Continuation (11 o	
C 733	95.5	7.1	298550	1	AP005029	AP005029 Streptomy	C 806	94	7.0	110000	2	CEV105E8_2	CEV105E8_2 Continuation (3 of	
C 734	95.5	7.1	300350	1	AP006574	AP006574 Gloebact	C 807	94	7.0	115751	8	AP003633	AP003633 Oryza sat	







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C 954	92.5	6.9	2517	6	AX317526	AX317526 Sequence	c1027	92.5	6.9	301700	1	AP005948	AP005948 Bradyrhiz
C 955	92.5	6.9	2517	6	AX317530	AX317530 Sequence	c1028	92.5	6.9	301708	1	AP016792	AP016792 Pseudomon
C 956	92.5	6.9	2517	6	AX317534	AX317534 Sequence	c1029	92.5	6.9	304500	1	AP005953	AP005953 Bradyrhiz
C 957	92.5	6.9	2520	6	AX410555	AX410555 Sequence	1030	92.5	6.9	305584	1	AE016920	AE016920 Chromobac
C 958	92.5	6.9	2520	6	AX410559	AX410559 Sequence	c1031	92.5	6.9	338579	1	AP003004	AP003004 Mesorhizo
C 959	92.5	6.9	2520	6	AX317219	AX317219 Sequence	c1032	92.5	6.9	349061	1	NMA222491	AL162753 Neisseria
C 960	92.5	6.9	2520	6	AX317502	AX317502 Sequence	1033	92	6.9	1035	6	AX479056	AX479056 Sequence
C 961	92.5	6.9	2520	6	AX317538	AX317538 Sequence	1034	92	6.9	1987	1	PASSSDAPP	X78478 Pseudomonas
C 962	92.5	6.9	2520	6	AX317540	AX317540 Sequence	1035	92	6.9	2396	6	CQ581775	CQ581775 Sequence
C 963	92.5	6.9	2520	6	AX317570	AX317570 Sequence	1036	92	6.9	2590	6	CQ599964	CQ599964 Sequence
C 964	92.5	6.9	2520	6	AX317574	AX317574 Sequence	1037	92	6.9	2675	9	BC023554	BC023554 Homo sapi
C 965	92.5	6.9	2526	6	AX410413	AX410413 Sequence	1038	92	6.9	2682	9	BC017210	BC017210 Homo sapi
C 966	92.5	6.9	2526	6	AX410418	AX410418 Sequence	1039	92	6.9	2720	9	BC023551	BC023551 Homo sapi
C 967	92.5	6.9	2526	6	AX410473	AX410473 Sequence	1040	92	6.9	2894	6	CQ599979	CQ599979 Sequence
C 968	92.5	6.9	2526	6	AX410475	AX410475 Sequence	c1041	92	6.9	2955	8	AK100088	AK100088 Oryza sat
C 969	92.5	6.9	2526	6	AX410508	AX410508 Sequence	1042	92	6.9	4256	3	AY122255	AY122255 Drosophil
C 970	92.5	6.9	2526	6	AX410509	AX410509 Sequence	c1043	92	6.9	5008	9	AX122704	AX122704 Homo sapi
C 971	92.5	6.9	2526	6	AX410510	AX410510 Sequence	c1044	92	6.9	5286	1	SCACT16	X63449 S.coelicolo
C 972	92.5	6.9	2526	6	AX410540	AX410540 Sequence	c1045	92	6.9	10369	1	AE005059	AE005059 Halobacte
C 973	92.5	6.9	2526	6	AX317100	AX317100 Sequence	1046	92	6.9	13197	1	AE004503	AE004503 Pseudomon
C 974	92.5	6.9	2526	6	AX317101	AX317101 Sequence	1047	92	6.9	14423	1	AE004532	AE004532 Pseudomon
C 975	92.5	6.9	2526	6	AX317114	AX317114 Sequence	1048	92	6.9	15280	9	AB107036	AB107036 Homo sapi
C 976	92.5	6.9	2526	6	AX317115	AX317115 Sequence	1049	92	6.9	24123	1	AF086815	AF086815 Acidovora
C 977	92.5	6.9	2526	6	AX317116	AX317116 Sequence	1050	92	6.9	102842	2	AC150097	AC150097 Callus ga
C 978	92.5	6.9	2526	6	AX317129	AX317129 Sequence	1051	92	6.9	106332	14	AY150217	AY150217 Ambystoma
C 979	92.5	6.9	2526	6	AX317264	AX317264 Sequence	c1052	92	6.9	110000	1	AE016822_15	Continuation (16 o
C 980	92.5	6.9	2526	6	AX317346	AX317346 Sequence	c1053	92	6.9	110000	1	AY16747_2	Continuation (3 of
C 981	92.5	6.9	2526	6	AX317370	AX317370 Sequence	c1054	92	6.9	110000	2	LMFLCHR12_00	AL390114 Leishmani
C 982	92.5	6.9	2526	6	AX317372	AX317372 Sequence	c1055	92	6.9	110000	2	LMFLCHR12_01	Continuation (2 of
C 983	92.5	6.9	2526	6	AX317376	AX317376 Sequence	c1056	92	6.9	110000	2	LMFLCHR12_16	Continuation (17 o
C 984	92.5	6.9	2526	6	AX317384	AX317384 Sequence	c1057	92	6.9	166421	8	AP003106	AP003106 Oryza sat
C 985	92.5	6.9	2526	6	AX317388	AX317388 Sequence	c1058	92	6.9	244273	2	AC106167	AC106167 Rattus no
C 986	92.5	6.9	2526	6	AX317392	AX317392 Sequence	c1059	92	6.9	252109	2	AC098630	AC098630 Rattus no
C 987	92.5	6.9	2526	6	AX317396	AX317396 Sequence	c1061	92	6.9	254439	2	AC150047	AC150047 Gallus ga
C 988	92.5	6.9	2526	6	AX317449	AX317449 Sequence	c1062	92	6.9	269985	2	AC127669	AC127669 Rattus no
C 989	92.5	6.9	2526	6	AX317452	AX317452 Sequence	c1063	92	6.9	298300	1	AP005025	AP005025 Streptomy
C 990	92.5	6.9	2526	6	AX317456	AX317456 Sequence	c1064	92	6.9	300029	1	SMES91786	AL591786 Sinorhizo
C 991	92.5	6.9	2526	6	AX317468	AX317468 Sequence	c1065	92	6.9	300950	1	AE016787	AE016787 Pseudomon
C 992	92.5	6.9	2526	6	AX317494	AX317494 Sequence	c1066	92	6.9	1707	3	AP005940	AP005940 Bradyrhiz
C 993	92.5	6.9	2526	6	AX317555	AX317555 Sequence	c1067	91.5	6.8	1787	9	HSPG5UT	AF012276 Toxoplas
C 994	92.5	6.9	2526	6	AX698683	AX698683 Sequence	c1068	91.5	6.8	2004	9	AY619993	Z14129 H.sapiens p
C 995	92.5	6.9	2526	6	AX698688	AX698688 Sequence	1069	91.5	6.8	2004	9	AY619994	AY619994 Homo sapi
C 996	92.5	6.9	2526	6	AX698691	AX698691 Sequence	c1071	91.5	6.8	2499	6	AR410430	AR410430 Sequence
C 997	92.5	6.9	2526	6	AX698694	AX698694 Sequence	c1072	91.5	6.8	2499	6	AX317076	AX317076 Sequence
C 998	92.5	6.9	2526	6	AX317460	AX317460 Sequence	c1073	91.5	6.8	2505	6	AR023938	AR023938 Sequence
C1000	92.5	6.9	2532	6	AX317464	AX317464 Sequence	c1074	91.5	6.8	2505	6	IL5439	IL5439 Sequence 9
C1001	92.5	6.9	2532	6	AX317560	AX317560 Sequence	c1075	91.5	6.8	2505	6	AR309011	AR309011 Sequence
C1002	92.5	6.9	2619	6	AX317556	AX317556 Sequence	c1076	91.5	6.8	2505	6	AR317142	AR317142 Sequence
C1003	92.5	6.9	2643	6	AX317556	AX317556 Sequence	c1077	91.5	6.8	2505	6	AR410544	AR410544 Sequence
C1004	92.5	6.9	3135	6	AX317478	AX317478 Sequence	c1078	91.5	6.8	2505	6	AR410544	AR410544 Sequence
C1005	92.5	6.9	4373	10	AK311166	AK311166 Mus muscu	c1079	91.5	6.8	2505	6	BD095935	BD095935 FEN-1 end
C1006	92.5	6.9	5956	9	AB058752	AB058752 Homo sapi	c1080	91.5	6.8	2511	6	AR309012	AR309012 Sequence
C1007	92.5	6.9	6245	1	AF202779	AF202779 Rhodobact	c1081	91.5	6.8	2511	6	AR317143	AR317143 Sequence
C1008	92.5	6.9	7282	1	AF548455	AF548455 Delftia a	c1082	91.5	6.8	2511	6	AR410362	AR410362 Sequence
C1009	92.5	6.9	11159	1	AE004919	AE004919 Pseudomon	c1083	91.5	6.8	2511	6	AR317241	AR317241 Sequence
C1010	92.5	6.9	11267	1	AE004763	AE004763 Pseudomon	c1084	91.5	6.8	2511	6	AR698678	AR698678 Sequence
C1011	92.5	6.9	11791	1	AE015066	AE015066 Shigella	c1085	91.5	6.8	2511	6	BD095936	BD095936 FEN-1 end
C1012	92.5	6.9	14253	1	AY281354	AY281354 Unculture	c1086	91.5	6.8	2640	6	I40148	I40148 Sequence 30
C1013	92.5	6.9	3263	9	AL713889	AL713889 Human DNA	c1087	91.5	6.8	2653	6	AX544044	AX544044 Sequence
C1014	92.5	6.9	54184	9	AL713889	AL713889 Human DNA	c1088	91.5	6.8	2653	6	AX876185	AX876185 Sequence
C1015	92.5	6.9	110000	2	AC150103	Continuation (13 o	c1089	91.5	6.8	2653	6	BD155996	BD155996 Primer fo
C1016	92.5	6.9	150372	2	AC150103	AC150103 Gallus ga	c1090	91.5	6.8	2653	6	AX876185	AX876185 Sequence
C1017	92.5	6.9	189505	9	AC092138	AC092138 Homo sapi	c1091	91.5	6.8	2653	6	BD155996	BD155996 Primer fo
C1018	92.5	6.9	203050	1	AX470161	AX470161 Zebrafish	c1092	91.5	6.8	3221	1	TTHPOA	AR405900 Sequence
C1019	92.5	6.9	241270	2	AC118119	AC118119 Rattus no	c1093	91.5	6.8	3221	1	TTTPOA	AR405900 Sequence
C1020	92.5	6.9	250891	2	AC111916	AC111916 Rattus no	c1094	91.5	6.8	3488	8	AK101762	AK101762 Oryza sat
C1021	92.5	6.9	262530	2	AC111916	AC111916 Rattus no	c1095	91.5	6.8	5022	12	AF112365	AF112365 Streptomy
C1022	92.5	6.9	265693	2	AC122319	AC122319 Mus muscu	c1096	91.5	6.8	5260	1	AF090329	AF090329 Pseudomon
C1023	92.5	6.9	292309	1	AE016979	AE016979 Shigella	c1097	91.5	6.8	7324	1	AF090329	AF090329 Pseudomon
C1024	92.5	6.9	299450	1	AP006580	AP006580 Gloebact	c1098	91.5	6.8	9972	1	AE003913	AE003913 Xylella f
C1025	92.5	6.9	299925	1	AP005045	AP005045 Streptomy	c1099	91.5	6.8	10029	1	AE012481	AE012481 Xanthomon



1100	91.5	6.8	10029	1	AE012523	Xanthomon	1173	91	6.8	110000	1	AE000516_32	Continuation (33 o
c1101	91.5	6.8	10087	1	AE004058	Xylella f	1174	91	6.8	110000	1	AE016822_00	AE016822 Xylella f
1102	91.5	6.8	10189	1	AE004715	Pseudomon	c1175	91	6.8	110000	2	AP006494_7	Continuation (8 of
c1103	91.5	6.8	10426	1	AE004699	Pseudomon	1176	91	6.8	110000	2	AP006501_07	Continuation (8 of
1104	91.5	6.8	11160	1	AE0009150	Agrobacte	1177	91	6.8	110000	2	LMFLCHR31_08	Continuation (9 of
c1105	91.5	6.8	11252	1	AE0005760	Caulobact	c1178	91	6.8	138203	1	AV310323	Streptomy
1106	91.5	6.8	11258	1	AE011803	Xanthomon	1179	91	6.8	152881	10	AC124353	Mus muscu
1107	91.5	6.8	11665	1	AE0008115	Agrobacte	1180	91	6.8	168916	10	AC124373	Mus muscu
c1108	91.5	6.8	11786	1	AE0004927	Pseudomon	1181	91	6.8	174139	2	AC116700	Mus muscu
1109	91.5	6.8	12675	1	AE011822	Xanthomon	1182	91	6.8	178376	2	AC125512	Papio anu
1110	91.5	6.8	20021	1	AE0004730	Leishmani	1183	91	6.8	193798	2	AC145535	Lemur cat
1111	91.5	6.8	35335	3	AC016161	Pseudomon	c1184	91	6.8	196216	9	AC099343	Homo sapi
c1112	91.5	6.8	61450	8	AP006556	Oryza sat	1185	91	6.8	202555	9	AC034159	Homo sapi
c1113	91.5	6.8	76196	1	AY354515	Streptomy	c1186	91	6.8	255809	2	AC108312	Rattus no
c1114	91.5	6.8	101385	5	CNS0595BW	Streptomy	1187	91	6.8	272101	1	AE017302	Thermus t
c1115	91.5	6.8	140933	8	AP005063	Theraodon	c1188	91	6.8	299425	1	AP005037	Streptomy
1116	91.5	6.8	141166	10	AC122423	Mus muscu	c1189	91	6.8	299425	1	AP005049	Streptomy
c1117	91.5	6.8	156840	2	AC146810	Zea mays	c1190	91	6.8	29986	1	AE017240	Mycobacte
1118	91.5	6.8	158749	8	AY360394	Oryza sat	c1191	91	6.8	300550	1	AP005030	Streptomy
1119	91.5	6.8	160541	8	AP004458	Oryza sat	c1192	91	6.8	300900	1	AP005939	Bradyrhiz
c1120	91.5	6.8	160681	2	AC118586	Pan trogl	c1193	91	6.8	301482	1	AE016916	Chromobac
c1121	91.5	6.8	163194	3	LMFP214	Leishmani	1194	91	6.8	301995	1	AE016779	Pseudomon
1122	91.5	6.8	164901	8	AY360393	Oryza sat	c1195	91	6.8	303226	1	AE016774	Pseudomon
c1123	91.5	6.8	174714	9	AC025280	Homo sapi	1196	91	6.8	307050	1	EX294140	Pirellula
c1124	91.5	6.8	180623	9	AC092341	Homo sapi	c1197	91	6.8	323000	3	TBBCHR1A3	Trypanoso
1125	91.5	6.8	181161	2	AC092347	Homo sapi	c1198	91	6.8	346362	1	EX640439	Bordetell
c1126	91.5	6.8	196204	9	AC073957	Homo sapi	c1199	91	6.8	346510	1	AP003011	Bordetell
1127	91.5	6.8	226460	2	AC114157	Rattus no	1200	91	6.8	347894	1	EX640431	Bordetell
c1128	91.5	6.8	247592	9	US2111	Homo sapien	1201	91	6.8	348411	1	AP003007	Bordetell
1129	91.5	6.8	263875	2	AC094237	Rattus no	1202	91	6.8	348642	1	EX640446	Bordetell
c1130	91.5	6.8	270418	1	AE017303	Thermus t	1203	91	6.8	348676	1	EX640458	Mycobacte
c1131	91.5	6.8	299225	1	AP005043	Streptomy	1204	90.5	6.7	909	6	BD179555	Highly th
1132	91.5	6.8	300425	1	AP005044	Streptomy	1205	90.5	6.7	1668	8	AX105185	Thermus t
c1133	91.5	6.8	300817	1	AE016756	Escherich	1206	90.5	6.7	1755	6	BD180277	Oryza sat
1134	91.5	6.8	313800	1	SC0939114	Streptomy	1207	90.5	6.7	2377	1	AE108682	Highly th
1135	91.5	6.8	314100	1	SC0939106	Streptomy	c1208	90.5	6.7	2526	6	AX410471	Streptomy
1136	91.5	6.8	325483	1	AP005050	Streptomy	c1209	90.5	6.7	2526	6	AX410471	Streptomy
c1137	91.5	6.8	333500	1	AP003590	Nostoc sp	c1210	90.5	6.7	3034	10	AX122327	Sequence
1138	91	6.8	906	6	AR386351	Sequence	c1211	90.5	6.7	3065	6	AR262597	Mus muscu
c1139	91	6.8	1092	12	AY659078	Synthetic	c1212	90.5	6.7	3077	9	BC006278	Sequence
1140	91	6.8	1125	12	AY659078	Synthetic	c1213	90.5	6.7	3306	10	AB017609	Homo sapi
1141	91	6.8	1500	6	BD180484	Highly th	c1214	90.5	6.7	3337	6	E30802	Mus muscu
c1142	91	6.8	1509	6	AX751797	Sequence	c1215	90.5	6.7	3360	10	AB017608	Novel prote
1143	91	6.8	1906	6	E01303	cDNA encodi	c1216	90.5	6.7	3674	6	E30801	Novel prote
1144	91	6.8	2016	4	BOVMIS	Bovine Mue	c1217	90.5	6.7	3674	6	E30801	Novel prote
1145	91	6.8	2085	6	AX078521	Sequence	c1218	90.5	6.7	3680	10	BC017126	Mus muscu
c1146	91	6.8	2299	6	AX664177	Sequence	1219	90.5	6.7	4449	10	CGU29946	Cricetulus
1147	91	6.8	2749	6	CQ767748	Sequence	c1220	90.5	6.7	5054	1	AF042276	Pseudomon
1148	91	6.8	2749	6	AR252737	Sequence	c1221	90.5	6.7	5054	1	AX105316	Sequence
1149	91	6.8	2749	6	AX403629	Sequence	c1222	90.5	6.7	8775	3	AY061650	Toxoplas
1150	91	6.8	2749	6	AX454474	Sequence	1223	90.5	6.7	10029	1	AE012488	Xanthomon
1151	91	6.8	2749	6	AX464252	Sequence	1224	90.5	6.7	10312	1	AE009781	Pyrabacul
1152	91	6.8	2749	6	AX490952	Sequence	c1225	90.5	6.7	10419	1	AE001865	Deinococ
1153	91	6.8	2749	9	AY358364	Homo sapi	c1226	90.5	6.7	10506	1	AE004806	Pseudomon
1154	91	6.8	2873	1	SHU41627	Homo sapi	1227	90.5	6.7	10761	1	AE014547	Bruceella
c1155	91	6.8	3456	1	RSP543650	Streptomyce	c1228	90.5	6.7	10963	1	AE011744	Xanthomon
1156	91	6.8	6175	1	AF064527	Rhodobact	c1229	90.5	6.7	11243	1	AE012067	Xanthomon
1157	91	6.8	7312	9	HUMCACL1G	Homo sapien	1230	90.5	6.7	12423	1	AE005155	Halobacte
1158	91	6.8	7417	9	HUMCACL1E	Homo sapien	c1231	90.5	6.7	12985	1	AE009710	Bruceella
1159	91	6.8	7499	9	HUMCACL1	Homo sapien	1232	90.5	6.7	13341	1	AE003964	Xylella f
1160	91	6.8	8940	9	HUMLVDCB	Homo sapien	c1233	90.5	6.7	14618	10	AF260753	Cricetulu
1161	91	6.8	10057	1	AE004871	Pseudomon	c1234	90.5	6.7	43514	9	AC005545	Homo sapi
c1162	91	6.8	10061	1	AE004314	Vibrio ch	1235	90.5	6.7	110000	2	LMFLCHR32_08	Continuation (9 of
1163	91	6.8	10429	1	AE0004875	Pseudomon	c1236	90.5	6.7	127952	8	OSJN00063_08	Continuation (9 of
1164	91	6.8	10518	1	AE012117	Xanthomon	1237	90.5	6.7	135638	1	AF484556	Oryza sat
1165	91	6.8	10895	1	AE004521	Pseudomon	c1238	90.5	6.7	156002	8	OSJN00050	Oryza sat
c1166	91	6.8	10950	1	AE012119	Xanthomon	c1239	90.5	6.7	158170	9	AC016757	Oryza sat
1167	91	6.8	10978	1	AE000490	Pseudomon	c1240	90.5	6.7	184631	2	AC141913	Rattus no
c1168	91	6.8	12031	1	AE0004648	Pseudomon	c1241	90.5	6.7	191762	10	AC107770	Rattus no
1169	91	6.8	12255	1	AE012255	Xanthomon	c1242	90.5	6.7	204050	1	AL646073	Ralstonia
1170	91	6.8	13138	1	AE012166	Xanthomon	c1243	90.5	6.7	210010	2	AC146135	Pan trogl
c1171	91	6.8	15446	1	AE000710	Aquifex a	1244	90.5	6.7	210614	1	AB088224	Streptomy
1172	91	6.8	110000	1	AE000516_31	Continuation (32 o	c1245	90.5	6.7	220622	2	AC118570	Lemur cat



1246	90.5	6.7	299800	1	AP005028	AP005028 Streptomy	cl319	90	6.7	225646	10	AC024915	AC024915 Mus muscu
1247	90.5	6.7	299800	1	AP005028	AP005028 Streptomy	1320	90	6.7	227773	10	AC034109	AC034109 Mus muscu
1248	90.5	6.7	308050	1	SC039124	AL939124 Streptomy	1321	90	6.7	230918	2	AC114190	AC114190 Rattus no
1249	90.5	6.7	340000	1	AP005274	AP005274 Coryneb	1322	90	6.7	242808	10	AC024069	AC024069 Mus muscu
1250	90.5	6.7	346274	1	EX640443	EX640443 Bordetell	cl323	90	6.7	249910	1	AE017307	AE017307 Thermus t
1251	90.5	6.7	346301	1	EX640432	EX640432 Bordetell	cl324	90	6.7	260860	2	AC125982	AC125982 Rattus no
1252	90.5	6.7	348014	1	EX640430	EX640430 Bordetell	cl325	90	6.7	273785	1	SME591793	AL591793 Sinorhizo
1253	90.5	6.7	348071	1	EX927148	EX927148 Coryneb	1326	90	6.7	298550	1	AP005047	AP005047 Streptomy
1254	90.5	6.7	348676	1	EX842581	EX842581 Mycobacte	cl327	90	6.7	300349	1	AE017319	AE017319 Desulfovi
1255	90.5	6.7	349876	1	EX640442	EX640442 Bordetell	cl328	90	6.7	303550	1	SC039118	AL939118 Streptomy
1256	90.5	6.7	349880	6	AX120085	AX120085 Sequence	cl329	90	6.7	308147	1	AE016915	AE016915 Chromobac
1257	90	6.7	934	1	AX1186970	AX1186970 Geothermo	cl330	90	6.7	308147	1	SME591792	AX1186970 Geothermo
1258	90	6.7	1069	6	AX452916	AX452916 Triticum	cl331	90	6.7	308147	1	SME591792	AX452916 Triticum
1259	90	6.7	1069	6	BT009567	BT009567 Triticum	cl332	90	6.7	308147	1	SME591792	BT009567 Triticum
1260	90	6.7	1176	1	AB014153	AB014153 Microbact	cl333	90	6.7	308147	1	SME591792	AB014153 Microbact
1261	90	6.7	1194	1	AB014944	AB014944 Rhodobact	cl334	90	6.7	308147	1	SME591792	AB014944 Rhodobact
1262	90	6.7	2016	6	AX653225	AX653225 Sequence	cl335	90	6.7	308147	1	SME591792	AX653225 Sequence
1263	90	6.7	2427	8	AF110494	AF110494 Neurospor	cl336	90	6.7	308147	1	SME591792	AF110494 Neurospor
1264	90	6.7	2451	8	AX640407	AX640407 Oryza sat	cl337	90	6.7	308147	1	SME591792	AX640407 Oryza sat
1265	90	6.7	2826	8	AX100795	AX100795 Oryza sat	cl338	90	6.7	308147	1	SME591792	AX100795 Oryza sat
1266	90	6.7	3115	1	AF225972	AF225972 Ralstonia	cl339	90	6.7	308147	1	SME591792	AF225972 Ralstonia
1267	90	6.7	3867	10	BC055076	BC055076 Mus muscu	cl340	90	6.7	308147	1	SME591792	BC055076 Mus muscu
1268	90	6.7	6676	1	AF031590	AF031590 Streptomy	cl341	90	6.7	308147	1	SME591792	AF031590 Streptomy
1269	90	6.7	8651	1	AY124589	AY124589 Agromyces	cl342	90	6.7	308147	1	SME591792	AY124589 Agromyces
1270	90	6.7	9427	1	AE011711	AE011711 Xanthomon	cl343	90	6.7	308147	1	SME591792	AE011711 Xanthomon
1271	90	6.7	9589	1	SC0001205	SC0001205 Streptomy	cl344	90	6.7	308147	1	SME591792	SC0001205 Streptomy
1272	90	6.7	10592	1	AE005729	AE005729 Caulobact	cl345	90	6.7	308147	1	SME591792	AE005729 Caulobact
1273	90	6.7	10901	1	AE012469	AE012469 Xanthomon	cl346	90	6.7	308147	1	SME591792	AE012469 Xanthomon
1274	90	6.7	11828	1	AF187159	AF187159 Methanosa	cl347	90	6.7	308147	1	SME591792	AF187159 Methanosa
1275	90	6.7	12198	1	AF187159	AF187159 Streptomy	cl348	90	6.7	308147	1	SME591792	AF187159 Streptomy
1276	90	6.7	12249	1	AE004632	AE004632 Pseudomon	cl349	90	6.7	308147	1	SME591792	AE004632 Pseudomon
1277	90	6.7	12372	1	AE004670	AE004670 Pseudomon	cl350	90	6.7	308147	1	SME591792	AE004670 Pseudomon
1278	90	6.7	15816	1	AB091692	AB091692 Sphingomo	cl351	90	6.7	308147	1	SME591792	AB091692 Sphingomo
1279	90	6.7	21931	1	AX149472	AX149472 Acinetoba	cl352	90	6.7	308147	1	SME591792	AX149472 Acinetoba
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Db	781	AGATC 786	
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LOCUS			
DEFINITION	913 bp mRNA linear PRI 30-JUN-2004		
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ACCESSION	BC023663.2	GI:40226187	
VERSION			
KEYWORDS			
SOURCE	MGC.		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 913)		
	Klausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G., Strausberg,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 913)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	On Dec 19, 2003 this sequence version replaced gi:23959051. Contact: MGC help desk		
	Email: <a href="mailto:cgapsb@mail.nih.gov">cgapsb@mail.nih.gov</a>		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),		
	Gaithersburg, Maryland;		
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>		
	Contact: <a href="mailto:nisc_mgc@nigr.nih.gov">nisc_mgc@nigr.nih.gov</a>		
	Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantiripop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Series: IRAL Plate: 39 Row: j Column: 6		
	This clone was selected for full length sequencing because it passed the following selection criteria: GenomesCan gene prediction, Similarity but not identity to protein.		
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 DEFINITION  
 ACCESSION BD222712  
 VERSION BD222712.1 GI:33032482  
 KEYWORDS JP 2002519030-A/58.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Yue, H., Patterson, C., Baughn, M.R., Akerblom, I.E., Young, J.A., Guegler, K.J., Reddy, R., Hillman, J.D. and Bandman, O.  
 Human signal peptide-containing protein  
 Patent: JP 2002519030-A 58 02-JUL-2002;  
 INCYTE PHARMACEUTICALS INC  
 OS Homo sapiens (human)  
 PN JP 2002519030-A/58  
 PD 02-JUL-2002  
 PF 25-JUN-1999 JP 2000557363  
 PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR  
 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI  
 LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,  
 PI MARIAN R BAUGHN, INGRID E AKERBLUM, JANICE AU YOUNG, HENRY YUE,  
 PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN  
 PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00,  
 PC A61P25/00,  
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RESULT 5  
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 ACCESSION AX201342  
 VERSION AX201342.1 GI:15391164  
 KEYWORDS  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 ASHENKAZI, A.J., GODDARD, A., GODOWSKI, P.J., GURNEY, A.L.,  
 HILLAN, K.J., MARSTERS, S.A., PAN, J., PITT, R.M., ROY, M.A., SMITH, V.,  
 STONE, D.M., WATANABE, C.K. and WOOD, W.I.



TITLE Compositions and methods for the treatment of tumour  
JOURNAL Patent: WO 0153486-A 21 26-JUL-2001;  
Genentech, Inc. (US)

FEATURES  
source

Location/Qualifiers  
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ORIGIN

Alignment Scores:  
Pred. No.: 6.4e-95 Length: 989  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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LOCUS AX697237  
DEFINITION Sequence 305 from Patent WO0078961.  
ACCESSION AX697237  
VERSION AX697237.1 GI:29498404  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Ferrarini, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 305 28-DEC-2000;  
Genentech Inc. (US)

TITLE

JOURNAL

FEATURES  
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ORIGIN

Alignment Scores:  
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DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x AX697237 (1-989)

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DEFINITION Sequence 1 from Patent WO0183719.  
ACCESSION AX338454  
VERSION AX338454.1 GI:18128893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Meyers, R.A. and Williamson, M.  
TITLE 25692, a novel human o-methyltransferase family member and uses thereof  
JOURNAL Patent: WO 0183719-A 1 08-NOV-2001;  
Millemmium Pharmaceuticals, Inc. (US)  
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ACCESSION BC047774  
VERSION BC047774.1 GI:28839536  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 1041)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Richards, S.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,  
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.  
TITLE Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 1041)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAR-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC help desk  
Email: gcgaps@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome



Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 Pred. No.: 6,78e-95 Length: 1041  
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 1  
 Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,  
 Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,  
 Nakamura, Y., Isogai, T. and Sugano, S.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 988)  
 Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,  
 Shibahara, T., Tanaka, T. and Nakamura, Y.  
 Direct Submission  
 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,  
 University of Tokyo, Laboratory of Genome Structure, Human Genome  
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
 (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
 Fax:81-3-5449-5416)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
 Research Association for Biotechnology; cDNA library construction;  
 5'- & 3'-end one pass sequencing; Department of Virology and Human  
 Genome Center, Institute of Medical Science, University of Tokyo  
 (partly supported by Science and Technology Agency!).  
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Tissue Procurement: Dr. Michael Brownstein	
cDNA Library Preparation: Michael Brownstein / Ted Udin	
Laboratory	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Genome Sequence Centre,	
BC Cancer Agency, Vancouver, BC, Canada	
<a href="mailto:info@bcgsc.bc.ca">info@bcgsc.bc.ca</a>	
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,	
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth	
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,	
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,	
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,	
Parvaneh Saedi, JR Santos, Angelique Schnerch, Ursula Skalska,	
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Clone distribution: MGC clone distribution information can be found	
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source	



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Db	694	CAGCCTCAGCCCAAGAACAGACTGTTGAATGTGTGCGGAACCTGAACGACGATCCTG	753
Qy	241	ArgaspVallArgValTrlSeLierleuProLeuGlyAspGlyLeuThrleuAlaPhe	260
Db	754	AGGAGACCCAGGGTCTACATCAGCCTCTGCCCTCGATGATGGCTCTCCTGGCCCTTT	813
Qy	261	Lysile 262	
Db	814	AAGATC 819	
RESULT 12			
AL390034/c			
LOCUS	AL390034	38679 bp DNA linear PRI 01-JAN-2002	
DEFINITION	Human DNA sequence from clone RP11-375G3 on chromosome 10, complete		
ACCESSION	AL390034	GI:18041549	
VERSION	AL390034.23		
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	Wray, P.		
AUTHORS	Direct Submission		
TITLE	Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxtton,		
JOURNAL	CambridgeShare, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk humquerry@sanger.ac.uk Clone request version replaced GI:18032099.		
COMMENT	On Jan 2, 2002 this sequence assembly data is compared from overlapping clones. During sequence assembly data is compared from overlapping clones. Where difference are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at <a href="http://www.sanger.ac.uk/projects/C_elegans/wormpep">http://www.sanger.ac.uk/projects/C_elegans/wormpep</a> This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr10">http://www.sanger.ac.uk/HGP/Chr10</a> RP11-375G3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <a href="http://www.chori.org/bacpac/home.htm">http://www.chori.org/bacpac/home.htm</a> VECTOR: pBACE3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-375G3 it may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-399K21 is at 36680 in this sequence. The true right end of clone RP11-487I5 is at 2000 in this sequence.		
FEATURES	Location/Qualifiers		



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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-375G3"
/clone_lib="RPC1-11.2"
29061..29121
misc_feature
/Note="Sequence from uni-directional dGTP big dye
terminator reads only."

ORIGIN
Alignment Scores:
Pred. No.:      8,97e-69      Length:      38679
Score:          1028.00      Matches:    261
Percent Similarity: 42.10%      Conservative: 0
Best Local Similarity: 42.10%      Mismatches: 1
Query Match:      76.55%      Indels:    259
DB:               9          Gaps:       6

US-10-017-407A-306 (1-262) x AL390034 (1-38679)

Qy      1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db      9448 ATGACCCAGCGGTGCCCCCGGCTCTCCGTGCCCGCGCTGGCCCTCGGCTCAGCCGCA 9389

Qy      21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db      9388 CTGGCGCGCGCTTCGCCCACTGGCCTCTTCCTGGGTGAGCAGGACCTGGTCCCGCGGGC 9329

Qy      31 ----- 31
Db      9328 GGGTGGCGGGCGCAGAGTAGGGCGCGGTGGCTCAGGTTAATCAACACCCCTCTCCCC 9269

Qy      32 ---- GlyArgArgCysProProTyrArgGlyArgGluGlnCysLeuLeuProGln 50
Db      9268 GTACAGCGCGCTGTGGCAGTATCTTCAGCGCTCCATGGGGAGCACCCGGCGGTGG 9149

Qy      70 gSerLeuArgLeu----- 74
Db      9148 AAGCCTGAGGTGGTCAGCAGGGCGCGGACGAAACGGGGTCCCTCTCGACCCCTCGC 9089

Qy      74 ----- 74
Db      9088 GGTCCCACTGGCTGTGTGA CTTGGGCTTGGGCCCTTGGCCCTTCCCTGGGCTTCGGGCTTC 9029

Qy      74 ----- 74
Db      9028 CTGGGCGGGTGGGTGGGTTCGAAAGGGCCAGTCCCCCAGGCCACGCCAGAACCG 8969

Qy      74 ----- 74
Db      8968 CGCCCTGGGCTTGGGACCCCGAGGGAAGTGGTGACTCGTCATGGCTGGTGCCACC 8909

Qy      75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetThrCysG1 89
Db      8908 CTCTCTTTACGCACTGACCTTGGAGCAGCCGCGAGGGGATTCATATGATGACCTGCGA 8849

Qy      89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuGlnAlaLysLysAlaLeuAspLe 109
Db      8848 CGAGGCCAGGCTCTTGGCCAACTGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCT 8789

Qy      109 u----- 109
Db      8788 GGGTAGGGGACGCGCGCGGATCCCGAGGGGCGAGGTTTCCGGGGCGACCCCACTCT 8729

Qy      110 -----GlyThrPheThrGlyTyrSerAlaLeuAla 120
Db      8728 GGGCTAGCCGCTGTGTCTGTGTCCTGGTCCAGGACCTTCACGGGCTACTTCGCGCCTGGGCC 8669

```

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Qy      120 euAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAlaAspAlaGlnProP 140
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Qy      140 roGluLeuGlyArgProLeuTyrArg----- 148
Db      8608 CGGAGCTGGGACGCGCCCTGTGGAGGAGGTGAGCGCCCGCGCTAGCTTCGACGCCCA 8549

Qy      149 -----GlnAlaGluAlaGluHisLysIleAsp 157
Db      8548 GCGGGGGCGCAACGGGTGACCCCGCTCCCTCGCAGCGCGGCGGAGGACCAAGATCGAC 8489

Qy      158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167
Db      8488 CTCCGGCTGAAGCCCGCTTCGAGACCTTGGGTAGCACCGAAGCGGAGGGCTTTGA 8430

Qy      167 ----- 167
Db      8429 AGCCATTCAATTGCAACGAGGCTGCTGTGTGGCCGAGCTGTGACTGGGCTTCGCGGGCAG 8370

Qy      167 ----- 167
Db      8369 GTTAAGGCGAGGGCGGCTTGTTCACAGAGCCCGGGCGCGCTGGGAGGGGCTTCAGGGCGC 8310

Qy      168 -----AspGluLeuLeuAla 172
Db      8309 CCGGGCGCGGACTCAGCCGACCTGCTCCCTCCCTCCCGCAAGACGAGCTGTGGCG 8250

Qy      173 AlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCysSer 192
Db      8249 CGGGCGAGGGCGGCACCTTCGAGTGGCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 8190

Qy      193 AlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArg 212
Db      8189 GCCTACTACGAGCGCTGCTGAGTCTGCTGAGTCTGCGAGCCCGAGGAGTCTCTCGCGTCTCAGA 8130

Qy      212 ----- 212
Db      8129 GTAAGGATCCACTGCTGGGGGAGGAGAACACCTGTCTGGGCGGGTCCCATCTTTTC 8070

Qy      212 ----- 212
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Qy      212 ----- 212
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Qy      212 ----- 212
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Qy      212 ----- 212
Db      7889 GAGACCCGCTCTCGTCTGGGACCTCCCTCCAAGACCCCGGCTCCCGCGCGGACCT 7830

Qy      212 ----- 212
Db      7829 CCCTCCAGTCCCGGCTTCGCGCGGAGCACCTCCCTCCGAGCCCGGCTCCCGCCCGG 7770

Qy      213 -----ValleuTyrArgGlyLysValLeuGlnProProLys 224
Db      7769 CCGGTTGGCCCGGCTCCCGCAGGTCTGTGGCGGGAGAGGTGTGCACTCCGAAA 7710

Qy      225 GlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArg 244
Db      7709 GGGGACGTGGGGCGGAGTGTGTGAAAACCTAAACGAAACGATCCGCGCGGAGCTCAGG 7650

Qy      245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db      7649 GTCTACATCAGCCTCTGCGCCCTGGCGATGGACTCACCTTTGGCTTCAAGATC 7596

```



RESULT 13

AC027393/c  
 LOCUS  
 DEFINITION Homo sapiens chromosome 10 clone RP11-770D23 map 10, WORKING DRAFT  
 AC027393  
 SEQUENCE, 28 unorderd pieces.  
 AC027393  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Brown,A., Burtett,G.,  
 Hovland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,  
 Melidrim,J., Meneus,L., Mirhova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Unpublished  
 2 (bases 1 to 169612)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Brown,A., Burtett,G.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,  
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burtett,G.,  
 Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczyk,J.,  
 Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,  
 Melidrim,J., Meneus,L., Mirhova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission  
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 169612)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Brown,A., Burtett,G.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,  
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burtett,G.,  
 Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczyk,J.,  
 Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,  
 Melidrim,J., Meneus,L., Mirhova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2000 this sequence version replaced gi:7652066.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L6572

Center clone name: 770 D.23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 155213 bases at least Q40

Consensus quality: 162022 bases at least Q30

Consensus quality: 164973 bases at least Q20

Insert size: 179000; agarose-fp

Insert size: 166912; sum-of-contigs

Quality coverage: 4.1 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently

consists of 28 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 1191: contig of 1191 bp in length

1192 1291: gap of 100 bp

1292 2404: contig of 1113 bp in length

2405 2504: gap of 100 bp

2505 3705: contig of 1201 bp in length

3706 3805: gap of 100 bp

3807 4734: contig of 929 bp in length

4735 4834: gap of 100 bp

4835 6570: contig of 1736 bp in length

6571 6570: gap of 100 bp

6571 8583: contig of 1913 bp in length

8584 8684: gap of 100 bp

8684 10290: contig of 1607 bp in length

10291 10391: gap of 100 bp

10391 11938: contig of 1548 bp in length

11939 12039: contig of 3801 bp in length

12039 15840 15939: gap of 100 bp

15840 19203: contig of 3264 bp in length

19204 19303: gap of 100 bp

19304 22581: contig of 3278 bp in length

22582 22681: gap of 100 bp

22682 24947: contig of 2266 bp in length

24948 25047: gap of 100 bp

25048 28167: contig of 3120 bp in length

28168 28267: gap of 100 bp

28268 32083: contig of 3816 bp in length

32084 32183: gap of 100 bp

32184 35333: contig of 3350 bp in length

35334 35634 35634: gap of 100 bp

35634 41517: contig of 5884 bp in length

41518 41617: gap of 100 bp

41618 47143: contig of 5526 bp in length

47144 47243: gap of 100 bp

47244 51694: contig of 4451 bp in length

51695 51794: gap of 100 bp

51795 57570: contig of 5776 bp in length

57571 57670: gap of 100 bp

57671 63190: contig of 5520 bp in length

63191 63290: gap of 100 bp

63291 70708: contig of 7418 bp in length

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86528 86628: gap of 100 bp

86628 99114: contig of 12487 bp in length

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Db 140839 GCCTACTACGAGCGCTGCTGCTGAGCTGTGGACCGGAGGCATCTCGCGTCTCTAGA 140780
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QY 212 ----- 212
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QY 212 ----- 212
Db 140659 CCGGGCTCCGGCCCGGTACCCAGGCTTCTCTCGCTTGTGTTCTGCTCCAGTCTGG 140600
QY 212 ----- 212
Db 140599 TCACCTCTGCGCGGCACCTCCCTCCGAGGCGCCGCTCCCGCCAGACACCTCCCTCC 140540
QY 212 ----- 212
Db 140539 GAGACCCCGCTTCGCTGCGGCACCTCCCTCCAGACCCGCTCCCGCGGGCACCT 140480
QY 212 ----- 212
Db 140479 CCCTCCAGTCCCGCTTCGCGCGGACCTCCCTCCGAAGCCCGCTCCACCGC 140420
QY 213 -----ValLeuTyrArgGlyIleValLeuGlnProProlys 224
Db 140419 CCGGTTGGCCCGCTCCCGCAGTCTCTGTGGCGGAGGTGCTGCAACCTCCGAA 140360
QY 225 GlyAspValAlaAlaGluCysValArgAenLeuAenGluArgIleArgAspValArg 244
Db 140359 GGGGAGCTGGCGCGCGAGTGTGGAAACCTTAACGAACGATCCGGGGGAGCTCAGG 140300
QY 245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheIle 262
Db 140299 GTCTACATCAGCTCTCTGCGCTCCGCGGATGGACTCACCTTGGCTTCAAGATC 140246

RESULT 14
AY294423_3/c
WPCOMMENT
Sequence split into 4 fragments LOCUS AY294423 Accession AY294423
Fragment Name Begin End
AY294423_0 1 110000
AY294423_1 100001 210000
AY294423_2 200001 310000
AY294423_3 300001 398888
Continuation (4 of 4) of AY294423 from base 300001 (AY294423 Mus musculus chromosome 17

Alignment Scores:
Pred. No.: 3 5e-56 Length: 89888
Score: 870.50 Matches: 223
Percent Similarity: 44.84% Conservative: 16
Best Local Similarity: 41.84% Mismatches: 23
Query Match: 64.82% Indels: 275
DB: 2 Gaps: 7

US-10-017-407A-306 (1-262) x AY294423_3 (1-89888)
QY 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20
Db 78332 ATGGCTCAGCCCGCTCCCTCGGCTATCTATCCAGCGCGACTGGCCCTGGGCTCGGCGCG 78273
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGly----- 32
Db 78272 CTGGGCGCGCCCTTCGCTACTGGTCTCTTCTGCTGGGTGAGCTGGGCTGGGCTGTCGATC 78213
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QY 33 -----ArgArgCys----- 35
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QY 36 -----ProProTyrArgGlyArgGlu 43
Db 78153 TGACTCGGCACCCCTCTCTCCCGGAGGAAACGGTGGCTCTCATGGGGGTCCAGGCGGCAA 78094
QY 44 GlnCysLeuLeuProProGluAspSerArgLeuTyrLeuLeuSerArgSerMet 63
Db 78093 GAGCGCTGCTGCGACCTAGGACAATCCCTCTGTGGCAGTATCTGCTGAGCGCTCCATG 78034
QY 64 ArgGluHisProAlaLeuArgSerLeuArgLeu----- 74
Db 78033 AGAGAGCACCCGCGCTGCGGAGCTGCGACTGTCAGTAGACTGGGACCGAGAACCG 77974
QY 74 ----- 74
Db 77973 CTCCCACTTCCAGCGTGTGGACCTCACGCTGGCTGTGTGACCTTGAGCTAGGCAGAAC 77914
QY 74 ----- 74
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QY 74 ----- 74
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Db 77733 GAAACAGGCCAGCTTCTGGCCACCTGCGCGGCTCATTAAGGCCAAGAAAGCTCTGGAT 77674
QY 109 Leu----- 109
Db 77673 CT-GGGTAGGAACACGACGACCATGCTCTGTGAAACACAGGGTCTACAGGGCAGCCCTGCAC 77615
QY 110 -----GlyThrPheThrGlyTyrSerAlaLeu 118
Db 77614 CTTGACCTGAGCTTGACAGTGTCCCTTCCACAGTACTTTCACGGGCTACTCGGCCCTG 77555
QY 119 AlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGln 138
Db 77554 GCCCTAGCTTGGCGCTTCCGAGGCTGGCGCGTGGTGTGACTGCGAGGTTGACGACAGAG 77495
QY 139 ProProGluLeuGlyArgProLeuTyrArg----- 148
Db 77494 CCCCCAAGCTGGGACGCGCCCATGTGGAA-GCAGGTGAGAGCCCCACACCTGCGGCCGTT 77436
QY 149 -----GlnAlaGluAlaGlu 153
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QY 154 HisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu----- 167
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QY 167 ----- 167
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QY 168 -----AspGluLeuLeu 171
Db 77256 GCTGAGACCTTAGCTCAGCCGCGCACATGCTCTCTGCTCTTAAGATGAGTCTCTTA 77197
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValValAspAlaAspLysGluAenCys 191
Db 77196 GCGGGCGCGAGCGCGAACTTTCACATAGTCCGCTGGTGGAGCGCGGACAAAGAACTGT 77137
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QY 192 SerAlaTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeu 211
Db 77136 ACCGCTACTAGCAGCGTGTCTGCAGCTCTACGTCCCGAGGCGTCTGCTGTACTC 77077
QY 212 Arg----- 212
Db 77076 AGAGTAAGGACTAGCTAAGGCAAAACTGCTGCTTCTGTGGGTGGGTACCCACTCTTCTC 77017
QY 212 ----- 212
Db 77016 AGCTTCTCCACCCACCCCGCCGCCCCCAAGCCACCCAGAGTATCATAGGTCC 76957
QY 212 ----- 212
Db 76956 CGCCCTCTGGCTAAGACTCTGGGTGGGTACCCCGCCACTTCCGACGCGCCGCCCTC 76897
QY 213 -----ValLeuTTPArgGlyLysValLeuGlnProProLysGlyAspValAlaAla 229
Db 76896 CATCTGTAGGTCTCTGTGGCGGAGAGTGTCTGCAGCTCAGCCCGAGCAAGACTGTT 76837
QY 230 GluCysValArgAsnLeuAsnGluArgIleArgAspValArgValTyrIleSerLeu 249
Db 76836 GAATGTGTGCGGAACCTGAACGACGATCTCTGAGGAGCGCCAGGCTCTACATCAGCCTC 76777
QY 250 LeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 76776 CTGCCCTGTGATGATGGCTCTCTCTGGCTTTAAGATC 76738

RESULT 15
LOCUS AC132590 161371 bp DNA linear ROD 01-JAN-2004
DEFINITION Mus musculus BAC clone RP24-273G1 from chromosome 14, complete
sequence.
ACCESSION AC132590
VERSION AC132590.3 GI:38564396
KEYWORDS HTG
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 161371)
AUTHORS Smeagen-Shahid, S., Shahid, S., Meyer, R. and Haglund, K.
TITLE The sequence of Mus musculus BAC clone RP24-273G1
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 161371)
AUTHORS Wilson, R.
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 161371)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 161371)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 161371)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 161371)
AUTHORS Wilson, R.
TITLE Direct Submission
JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Nov 27, 2003 this sequence version replaced gi:23683300.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
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Contact: submissions@watson.wustl.edu  
----- Summary Statistics  
Center project name: M\_BB0273G01  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

#### SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC129590.

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Job time : 3522 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 12, 2005, 21:38:38 ; Search time 2958 Seconds

(without alignments)

3227.589 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 32822875 seqs, 18219865908 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Database :

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2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1259	93.7	814	4	BM051236 AGENCOURT
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5	1188	88.5	921	2	BF664198 602145812
6	1186.5	88.3	772	2	BF796570 601592247
7	1181.5	88.0	1321	3	CR625911 full-length
8	1180	87.9	750	6	CR852718 UI-CF-FNO
9	1177	87.6	779	2	BF663695 602145414

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11	1156	86.1	919	3	AK007659
12	1156	86.1	2243	3	AK054334 Mus muscu
13	1126	83.8	910	6	BY707694
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us-10-017-407a-306.p2n.rst

Thu Jan 13 11:25:09 2005

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C 105	627	46.7	411	4	BM768965	BM768965 K-EST0052	178	559	41.6	581	5	CA353706	CA353706 625267 NC
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C 110	608	45.3	769	6	CA346219	CA346219 677059 NC	183	553.5	41.2	871	3	CR653669	CR653669 Tetraodon
C 111	605	45.0	539	2	BF769048	BF769048	184	553.5	41.2	878	3	CR653482	CR653482 Tetraodon
C 112	604	45.0	515	6	CF181537	CF181537 818378 MA	185	553	41.2	428	5	BY041621	BY041621
C 113	600	44.7	414	1	AI325680	AI325680 mm60d11.y	186	552.5	41.1	885	3	CR633632	CR633632 Tetraodon
C 114	598	44.5	402	6	CG95780	CG95780 359409 MA	187	551.5	41.1	1200	3	CR698066	CR698066 Tetraodon
C 115	598	44.5	499	4	BG95780	BG95780 359409 MA	188	551	41.0	569	5	BQ480163	BQ480163 faa86g07.
C 116	593	44.2	414	1	AI892364	AI892364 mm60d11.y	189	549.5	40.9	913	3	CR638711	CR638711 Tetraodon
C 117	592.5	44.1	1235	3	CR721460	CR721460 Tetraodon	190	547	40.7	1188	3	CR690884	CR690884 Tetraodon
C 118	592	44.1	507	4	BM129438	BM129438 if22d02.x	191	546.5	40.7	860	3	CR655148	CR655148 Tetraodon
C 119	591.5	44.0	1171	3	CR731130	CR731130 Tetraodon	192	546.5	40.7	861	3	CR634105	CR634105 Tetraodon
C 120	590	43.9	1232	3	CR646763	CR646763 Tetraodon	193	546.5	40.7	862	3	CR645383	CR645383 Tetraodon
C 121	590	43.9	1232	3	CR646763	CR646763 Tetraodon	194	546.5	40.7	1186	3	CR690706	CR690706 Tetraodon
C 122	589	43.9	881	6	CF250863	CF250863 esa018.a1	195	545.5	40.6	860	3	CR656656	CR656656 Tetraodon
C 123	588	43.8	1275	3	CR686979	CR686979 Tetraodon	196	545.5	40.6	863	3	CR651698	CR651698 Tetraodon
C 124	587	43.7	1133	3	CR640078	CR640078 Tetraodon	197	545.5	40.6	874	3	CR651698	CR651698 Tetraodon
C 125	586.5	43.7	1183	3	CR696893	CR696893 Tetraodon	198	545.5	40.6	876	3	CR649975	CR649975 Tetraodon
C 126	586.5	43.7	1194	3	CR725106	CR725106 Tetraodon	199	545.5	40.6	881	3	CR656653	CR656653 Tetraodon
C 127	584.5	43.5	1211	3	CR728184	CR728184 Tetraodon	200	544.5	40.5	862	3	CR650550	CR650550 Tetraodon
C 128	584	43.5	470	6	CA777819	CA777819 ip21g07.y	201	544.5	40.5	873	3	CR733986	CR733986 Tetraodon
C 129	584	43.5	747	6	CA388383	CA388383 670627 NC	202	544	40.5	454	5	BU500439	BU500439 AGENCOURT
C 130	582.5	43.4	1216	3	CR685301	CR685301 Tetraodon	203	542.5	40.4	864	3	CR653465	CR653465 Tetraodon
C 131	581.5	43.3	1238	3	CR682588	CR682588 Tetraodon	204	542.5	40.4	884	3	CR653782	CR653782 Tetraodon
C 132	581	43.3	1229	3	CR701700	CR701700 Tetraodon	205	542.5	40.4	904	3	CR639009	CR639009 Tetraodon
C 133	579.5	43.1	1224	3	CR662508	CR662508 Tetraodon	206	542.5	40.4	910	3	CR637704	CR637704 Tetraodon
C 134	579.5	43.1	1224	3	CR698208	CR698208 Tetraodon	207	542.5	40.4	924	3	CR655129	CR655129 Tetraodon
C 135	577	43.0	413	5	BY094423	BY094423 BY094423	208	542.5	40.4	1181	3	CR692840	CR692840 Tetraodon
C 136	577	43.0	487	7	CK819654	CK819654 if22d02.x	209	542	40.4	796	7	CF931709	CF931709 EST0141.A
C 137	576	42.9	528	1	AI548694	AI548694 UI-R-C3-t	210	542	40.4	905	4	BM439118	BM439118 Iplv0184
C 138	575	42.9	1292	3	CR681700	CR681700 Tetraodon	211	542	40.4	1211	3	CR698267	CR698267 Tetraodon
C 139	575	42.8	1218	3	CR687075	CR687075 Tetraodon	212	542	40.4	858	3	CR641707	CR641707 Tetraodon
C 140	575	42.8	1290	3	CR647544	CR647544 Tetraodon	213	541.5	40.3	863	3	CR637158	CR637158 Tetraodon
C 141	574.5	42.8	1144	3	CR700317	CR700317 Tetraodon	214	541.5	40.3	1189	3	CR734171	CR734171 Tetraodon
C 142	574	42.7	459	1	AI929284	AI929284 au9e03.x	215	541.5	40.3	555	4	BM154433	BM154433 fv85a10.y
C 143	573	42.7	582	4	BM574123	BM574123 fx59d04.y	216	541	40.3	555	4	BM186124	BM186124 fv98c04.y
C 144	572	42.6	458	6	CB739243	CB739243 AGNNUC:N	217	541	40.3	561	4	BM186124	BM186124 fv98c04.y
C 145	572	42.6	1226	3	CR683190	CR683190 Tetraodon	218	541	40.3	1188	3	CR698292	CR698292 Tetraodon
C 146	572	42.6	1245	3	CR685973	CR685973 Tetraodon	219	540.5	40.2	1263	3	CR727342	CR727342 Tetraodon
C 147	571.5	42.6	1156	3	CR660388	CR660388 Tetraodon	220	540	40.2	581	5	BQ783563	BQ783563 fab31c01.
C 148	571.5	42.6	1178	3	CR633873	CR633873 Tetraodon	221	539	40.1	720	6	CA360096	CA360096 633318 NC
C 149	571.5	42.6	1201	3	CR633873	CR633873 Tetraodon	222	539	40.1	375	2	BQ653217	BQ653217 UI-N-AMO-
C 150	571.5	42.6	1205	3	CR692309	CR692309 Tetraodon	223	538	40.1	756	4	BJ739050	BJ739050 BJ739050
C 151	571.5	42.6	1215	3	CR676419	CR676419 Tetraodon	224	538	40.1	764	4	BJ716953	BJ716953 BJ716953
C 152	571.5	42.6	1572	3	CR693937	CR693937 Tetraodon	225	537	40.0	553	4	BM186049	BM186049 fv97a10.y
C 153	571	42.5	453	1	AI969924	AI969924 wq77f05.x	226	537	40.0	868	7	CK406586	CK406586 AUF_Iflvr
C 154	570.5	42.5	1150	3	CR684437	CR684437 Tetraodon	227	537	40.0	869	7	CK409595	CK409595 AUF_Iflvr
C 155	570.5	42.5	1162	3	CR683289	CR683289 Tetraodon	228	537	40.0				



229 537 40.0 943 7 CK409493 AUF Iflvr  
 230 535 39.8 1215 3 CR726092 Tetraodon  
 231 532 39.6 688 6 CA350955 621897 NC  
 232 531.5 39.5 531.5 9 CG567423 OST193749  
 233 530 39.5 426 2 BR233897 140418 MA  
 234 529 39.4 479 2 AW251950 UI-R-BJO-  
 235 528 39.3 855 7 CN985363 58335 126  
 236 527 39.2 537 4 BM534699 fx70d07.Y  
 237 526 39.1 921 7 CK409380 AUF Iflvr  
 238 525 39.0 918 7 CK406607 AUF Iflvr  
 239 524 39.0 400 5 BY050241 BY050241  
 240 524 39.0 854 3 CR651708 Tetraodon  
 241 524 39.0 934 7 CK406893 AUF Iflvr  
 242 522 38.9 422 2 BF593185 7050a03.x  
 243 521 38.8 678 7 CN974704 23486 125  
 244 520 38.7 869 7 CN985211 57529 127  
 245 519 38.6 629 1 AU179577 AU179577  
 246 518 38.6 460 1 A1340993 qo82g09.x  
 247 518 38.6 614 1 AU180003 AU180003  
 248 518 38.6 896 7 CK407472 AUF Iflvr  
 249 512 38.1 645 2 AW299522 x840h01.x  
 250 512 38.1 421 4 BJ705610 BJ705610  
 251 512 38.1 660 4 BJ727162 BJ727162  
 252 511 38.0 902 7 CK409572 AUF Iflvr  
 253 511 38.0 956 7 CK406337 AUF Iflvr  
 254 509.5 37.9 491 4 BJ708514 BJ708514  
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 256 509 37.9 643 6 CB512007 ssalrgb53  
 257 509 37.9 722 5 BQ208081 UI-R-BJO-  
 258 509 37.9 837 6 C23373 C23373 Japa  
 259 508.5 37.9 1205 3 CR652934 Tetraodon  
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 263 503 37.5 612 4 B1304044 UI-R-BJO-  
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 265 495 36.9 415 1 A1340991 A1340991 qo82g07.x  
 266 495 36.9 638 4 B0711589 B0711589  
 267 494 36.8 905 7 CK407588 AUF Iflvr  
 268 492 36.6 670 6 CA355616 627543 NC  
 269 490 36.5 731 4 BJ722907 BJ722907  
 270 490 36.5 866 7 CN175149 AGENCOURT  
 271 489 36.4 587 7 CK896420 SGP158963  
 272 488 36.3 642 1 A1477552 fb58g04.Y  
 273 486 36.2 401 6 CB969899 AMGNNUC:N  
 274 485.5 36.2 527 5 BQ615750 fab14b01.  
 275 484 36.0 371 5 BY048974 BY048974  
 276 481 35.8 704 2 BF228537 BF228537  
 277 479 35.7 434 2 BB787832 BB787832  
 278 478 35.6 405 1 A1912836 tz86c05.x  
 279 477 35.5 374 5 BY037587 BY037587  
 280 477 35.5 579 7 CK895655 SGP158175  
 281 477 35.5 874 7 CN169125 AGENCOURT  
 282 476 35.4 513 5 BQ783421 fab29f02.  
 283 471.5 35.1 1206 3 CK641100 Tetraodon  
 284 471 35.1 360 5 BY057583 BY057583  
 285 470 35.0 746 7 CN988270 64067 125  
 286 468 34.8 436 2 AW251225 UI-R-BJO-  
 287 464 34.5 598 7 CK895107 SGP154357  
 288 463 34.5 661 4 B1468189 EST00596  
 289 461 34.3 551 7 CK896911 SGP159468  
 290 459.5 34.2 1211 3 CN683715 Tetraodon  
 291 458 34.1 372 5 BY042000 BY042000  
 292 457.5 34.1 812 7 C0804908 K-EST0139  
 293 454 33.8 292 4 BM856156 K-EST0139  
 294 453.5 33.8 644 6 CA333572 haa85h10.  
 295 451 33.7 503 4 BQ669239 BQ669239  
 296 450 33.6 373 5 BY041991 BY041991  
 297 451 33.6 963 7 CK409756 AUF Iphdk  
 298 445 33.1 423 2 AW252701 UI-R-BJO-  
 299 445 33.1 473 6 CA395926 c870g11.Y  
 300 444 33.1 600 6 C23352 C23352 Japa  
 301 444 33.1 469 4 B010311 B010311

302 444 33.1 566 7 CK885643  
 303 444 33.0 781 5 BU296625 SGP166021  
 304 443 33.0 362 5 BY045218 BU296625  
 305 441 32.8 344 6 BY057551 BU296625  
 306 441 32.8 543 6 C23048 C23048  
 307 438 32.6 370 1 A1341293 A1341293  
 308 437.5 32.6 917 7 CK406909 AUF Iflvr  
 309 436 32.5 808 7 CN977279 27484 125  
 310 434 32.3 336 5 BY048400 BY048400  
 311 433 32.2 413 2 AW252346 UI-R-BJO-  
 312 432 32.2 499 1 AL919863 AL919863  
 313 431 32.1 613 7 CK896516 SGP159062  
 314 430 32.0 298 2 AW664650 hi84b01.x  
 315 427 31.8 610 7 CK896728 SGP159280  
 316 426 31.7 411 2 AW251159 UI-R-BJO-  
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 318 420 31.3 598 7 CK895980 SGP158514  
 319 420 31.3 847 7 CN175403 AGENCOURT  
 320 419 31.2 616 3 CR647326 Tetraodon  
 321 419 31.2 937 6 CA458592 AGENCOURT  
 322 416.5 31.0 671 5 BX864474 BX864474  
 323 416 31.0 737 2 AW012934 Ldt-0102  
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 325 409.5 30.5 720 7 CN989253 65281 125  
 326 408 30.4 416 5 BQ479917 faa84a07.  
 327 408 30.4 439 5 BY447416 BY447416  
 328 407.5 30.3 766 5 BU010720 QGJ14E17.  
 329 407 30.3 539 6 CA333551 haa85c09.  
 330 406 30.2 526 5 BY468703 BY468703  
 331 404 30.1 351 5 BY085557 BY085557  
 332 404 30.1 808 7 CN991683 68533 125  
 333 403 30.0 406 4 B1288752 UI-R-DKO-  
 334 403 30.0 599 1 A1981881 pat.pk006  
 335 403 30.0 635 7 CN984292 53247 126  
 336 401.5 29.9 753 6 CA782445 sat28h08.  
 337 401 29.9 243 4 B1832844 B1832844  
 338 401 29.9 878 7 CO366616 RTKJ\_29\_A  
 339 399 29.7 362 2 BF509580 UI-H-B14-  
 340 399 29.7 882 7 CK605765 gmrhRW6-  
 341 398 29.6 1045 3 CN50A6FG Arabidops  
 342 397 29.6 341 1 A1650609 wbo1f04.x  
 343 397 29.6 857 7 CN172476 AGENCOURT  
 344 396.5 29.5 779 4 BQ647257 EST050886  
 345 396 29.5 826 7 CK189143 EST778458  
 346 396 29.5 866 6 CB650869 OSUNEB15J  
 347 396 29.5 873 7 CK189144 EST778459  
 348 395 29.4 365 6 CB050636 NISC 9118  
 349 395 29.4 365 6 CB050637 NISC\_9118  
 350 395 29.4 635 6 C23181 C23181  
 351 394.5 29.4 720 7 CO532807 CO532807  
 352 394 29.3 398 4 BM573972 fx57d11.Y  
 353 394 29.3 593 7 CK888688 SGP160680  
 354 394 29.3 1064 7 CK163121 FGAS01573  
 355 393 29.3 683 2 BB594747 BB594747  
 356 392.5 29.2 818 6 CF203341 RR890915N  
 357 392 29.2 419 7 CN542838 UI-R-EAO-  
 358 392 29.2 465 4 BJ498661 BJ498661  
 359 392 29.2 499 4 BJ527812 BJ527812  
 360 392 29.2 515 4 BJ490344 BJ490344  
 361 392 29.2 562 4 BJ496988 BJ496988  
 362 391.5 29.2 833 6 CF215293 CF215293  
 363 391.5 29.2 924 7 CF652643 CAP0004\_I  
 364 391.5 29.2 942 7 CF516928 CAP0004\_I  
 365 391.5 29.2 1003 3 CN50A315 Arabidops  
 366 391.5 29.2 1024 5 BY398556 BY398556  
 367 391 29.1 370 5 BY398556 BY398556  
 368 390.5 29.1 810 6 CF213611 CGF100079  
 369 390 29.0 488 6 CD737778 CD737778  
 370 390 29.0 658 4 BJ510111 BJ510111  
 371 390 29.0 712 7 CN975952 25862 125  
 372 389.5 29.0 789 4 B1308775 EST0530185  
 373 389 29.0 388 5 BY405666 BY405666  
 374 389 29.0 505 7 CK895885 SGP158415

375 389 29.0 505 7 CK895885 SGP158415



C 375	388.5	28.9	655	7	CF626673	CF626673 ZMRW05_0	448	368.5	27.4	649	6	CB870888	CB870888 HCL5J04W
376	388.5	28.9	780	5	BQ752940	BQ752940 WHE4120_H	449	368.5	27.4	749	7	CF833684	CF833684 GEOL15_E
377	388.5	28.9	907	2	BE412589	BE412589 MCG002_C1	450	368.5	27.4	750	7	CF0198619	CF0198619 GEOL15_E
C 378	387.5	28.9	668	4	BM072891	BM072891 MEST55-D0	C 451	368.5	27.4	788	4	BI9711175	BI9711175 CAP0004_I
C 379	387.5	28.9	785	6	CB346952	CB346952 CAB28G000	C 452	368.5	27.4	819	7	CF517012	CF517012 CAP0004_I
C 380	387	28.8	648	4	BU024113	BU024113 BJ024113	C 453	368.5	27.4	830	7	CF838016	CF838016 OGLA080TV
C 381	387	28.8	1126	7	CK211108	CK211108 FGAS02294	C 454	368.5	27.4	899	9	CG297599	CG297599 OGLA080TV
C 382	386.5	28.8	808	6	CA917180	CA917180 EST641327	C 455	368	27.4	546	7	CK896580	CK896580 SGP159129
C 383	386.5	28.8	896	6	CF215012	CF215012 CAST0001	C 456	367.5	27.4	798	7	CO533605	CO533605 3530_1_22
C 384	386	28.7	264	2	AW477994	AW477994 18030_MAR	C 457	367.5	27.4	754	5	BO991252	BO991252 QGF22F21
C 385	386	28.7	854	3	CO363617	CO363617 RTKL10_G	C 458	367	27.3	357	5	BY406134	BY406134 BY406134
C 386	386	28.7	1146	3	AY104406	AY104406 Zea may	C 459	367	27.3	540	6	CB23049	CB23049 C23049 Japa
C 387	385.5	28.7	769	6	CA784719	CA784719 sat88a11	C 460	367	27.3	741	5	BX074245	BX074245 BX074245
C 388	385.5	28.7	1121	7	BQ752791	BQ752791 WHE4119_B	C 461	366.5	27.3	849	7	CK136380	CK136380 MM2_1_4_H
C 389	385	28.6	795	5	BQ752791	BQ752791 WHE4119_B	C 462	366	27.3	326	1	AK279840	AK279840 z89302_B
C 390	384.5	28.6	986	4	BG381333	BG381333 GC01_06D0	C 463	366	27.3	558	7	CK889558	CK889558 SGP161584
C 391	384	28.6	580	7	CK889037	CK889037 SGP161594	C 464	366	27.3	680	4	BG043486	BG043486 su33906_Y
C 392	384	28.6	582	7	CK889567	CK889567 SGP161594	C 465	365.5	27.2	708	6	CD878344	CD878344 AZO4_1021
C 393	384	28.6	822	7	CO364711	CO364711 RTKL_21_H	C 466	365.5	27.2	731	7	CN190617	CN190617 UCRCS06_0
C 394	383.5	28.6	816	2	BF064997	BF064997 HV_CEB002	C 467	365.5	27.2	1038	7	CK213384	CK213384 FGAS02529
C 395	383.5	28.6	900	7	CO488021	CO488021 GQ0255_B3	C 468	365	27.2	363	5	BY400948	BY400948 BY400948
C 396	382.5	28.5	787	7	CF838445	CF838445 UCRCS03_0	C 469	364.5	27.1	715	7	CK939864	CK939864 CGF100474
C 397	382.5	28.5	812	7	CF838788	CF838788 UCRCS03_0	C 470	364.5	27.1	817	7	CF831643	CF831643 UCRCS01_0
C 398	382.5	28.5	880	7	CN191185	CN191185 UCRCS06_0	C 471	364	27.1	386	5	BY394806	BY394806 BY394806
C 399	381.5	28.4	673	7	CF389114	CF389114 RTDR2_13	C 472	364	27.1	773	4	CG582119	CG582119 EST483858
C 400	381.5	28.4	780	2	AW624860	AW624860 EST313689	C 473	362.5	27.0	628	6	BE785237	BE785237 601474760
C 401	381.5	28.4	848	7	CN191778	CN191778 UCRCS06_0	C 474	362.5	27.0	612	7	CN009676	CN009676 WHE3861_E
C 402	381.5	28.4	860	7	CK933305	CK933305 CGF100428	C 475	362.5	27.0	1002	2	CF814191	CF814191 VDO009H02
C 403	381	28.4	449	1	AI132590	AI132590 Z020D02_I	C 476	361.5	26.9	528	7	CF833321	CF833321 UCRCS02_0
C 404	381	28.4	809	7	CO165036	CO165036 FLOD1_51_H	C 477	361.5	26.9	629	6	CK887538	CK887538 SGP164404
C 405	381	28.4	841	7	CO367905	CO367905 RTKL_37_A	C 478	361.5	26.9	645	8	BZ628759	BZ628759 ih62B02_G
C 406	380.5	28.3	673	5	BQ752785	BQ752785 WHE4119_B	C 479	361.5	26.9	607	7	CK439808	CK439808 GQ0021b_B
C 407	380.5	28.3	720	1	AI489305	AI489305 EST247644	C 480	361	26.9	658	1	AU267636	AU267636 AU267636
C 408	380.5	28.3	808	4	BM113258	BM113258 IN	C 481	361	26.9	664	1	AU261652	AU261652 AU261652
C 409	380.5	28.3	841	9	CG847727	CG847727 ZMMBB031	C 482	361	26.9	720	6	CA172879	CA172879 SCUTB103
C 410	380.5	28.3	856	7	CO117389	CO117389 GR_EB01C	C 483	361	26.9	799	7	CN010817	CN010817 WHE3876_E
C 411	380.5	28.3	1072	3	AY108449	AY108449 Zea may	C 484	361	26.9	789	7	CF833321	CF833321 UCRCS02_0
C 412	380.5	28.3	757	5	BQ871360	BQ871360 QG11J23	C 485	360.5	26.8	730	7	CF636603	CF636603 ZMRW00_0
C 413	380	28.3	833	7	CK934159	CK934159 CGF100454	C 486	360.5	26.8	867	7	CO239360	CO239360 WSO0725_B
C 414	379.5	28.3	854	4	AI422985	AI422985 EST705443	C 487	360.5	26.8	911	7	CO239360	CO239360 WSO0725_B
C 415	379.5	28.3	854	4	AI422985	AI422985 EST705443	C 488	360	26.8	1054	4	BJ543510	BJ543510 FGAS02510
C 416	379	28.2	360	1	AA279903	AA279903 SGP159460	C 489	360	26.8	635	5	BU044203	BU044203 PP_LBA001
C 417	378.5	28.2	696	4	BG935676	BG935676 SL1_1037	C 490	359.5	26.8	744	7	CF838018	CF838018 UCRCS03_0
C 418	378.5	28.2	775	6	CD576142	CD576142 UCRPT01_0	C 491	359.5	26.8	752	7	CO172079	CO172079 ND11_27_B
C 419	378.5	28.2	919	7	CK259365	CK259365 EST705443	C 492	359.5	26.8	829	4	BG323539	BG323539 60242001
C 420	378.5	28.2	949	7	CK259366	CK259366 EST705443	C 493	359.5	26.8	829	4	BG323539	BG323539 60242001
C 421	378	28.1	436	7	CK896903	CK896903 SGP159460	C 494	359	26.7	756	6	CB650397	CB650397 OSUNED14N
C 422	378	28.1	930	7	CK270847	CK270847 EST716925	C 495	359	26.7	799	7	CF589246	CF589246 EST00H03
C 423	378	28.1	976	3	AY104670	AY104670 Zea may	C 496	359	26.7	799	7	CF589246	CF589246 EST00H03
C 424	377.5	28.1	840	7	CN191650	CN191650 UCRCS06_0	C 497	359	26.7	621	2	AW306951	AW306951 SF50H03_Y
C 425	377.5	28.1	1088	4	BG338516	BG338516 602436241	C 498	358.5	26.7	751	5	BQ986770	BQ986770 QGF10G12
C 426	377.5	28.1	1148	7	CK162427	CK162427 FGAS01502	C 499	358.5	26.7	704	7	CN549757	CN549757 GQ0244_B3
C 427	376.5	28.0	685	5	BX253301	BX253301 BX253301	C 500	357.5	26.6	407	5	BY395434	BY395434 BY395434
C 428	376	28.0	794	7	CK193235	CK193235 FGAS00164	C 501	357	26.6	588	1	AU261478	AU261478 AU261478
C 429	375.5	28.0	715	5	BP176249	BP176249 BP176249	C 502	357	26.6	734	2	BF519859	BF519859 EST457324
C 430	375	27.9	365	5	BY079881	BY079881 sd88q11_Y	C 503	357	26.6	734	2	BF519859	BF519859 EST457324
C 431	375	27.9	735	2	AW102461	AW102461 AJ792459	C 504	356.5	26.5	585	1	AI166541	AI166541 xyllem.est
C 432	375	27.9	762	1	AW792459	AW792459 AJ792459	C 505	356.5	26.5	648	1	AJ560061	AJ560061 AJ560061
C 433	374.5	27.9	677	7	CF806867	CF806867 psH016XM	C 506	356.5	26.5	665	8	BZ641948	BZ641948 OGRAMK72TM
C 434	374.5	27.9	685	4	BG450822	BG450822 NFQ93D04D	C 507	356.5	26.5	683	2	AW030189	AW030189 EST273444
C 435	374.5	27.9	802	6	CA917727	CA917727 EST61874	C 508	356.5	26.5	692	7	CF806637	CF806637 psH014XG
C 436	374.5	27.9	1100	7	CK161647	CK161647 FGAS01421	C 509	356.5	26.5	721	8	CF833360	CF833360 UCRCS02_0
C 437	374	27.8	857	7	CO367832	CO367832 RTKL_37_A	C 510	356.5	26.5	781	6	CH012959	CH012959 TDGAQ60TH
C 438	373.5	27.8	832	6	CF215096	CF215096 CAST0001	C 511	356.5	26.5	715	6	CH012959	CH012959 TDGAQ60TH
C 439	373.5	27.8	1138	7	CK163513	CK163513 FGAS01614	C 512	356	26.5	724	1	AU2666351	AU2666351 AU2666351
C 440	372	27.7	1142	7	CK162127	CK162127 FGAS01471	C 513	355.5	26.5	749	2	BF626523	BF626523 HVSWEA001
C 441	371	27.6	1052	7	CK210051	CK210051 FGAS02184	C 514	355.5	26.5	872	7	CO064791	CO064791 est_k_bre
C 442	370	27.6	371	5	BY404587	BY404587 BY404587	C 515	355.5	26.5	749	2	BF626523	BF626523 HVSWEA001
C 443	369.5	27.5	764	7	CO488866	CO488866 GQ0259_B3	C 516	354.5	26.4	802	6	CF470308	CF470308 RTDNT1_45
C 444	369.5	27.5	859	7	CN127238	CN127238 RHOH1_21	C 517	354	26.4	745	7	CF470308	CF470308 RTDNT1_45
C 445	369.5	27.5	868	7	CO083020	CO083020 GR_Ea470	C 518	353.5	26.3	739	5	BQ986844	BQ986844 QGF10J16
C 446	369	27.5	996	4	BG837909	BG837909 Zml0_09g1	C 519	353.5	26.3	747	1	AJ614420	AJ614420 AJ614420



521	353.5	26.3	775	7	CF390634	RTD2_20	CF390634	RTD2_20	594	344.5	25.7	695	6	CA090038	SCSGAM207
522	353.5	26.3	781	4	BM407902	EST582229	BM407902	EST582229	595	344.5	25.7	709	7	CN825707	LJPEST9F3
523	353.5	26.3	801	6	C23213	Japa	C23213	C23213	596	344.5	25.7	814	7	CK200458	CK200458
524	353.5	26.3	860	6	CB893812	EST646604	CB893812	EST646604	597	344.5	25.7	815	7	CO165535	PLD1_55_E
525	352.5	26.2	715	5	B0123287	EST608863	B0123287	EST608863	598	344.5	25.7	817	7	CO364800	RTK1_21_H
526	352.5	26.2	864	6	CB823986	EST_5210	CB823986	EST_5210	599	344.5	25.6	647	2	AW648499	EST726953
527	352	26.2	439	5	BY599654	BY599654	BY599654	BY599654	600	343.5	25.6	398	1	AA132529	ZO2002_18
528	352	26.2	686	5	BP184507	BP184507	BP184507	BP184507	601	343.5	25.6	563	4	BI308179	EST529589
529	352	26.2	774	9	CG694438	CGUJH61TH	CG694438	CGUJH61TH	602	343.5	25.6	615	6	CA246946	SCSGFL5C0
530	352	26.2	783	1	AJ787529	AJ787529	AJ787529	AJ787529	603	343.5	25.6	662	2	AW584279	N210278e
531	352	26.2	864	7	CK195971	FGAS00441	CK195971	FGAS00441	604	343.5	25.6	751	6	CD820878	BN25_040B
532	351.5	26.2	588	4	BM520677	sa197b12	BM520677	sa197b12	605	343.5	25.6	751	6	CD821098	BN25_040N
533	351.5	26.2	693	6	CA153085	SCSBR2202	CA153085	SCSBR2202	606	343.5	25.6	781	7	CF447177	EST683522
534	351.5	26.2	714	6	CD864630	AZ02_001G	CD864630	AZ02_001G	607	343.5	25.6	792	7	CO363528	RTK1_10_G
535	351.5	26.2	752	7	CN012179	WHE3893_E	CN012179	WHE3893_E	608	343.5	25.6	810	7	CK197247	FGAS00571
536	351.5	26.2	764	5	BQ804819	WHE3893_C	BQ804819	WHE3893_C	609	343.5	25.6	843	7	CO164960	FLD1_51_H
537	351	26.1	665	6	CD860328	TE_002B22	CD860328	TE_002B22	610	343	25.5	658	1	AJ805285	AJ805285
538	350.5	26.1	620	2	AW585897	EST717520	AW585897	EST717520	611	343	25.5	694	6	CD937240	OV_106G10
539	350.5	26.1	667	2	BF636068	NF069E08D	BF636068	NF069E08D	612	343	25.5	705	2	BE519617	HV_CEB001
540	350.5	26.1	697	2	BF634788	NF069G09D	BF634788	NF069G09D	613	343	25.5	807	2	BF065240	HV_CEB002
541	350.5	26.1	703	4	BI308339	EST529749	BI308339	EST529749	614	343	25.5	930	4	BI956791	HVSMEN000
542	350.5	26.1	795	5	BQ255166	MTWAE30TK	BQ255166	MTWAE30TK	615	343	25.5	1106	7	CK217545	FGAS02954
543	350.5	26.1	877	6	CA755835	BR0300290	CA755835	BR0300290	616	342.5	25.5	516	1	AU261400	AU261400
544	350.5	26.1	1078	4	BG338728	603436489	BG338728	603436489	617	342.5	25.5	571	2	BE803196	gr53all.y
545	349.5	26.0	590	4	BM660518	952039C01	BM660518	952039C01	618	342.5	25.5	649	2	BE216025	HV_CEB000
546	349.5	26.0	631	4	BG045213	sa239a10	BG045213	sa239a10	619	342.5	25.5	653	7	CO170754	NDL1_16_D
547	349.5	26.0	713	6	CD869948	AZ02_113A	CD869948	AZ02_113A	620	342.5	25.5	709	7	CO165605	FLD1_55_E
548	349.5	26.0	729	6	CD885596	G118_0010	CD885596	G118_0010	621	342.5	25.5	714	7	CN183738	UCRCS04_0
549	349.5	26.0	759	2	BF259495	HVSMEN001	BF259495	HVSMEN001	622	342.5	25.5	772	6	CF235114	PEAXT001
550	349.5	26.0	789	7	CK119117	214h16.p1	CK119117	214h16.p1	623	342	25.5	352	1	AI712475	UI-AFP1
551	349	26.0	553	5	BQ036499	SL5-0018	BQ036499	SL5-0018	624	342	25.5	584	1	AJ802385	AJ802385
552	349	26.0	711	6	CD873066	AZ02_122E	CD873066	AZ02_122E	625	342	25.5	652	4	BI960399	HVSMEN002
553	349	26.0	731	6	CD885623	G118_001P	CD885623	G118_001P	626	342	25.5	660	6	CA123437	SCMCLRL01
554	349	26.0	762	6	CB649583	OSJNEB13J	CB649583	OSJNEB13J	627	342	25.5	753	5	BQ518760	EST626175
555	348.5	25.9	605	4	BM660519	952039C01	BM660519	952039C01	628	342	25.5	837	3	CNS086PN	ARABIDOP8
556	348.5	25.9	689	4	BM654230	sa239a10	BM654230	sa239a10	629	341.5	25.4	665	5	BQ838311	WHE2909_A
557	348.5	25.9	693	1	AU270835	AU270835	AU270835	AU270835	630	341.5	25.4	666	4	BG453602	Q998F01L
558	348.5	25.9	717	4	BI434036	EST536797	BI434036	EST536797	631	341.5	25.4	669	2	BF474987	WHE2104_D
559	348.5	25.9	737	2	BE559087	HV_CEB002	BE559087	HV_CEB002	632	341.5	25.4	691	1	AJ501241	AJ501241
560	347.5	25.9	622	4	BG045242	sa239d08	BG045242	sa239d08	633	341.5	25.4	696	6	CD832570	UCRCS06_0
561	347.5	25.9	619	1	AI637136	603001A11	AI637136	603001A11	634	341.5	25.4	740	7	CN192131	CN192131
562	347.5	25.9	630	2	AW757356	8132c10.y	AW757356	8132c10.y	635	341.5	25.4	745	7	CF835276	UCRCS08_0
563	347.5	25.9	639	2	BE203346	EST403368	BE203346	EST403368	636	341.5	25.4	813	7	CK199240	FGAS000773
564	347.5	25.9	657	5	BQ624016	USDA-FP_0	BQ624016	USDA-FP_0	637	341.5	25.4	1141	7	CK210321	FGAS02212
565	347.5	25.9	676	2	BF642362	NF051D11	BF642362	NF051D11	638	341	25.4	746	7	CO520722	3530_1_13
566	347.5	25.9	686	2	AW584562	N210630e	AW584562	N210630e	639	341	25.4	780	7	CO528134	3530_1_18
567	347.5	25.9	728	2	AW75400	EST334465	AW75400	EST334465	640	341	25.4	809	7	CN138077	OX1_51_C0
568	347.5	25.9	752	6	CA918307	EST641054	CA918307	EST641054	641	340.5	25.4	646	6	CD864631	AZ02_001G
569	347.5	25.9	803	7	CF395282	RTD2_10	CF395282	RTD2_10	642	340.5	25.4	655	4	BI270143	NF052B07F
570	347	25.8	597	4	BJ505563	BJ505563	BJ505563	BJ505563	643	340.5	25.4	683	5	BQ146393	NF069F03F
571	347	25.8	697	2	BE216491	HV_CEB001	BE216491	HV_CEB001	644	340.5	25.4	689	6	CF233668	PEAXT0002
572	347	25.8	700	1	AL503249	AL503249	AL503249	AL503249	645	340.5	25.4	728	7	CF418067	USDA-FP_1
573	347	25.8	714	2	BE519891	HV_CEB002	BE519891	HV_CEB002	646	340.5	25.4	763	7	CK121692	202c15.p1
574	347	25.8	723	6	CB653598	OSNNEC04M	CB653598	OSNNEC04M	647	340.5	25.4	799	7	CF635242	zmrw00_0
575	347	25.8	880	4	BI950057	HVSMEN001	BI950057	HVSMEN001	648	340	25.3	816	3	CNS0A6LK	AX23743
576	346.5	25.8	630	4	BI960166	HVSMEN002	BI960166	HVSMEN002	649	340	25.3	915	6	CA213294	SCQGSB113
577	346.5	25.8	673	4	BN370604	EBT008_SO	BN370604	EBT008_SO	650	340	25.3	1080	7	CK213716	FGAS02562
578	346.5	25.8	692	6	CD866963	AZ02_1040	CD866963	AZ02_1040	651	339.5	25.3	627	6	CB910128	VVD174D02
579	346.5	25.8	694	2	BE214450	HV_CEB000	BE214450	HV_CEB000	652	339.5	25.3	658	7	CK240496	VRJ324177
580	346.5	25.8	708	6	CA836411	MCU007A06	CA836411	MCU007A06	653	339.5	25.3	676	4	BI263612	NF089A09P
581	346.5	25.8	804	2	BF624054	HVSMEN000	BF624054	HVSMEN000	654	339.5	25.3	721	5	BQ838009	WHE2905_E
582	346	25.8	429	5	BY412806	BY412806	BY412806	BY412806	655	339.5	25.3	802	9	CG615544	OGWDE123TV
583	346	25.8	732	6	CD939542	OV_113024	CD939542	OV_113024	656	339.5	25.3	807	2	BF259949	HVSMEN002
584	346	25.8	819	7	CK193277	FGAS00169	CK193277	FGAS00169	657	339	25.2	808	6	CD827397	BN25_067F
585	346	25.8	836	7	CK193388	FGAS00382	CK193388	FGAS00382	658	339	25.2	889	6	CA159865	SCUPR23C0
586	345.5	25.7	540	4	BG842718	MEST39-C0	BG842718	MEST39-C0	659	338.5	25.2	601	2	BE998051	EST429774
587	345.5	25.7	595	1	AI857214	603008D06	AI857214	603008D06	660	338.5	25.2	662	2	BE610562	B610562
588	345.5	25.7	622	2	BF005553	EST434051	BF005553	EST434051	661	338.5	25.2	666	4	BI265049	sq07h11.y
589	345.5	25.7	815	7	CO083019	GR_E4470	CO083019	GR_E4470	662	338.5	25.2	818	6	CD575294	UCRPT01_0
590	345	25.7	682	1	AJ612197	AJ612197	AJ612197	AJ612197	663	338	25.2	797	6	CD868553	AZ02_105E
591	345	25.7	706	2	BF625981	HVSMEN001	BF625981	HVSMEN001	664	337.5	25.1	548	4	BM527768	sa165f09
592	345	25.7	731	5	BQ752847	WHE4119_G	BQ752847	WHE4119_G	665	337.5	25.1	637	2	BF520898	EST458371
593	345	25.7	794	7	CO174177	NDL1_42_G	CO174177	NDL1_42_G	666	337.5	25.1	651	4	BI270050	NF003E10F



667	337.5	25.1	673	7	CN190619	CN190619	UCRCS06_0	740	331.5	24.7	681	5	BQ987553	BQ987553	QGF12119.
668	337.5	25.1	674	2	AW560150	AW560150	EST315198	741	331.5	24.7	683	2	AW030736	AW030736	EST273991
669	337.5	25.1	683	2	BF520049	BF520049	EST457517	742	331.5	24.7	683	2	BI922821	BI922821	EST542725
670	337.5	25.1	683	6	CD930335	CD930335	GR45.110P	743	331.5	24.7	714	6	CA918225	CA918225	EST642372
671	337.5	25.1	699	5	BQ624767	BQ624767	USDA-FP_0	744	331.5	24.7	726	5	BQ838107	BQ838107	WHE2906_F
672	337.5	25.1	718	6	CD938268	CD938268	OV.109I23	745	331.5	24.7	750	5	CF921444	CF921444	gmthrw3-
673	337.5	25.1	718	6	CD938289	CD938289	OV.109K04	746	331	24.6	606	2	BE021597	BE021597	gmthrw3-
674	337.5	25.1	746	6	CK215205	CK215205	FGAS02715	747	331	24.6	946	6	CA270677	CA270677	SCRULB206
675	337	25.1	629	6	CD478576	CD478576	eca01-14m	748	330.5	24.6	519	2	BF636493	BF636493	NF0880606
676	337	25.1	732	7	CF4338087	CF4338087	EST674432	749	330.5	24.6	596	2	BE403578	BE403578	WHE0434_C
677	337	25.1	739	5	BQ115361	BQ115361	EST600937	750	330.5	24.6	631	2	BF473218	BF473218	WHE0922_H
678	336.5	25.1	543	1	AI939180	AI939180	sc67h02_Y	751	330.5	24.6	652	7	CN192437	CN192437	UCRCS06_0
679	336.5	25.1	617	2	BE405650	BE405650	WHE1209_G	752	330.5	24.6	658	7	CF836276	CF836276	UCRCS03_0
680	336.5	25.1	618	2	BE801899	BE801899	sc70h08_Y	753	330.5	24.6	658	7	CN191414	CN191414	UCRCS06_0
681	336.5	25.1	653	4	BI957460	BI957460	HVSMEN000	754	330.5	24.6	731	1	AJ803420	AJ803420	AJ803420
682	336.5	25.1	704	6	CD817128	CD817128	BN20.040N	755	330.5	24.6	772	6	CD839679	CD839679	RFO2.116D
683	336.5	25.1	786	7	CK137489	CK137489	OX1_57_D0	756	330.5	24.6	1121	6	CA131093	CA131093	SCBFR106
684	336.5	25.1	797	7	CK193862	CK193862	FGAS00228	757	330	24.6	569	7	CK439809	CK439809	G00021b_B
685	336	25.0	442	7	CN967135	CN967135	14632_100	758	330	24.6	706	7	CF517412	CF517412	CAP0005_I
686	336	25.0	646	4	BJ466490	BJ466490	BJ466490	759	330	24.6	712	7	CF389766	CF389766	RTRW2_19
687	336	25.0	675	4	BM814917	BM814917	EST593011	760	330	24.6	712	7	CF473897	CF473897	RTRW3_21
688	336	25.0	733	5	BQ838231	BQ838231	WHE2908_A	761	330	24.6	718	7	CF478998	CF478998	RTRW2_19
689	336	25.0	733	5	CD989674	CD989674	G174.109L	762	330	24.6	747	7	CF396117	CF396117	RTRW2_19
690	336	25.0	776	5	BQ618942	BQ618942	RNOSEQLF0	763	329.5	24.5	562	2	BE205077	BE205077	EST397753
691	335.5	25.0	530	6	CB395923	CB395923	OSTR163G7	764	329.5	24.5	606	2	BE205077	BE205077	EST397753
692	335.5	25.0	559	2	AW102353	AW102353	sg86f04_Y	765	329.5	24.5	638	4	BI959367	BI959367	HVSMEN001
693	335.5	25.0	623	8	BK641943	BK641943	OGAMK72TC	766	329.5	24.5	651	1	AL504625	AL504625	AL504625
694	335.5	25.0	731	2	AW348485	AW348485	GM210002B	767	329.5	24.5	666	1	AL504625	AL504625	AL504625
695	335.5	25.0	737	2	AW348485	AW348485	GM210002B	768	329.5	24.5	672	2	AW442463	AW442463	EST5758025
696	335	24.9	747	7	CF474427	CF474427	RTRW2_20	769	329.5	24.5	684	4	BM110489	BM110489	GF-FV-P3C
697	335	24.9	747	7	CF478537	CF478537	RTRW3_20	770	329.5	24.5	693	2	BM284958	BM284958	GF-FV-P3C
698	335	24.9	747	7	CF478537	CF478537	RTRW3_20	771	329.5	24.5	693	2	BM284958	BM284958	GF-FV-P3C
699	334.5	24.9	531	4	BI426741	BI426741	sa6f5902	772	329	24.5	672	2	BF473981	BF473981	WHE0839_F
700	334.5	24.9	598	4	BI321639	BI321639	sa6f5902	773	329	24.5	640	2	AW218547	AW218547	EST303730
701	334.5	24.9	644	6	CD930761	CD930761	WHE2909_A	774	328.5	24.5	646	2	AW218547	AW218547	EST303730
702	334.5	24.9	646	5	BQ838318	BQ838318	WHE2909_A	775	328.5	24.5	646	2	AW218547	AW218547	EST303730
703	334.5	24.9	724	7	CF921036	CF921036	gmthrw3-	776	328.5	24.5	649	6	CF227474	CF227474	PLAD6D5D0
704	334	24.9	646	5	BI176248	BI176248	BP176248	777	328.5	24.5	655	4	BI960120	BI960120	HVSMEN002
705	334	24.9	659	1	AJ6515423	AJ6515423	AJ6515423	778	328.5	24.5	762	7	CO171539	CO171539	NDL1_22_C
706	334	24.9	661	4	BJ247474	BJ247474	BJ247474	779	328.5	24.5	797	7	CF833015	CF833015	UCRCS02_0
707	334	24.9	692	6	CD868552	CD868552	AZ02.109E	780	328.5	24.5	800	7	CF833320	CF833320	UCRCS02_0
708	333.5	24.8	630	4	BG449728	BG449728	NF007D111	781	328.5	24.5	859	6	CB823461	CB823461	EST_4685
709	333.5	24.8	632	2	BE325133	BE325133	SCBGR104	782	328.5	24.5	743	6	CA180815	CA180815	SCAST316
710	333.5	24.8	654	6	CA131555	CA131555	SCBGR104	783	328.5	24.5	621	5	BQ743179	BQ743179	WHE4101_C
711	333.5	24.8	662	2	BF597864	BF597864	su8c03_Y	784	327.5	24.4	623	6	CA821361	CA821361	RSN01405
712	333.5	24.8	682	2	BF641947	BF641947	NF011B121	785	327.5	24.4	635	1	AJ560090	AJ560090	AJ560090
713	333.5	24.8	684	5	BU875316	BU875316	V005C03_P	786	327.5	24.4	637	4	BI960118	BI960118	HVSMEN002
714	333.5	24.8	694	5	BU877332	BU877332	V032G08_P	787	327.5	24.4	654	6	CD839960	CD839960	SCSBAD108
715	333.5	24.8	699	1	AJ615461	AJ615461	AJ615461	788	327.5	24.4	721	6	CA196132	CA196132	SCSBAD108
716	333.5	24.8	709	5	CN184479	CN184479	UCRCS04_0	789	327.5	24.4	667	6	CF472622	CF472622	RTRW1_10
717	333.5	24.8	709	5	BO752659	BO752659	WHE4117_F	790	327	24.3	629	4	BI959561	BI959561	HVSMEN002
718	333.5	24.8	716	5	BU874994	BU874994	V001B12_P	791	327	24.3	636	6	CA020338	CA020338	HZ36A04R
719	333.5	24.8	722	5	BF630744	BF630744	HVSMEN001	792	326.5	24.3	637	5	BO623195	BO623195	USDA-FP_0
720	333.5	24.8	756	2	BF630744	BF630744	HVSMEN001	793	326.5	24.3	643	5	BU977235	BU977235	HALL1B05F
721	333	24.8	417	1	AI477667	AI477667	FD58904_X	794	326.5	24.3	648	4	BI959235	BI959235	HVSMEN001
722	333	24.8	664	5	BI184560	BI184560	BP184560	795	326.5	24.3	650	7	CK987645	CK987645	SP7-A3(P1
723	333	24.8	667	4	BI957447	BI957447	HVSMEN000	796	326.5	24.3	656	7	CK987645	CK987645	SP7-A3(P1
724	333	24.8	738	7	CK961883	CK961883	33001_In	797	326.5	24.3	675	7	CF932162	CF932162	P1-A3-REV
725	333	24.8	743	4	BJ252414	BJ252414	BJ252414	798	326.5	24.3	675	7	CF932162	CF932162	P1-A3-REV
726	333	24.8	766	7	CO173178	CO173178	NDL1_34_B	799	326.5	24.3	712	6	CD841037	CD841037	P1-A4_A_8
727	333	24.8	882	7	CN201625	CN201625	Tor1690_G	800	326.5	24.3	712	6	CD841037	CD841037	P1-A4_A_8
728	332.5	24.8	645	2	BF642662	BF642662	NF072H071	801	326.5	24.3	719	7	CF833209	CF833209	RFO2.121J
729	332.5	24.8	671	4	BM063898	BM063898	KS01060G0	802	326.5	24.3	774	6	CA065807	CA065807	RFO2.121J
730	332.5	24.8	725	6	CD823678	CD823678	BN25.049J	803	326.5	24.3	823	2	BF264389	BF264389	RFO2.117E
731	332.5	24.8	739	7	CN190771	CN190771	UCRCS06_0	804	326.5	24.3	1086	7	CK213734	CK213734	FGAS02564
732	332.5	24.8	807	7	CK932928	CK932928	CGF100434	805	326.5	24.3	336	5	BY398227	BY398227	BY398227
733	332.5	24.8	817	7	CK197926	CK197926	GF100434	806	326.5	24.3	360	5	CD899633	CD899633	G174.113A
734	332	24.7	208	2	BE853865	BE853865	UX220608_Y	807	326	24.3	366	5	CD899633	CD899633	G174.113A
735	332	24.7	511	7	CK197926	CK197926	GF100434	808	326	24.3	366	5	CD899633	CD899633	G174.113A
736	331.5	24.7	865	7	CO102007	CO102007	GR_EB002	809	326	24.3	817	7	CK194117	CK194117	FGA000253
737	331.5	24.7	649	6	CD879761	CD879761	sa82f01.	810	325.5	24.2	543	4	BI788368	BI788368	sa82f01.
738	331.5	24.7	665	1	AI898029	AI898029	AZ04.106E	811	325.5	24.2	574	4	BM731352	BM731352	sal70h05.
739	331.5	24.7	681	5	BQ875399	BQ875399	QGI8A03_Y	812	325.5	24.2	610	5	BQ467961	BQ467961	HR01H17F



813	325.5	24.2	624	6	CA021273	CA021273 HZ39J21r	886	319	23.8	853	2	BF256079	BF256079 HVSNEf000
814	325.5	24.2	630	7	CN010185	CN010185 WHE3867_G	887	318.5	23.7	549	4	BG155028	BG155028 sabb40b01.
815	325.5	24.2	647	7	B1960119	B1960119 HVSME002	888	318.5	23.7	570	6	CA279207	CA279207 SCBFLB209
816	325.5	24.2	660	7	CF418675	CF418675 USDA-FP_1	889	318.5	23.7	608	7	CK750439	CK750439 pam01-6ns
817	325.5	24.2	681	1	AV782400	AV782400 AV782400	890	318.5	23.7	609	4	BM065108	BM065108 KS01075A0
818	325.5	24.2	698	5	B0896211	B0896211 X037C08_P	891	318.5	23.7	623	4	BM111532	BM111532 EST559068
819	325.5	24.2	714	1	AJ778942	AJ778942 AJ778942	892	318.5	23.7	687	6	CA192398	CA192398 SCCGST3C0
820	325.5	24.2	734	9	CG327759	CG327759 OGF0308TH	893	318.5	23.7	694	4	B0261281	B0261281 BJC21281
821	325.5	24.2	788	7	CF669731	CF669731 RCMNT1_45	894	318.5	23.7	745	6	CA918812	CA918812 EST636530
822	325.5	24.2	684	6	CA142702	CA142702 SCTCNT1_45	895	318.5	23.7	753	7	CF436915	CF436915 EST673260
823	325.5	24.2	757	7	CF395287	CF395287 RTD82_10	896	318.5	23.7	856	7	CK202105	CK202105 FGAS01062
824	324.5	24.2	557	2	BE404145	BE404145 WHE1201_G	897	318	23.7	695	5	BX252395	BX252395 BX252395
825	324.5	24.2	591	5	B0753204	B0753204 WHE4124_C	898	318	23.7	720	6	CA221618	CA221618 SCSGFLA03
826	324.5	24.2	624	5	B0744417	B0744417 WHE4115_D	899	318	23.7	787	5	B0515541	B0515541 EST622956
827	324.5	24.2	627	5	B0788936	B0788936 WHE4155_E	900	317.5	23.6	510	2	AW424002	AW424002 sh59c10.Y
828	324.5	24.2	628	5	B0744183	B0744183 WHE4112_F	901	317.5	23.6	711	5	BQ139680	BQ139680 NF023A10P
829	324.5	24.2	664	6	CD079415	CD079415 MA3-9999U	902	317.5	23.6	720	7	CF921163	CF921163 gmrbw3
830	324.5	24.2	680	4	B1179085	B1179085 EST520030	903	317.5	23.6	756	6	CD849237	CD849237 DHOAC017Z
831	324.5	24.2	694	4	BG646445	BG646445 EST508064	904	317	23.6	468	7	CK895492	CK895492 SGP158009
832	324.5	24.2	707	4	BG587428	BG587428 EST489200	905	317	23.6	605	6	CA155532	CA155532 SCACR2310
833	324.5	24.2	719	7	CN146340	CN146340 WOUND1_39	906	317	23.6	663	6	CA280962	CA280962 SCRFSD101
834	324	24.1	588	2	BE493850	BE493850 WHE1276_H	907	317	23.6	681	4	BM267355	BM267355 MEST365-F
835	324	24.1	624	5	BP184421	BP184421 BP184421	908	317	23.6	893	4	BI952091	BI952091 HVSME000
836	324	24.1	640	5	B0743388	B0743388 WHE4103_D	909	316.5	23.6	515	7	CK864045	CK864045 35355_In
837	324	24.1	641	4	EM813932	EM813932 EST592025	910	316.5	23.6	559	2	BE802841	BE802841 sr45d12.Y
838	324	24.1	649	6	CA290596	CA290596 SCUTSD102	911	316.5	23.6	566	2	BE942838	BE942838 EST422417
839	324	24.1	791	3	CNS0AB15	BE18211 Arabidops	912	316.5	23.6	571	7	CN008321	CN008321 WHE2639_H
840	323.5	24.1	546	4	BG096397	BG096397 EST460916	913	316.5	23.6	578	2	AW695176	AW695176 NF092D12S
841	323.5	24.1	564	5	B0762327	B0762327 EBrco01_SQ	914	316.5	23.6	580	7	CNS17425	CNS17425 QO092_B3
842	323.5	24.1	669	6	CD073590	CD073590 MA3-000IU	915	316.5	23.6	590	2	BF006247	BF006247 EST434745
843	323.5	24.1	669	6	CF507287	CF507287 USDA-FP_1	916	316.5	23.6	595	6	CF092647	CF092647 QHNT1F02
844	323.5	24.1	709	6	CA146291	CA146291 SCVPRT307	917	316.5	23.6	598	2	BE124003	BE124003 EST394128
845	323.5	24.1	796	2	BE034896	BE034896 ML05H01_M	918	316.5	23.6	637	5	BQ765794	BQ765794 EBrco03_SQ
846	323.5	24.1	846	7	CK195394	CK195394 FGAS00383	919	316.5	23.6	643	7	CF518411	CF518411 CAP0007_I
847	323	24.1	803	7	CK200685	CK200685 FGAS00920	920	316	23.5	669	6	CA187131	CA187131 SCUTST308
848	322.5	24.0	633	7	CF418893	CF418893 USDA-FP_1	921	316	23.5	691	1	AJ613139	AJ613139 AJ613139
849	322.5	24.0	674	7	CK739670	CK739670 USDA-FP_16	922	316	23.5	836	9	CG323590	CG323590 OGWI857TV
850	322.5	24.0	840	7	CO234257	CO234257 WS0261_B2	923	315.5	23.5	529	6	CF059783	CF059783 QCS16904.
851	322	24.0	640	6	CA191213	CA191213 SCCCT2C0	924	315.5	23.5	536	2	AW980337	AW980337 EST391490
852	322	24.0	649	6	CD904272	CD904272 G356_112P	925	315.5	23.5	561	4	BM732615	BM732615 sal79d10.
853	322	24.0	716	4	BI960085	BI960085 HVSME002	926	315.5	23.5	631	2	AW776700	AW776700 EST335765
854	322	24.0	736	2	BF630555	BF630555 HVSNEB001	927	315.5	23.5	702	6	CA179873	CA179873 SCCGST200
855	322	24.0	807	7	CF443345	CF443345 EST679690	928	315	23.5	442	7	CN966263	CN966263 13760_100
856	321.5	23.9	647	7	CN012727	CN012727 WHE3952_B	929	315	23.5	660	5	BQ086305	BQ086305 WHE3577_C
857	321.5	23.9	686	7	CF833210	CF833210 UCRCS02_0	930	315	23.5	739	9	CG320079	CG320079 QGXD727TV
858	321.5	23.9	754	4	BG584701	BG584701 EST486462	931	315	23.5	852	9	CN013071	CN013071 WHE3956_D
859	321.5	23.9	770	4	BI967327	BI967327 GM830001B	932	315	23.5	880	9	CG229531	CG229531 QG3DO60TH
860	321	23.9	616	4	BE259369	BE259369 BJ259369	933	314.5	23.4	540	4	BG789661	BG789661 sae33e08.
861	321	23.9	678	6	CA071322	CA071322 SCACAM107	934	314.5	23.4	562	2	AW683492	AW683492 NF012H09L
862	321	23.9	737	7	CF397756	CF397756 RTD83_1_C	935	314.5	23.4	598	5	BU008292	BU008292 QGH7C13_Y
863	321	23.9	881	7	CK196097	CK196097 FGAS00454	936	314.5	23.4	616	5	BQ788665	BQ788665 WHE4152_E
864	320.5	23.9	637	7	CN189395	CN189395 UCRCS06_0	937	314.5	23.4	625	2	AW034347	AW034347 EST277918
865	320.5	23.9	643	2	AW695080	AW695080 NF091D1S	938	314.5	23.4	708	6	CF213537	CF213537 CGF100060
866	320.5	23.9	681	4	BI959659	BI959659 HVSME002	939	314.5	23.4	776	7	CN987035	CN987035 62721_125
867	320.5	23.9	744	4	BM408348	BM408348 EST582675	940	314	23.4	684	2	BF627066	BF627066 HVSMEB000
868	320.5	23.9	904	2	BF972265	BF972265 602240747	941	313.5	23.3	472	5	BQ460884	BQ460884 HE01017r
869	320	23.8	712	5	BU672830	BU672830 NL_6_90_D	942	313.5	23.3	573	2	BE998050	BE998050 EST429773
870	320	23.8	770	3	CN050A83	CN050A83 Arabidops	943	313.5	23.3	605	5	BQ970451	BQ970451 QHB42B22.
871	320	23.8	835	4	BM407184	BM407184 EST581511	944	313.5	23.3	612	5	BQ699842	BQ699842 NXRVL22_D
872	319.5	23.8	605	1	AI486500	AI486500 EST244821	945	313.5	23.3	635	5	BU888753	BU888753 P012B02_P
873	319.5	23.8	662	6	CA916813	CA916813 EST640960	946	313	23.3	486	3	CK640865	CK640865 Tetraodon
874	319.5	23.8	666	6	CB869763	CB869763 NF12G06V	947	313	23.3	702	4	BI073165	BI073165 PIP2A_F04
875	319.5	23.8	670	4	BG455746	BG455746 HFO66H01P	948	313	23.3	679	6	CA262688	CA262688 SCPTLB202
876	319.5	23.8	740	7	CN011226	CN011226 WHE3881_F	949	313	23.3	881	7	CK202172	CK202172 FGAS01069
877	319.5	23.8	748	5	BU635690	BU635690 O04G05_In	950	312.5	23.3	539	7	CO415038	CO415038 Mdfw2041m
878	319.5	23.8	789	5	BU894945	BU894945 X017B10_P	951	312.5	23.3	540	4	BI788174	BI788174 saeg7f01.
879	319	23.8	644	1	AI895091	AI895091 EST264534	952	312.5	23.3	545	2	AW620537	AW620537 sj06d09.Y
880	319	23.8	675	6	CA209393	CA209393 SCCGST3C1	953	312.5	23.3	577	5	BQ490451	BQ490451 24-E01178
881	319	23.8	684	1	AL821924	AL821924 AL821924	954	312.5	23.3	606	7	CF807049	CF807049 pBH019xK
882	319	23.8	711	4	BJ253542	BJ253542 BJ253542	955	312.5	23.3	656	2	BF650456	BF650456 NF097D11E
883	319	23.8	756	6	CB680447	CB680447 OSUNEF05C	956	312.5	23.3	670	5	BU816246	BU816246 N062C10_P
884	319	23.8	756	7	CF428636	CF428636 PH1_9_G09	957	312.5	23.3	676	6	CD817919	CD817919 BN20_043K
885	319	23.8	819	7	CN127149	CN127149 RHOH1_21_	958	312.5	23.3	704	5	BU814263	BU814263 N027B09_P



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959	312.5	23.3	706	6	CF233163	PLAJX0002	1032	305	22.7	646	7	CK860977	32005	IN
960	312.5	23.3	754	1	AJ806917	AJ806917	1033	305	22.7	713	6	AW221136	ECZFL404	
961	312.5	23.3	815	2	BE642551	Cr12_6_F2	1034	304.5	22.7	569	2	AW736350	SCST32269	
962	312.5	23.3	817	7	CK193931	FGAS00235	1035	304.5	22.7	594	2	CK319292	RTP09B04	
963	312.5	23.3	963	7	BG935465	SU1-0818	1036	304.5	22.7	745	5	CF397680	RF02_114A	
964	312	23.2	647	4	BJ264257	BJ264257	1037	304.5	22.7	768	6	CD839106	FGAS01030	
965	312	23.2	726	6	CA158055	CA158055	1038	304.5	22.7	831	7	CK201781	FGAS01030	
966	312	23.2	816	8	BZ541105	BZ541105	1039	304	22.6	302	2	BF605771	272357	MA
967	311.5	23.2	605	6	CA733178	CA733178	1040	304	22.6	592	4	BM660366	952037B06	
968	311.5	23.2	611	4	BL957501	BL957501	1041	304	22.6	622	6	CA182599	SCCST314	
969	311.5	23.2	622	7	CF395203	CF395203	1042	304	22.6	647	6	CA285613	SCSBHR105	
970	311	23.2	742	6	CA146092	CA146092	1043	304	22.6	661	6	CA107862	TALR1141H	
971	310.5	23.1	559	4	BI894075	BI894075	1044	304	22.6	677	4	BG905724	SCBGLR109	
972	310.5	23.1	608	7	CK318739	CK318739	1045	304	22.6	685	6	CA121225	SCBGLR109	
973	310.5	23.1	616	5	BQ139156	BQ139156	1046	303.5	22.6	511	7	CF603338	BACCA01_0	
974	310.5	23.1	624	7	CF411750	CF411750	1047	303.5	22.6	618	7	CF6010871	WH3877_C	
975	310.5	23.1	638	4	BI957710	BI957710	1048	303.5	22.6	632	1	AI486948	WET245270	
976	310.5	23.1	650	2	BF646063	BF646063	1049	303.5	22.6	609	1	AU263882	AU263882	
977	310.5	23.1	735	5	BH835879	BH835879	1050	303	22.6	679	6	CD823836	BN25_050C	
978	310.5	23.1	756	7	CK215844	CK215844	1051	303	22.6	814	7	CK201094	FGAS00961	
979	310	23.1	447	7	CK879029	CK879029	1052	302.5	22.5	577	2	AW703717	SK23607.Y	
980	310	23.1	654	6	CK175542	CK175542	1053	302.5	22.5	588	1	AL808354	AL808354	
981	310	23.1	699	5	BK251392	BK251392	1054	302.5	22.5	659	6	CA089962	SCSGAM207	
982	310	23.1	802	2	BF261040	BF261040	1055	302	22.5	636	4	BJ259464	BJ259464	
983	309.5	23.0	505	4	BG835402	BG835402	1056	302	22.5	674	5	BK251216	BJ251216	
984	309.5	23.0	565	2	AW625126	AW625126	1057	302	22.5	675	5	BK254999	EX254999	
985	309.5	23.0	613	4	BI309404	BI309404	1058	302	22.5	689	5	EX250520	EX250520	
986	309.5	23.0	691	7	CN524624	CN524624	1059	302	22.5	692	6	CA142664	CA142664	
987	309.5	23.0	756	6	CD842250	CD842250	1060	302	22.5	784	6	CD840817	FGAS01088	
988	309.5	23.0	781	5	BH895541	BH895541	1061	302	22.5	814	7	CK203256	EST68670	
989	309	23.0	489	7	CF931812	CF931812	1062	302	22.4	548	1	AI899227	EST68670	
990	309	23.0	536	2	BF484161	BF484161	1063	301.5	22.4	588	1	AL822798	AL822798	
991	309	23.0	638	7	CK975309	CK975309	1064	301.5	22.4	543	5	BH800080	UW417B11	
992	309	23.0	718	6	CF972935	CF972935	1065	301.5	22.4	643	5	AW306980	8F51C05.Y	
993	308.5	23.0	507	7	CF972935	CF972935	1066	301	22.4	600	2	AW306980	8F51C05.Y	
994	308.5	23.0	585	2	AW690185	AW690185	1067	301	22.4	622	4	BM068669	BM068669	
995	308.5	23.0	712	7	CO361980	CO361980	1068	301	22.4	652	6	CA142587	CA142587	
996	308.5	23.0	759	6	CD879592	CD879592	1069	301	22.4	666	7	CO532808	CO532808	
997	308.5	23.0	772	6	CF233249	CF233249	1070	301	22.4	702	7	CO230270	CO230270	
998	308.5	23.0	834	7	CO489149	CO489149	1071	300.5	22.4	560	4	BM885724	BM885724	
999	308	22.9	520	1	AU164541	AU164541	1072	300.5	22.4	578	4	BM068669	BM068669	
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1001	307.5	22.9	535	5	BQ624278	BQ624278	1074	300.5	22.4	600	4	AA660318	AA660318	
1002	307.5	22.9	598	2	AW077192	AW077192	1075	300.5	22.4	636	7	CK606552	CK606552	
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1006	307.5	22.9	775	6	CD839277	CD839277	1079	300.5	22.4	800	5	BQ518761	BQ518761	
1007	307	22.9	606	6	CD895487	CD895487	1080	300	22.3	550	6	CA107671	CA107671	
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1009	306.5	22.8	534	2	AW287882	AW287882	1082	300	22.3	685	5	BU103556	BU103556	
1010	306.5	22.8	535	2	BE574803	BE574803	1083	300	22.3	685	5	BU103556	BU103556	
1011	306.5	22.8	580	1	AL827353	AL827353	1084	299.5	22.3	516	4	BM402624	BM402624	
1012	306.5	22.8	546	4	AU261430	AU261430	1085	299.5	22.3	551	1	AL828595	AL828595	
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1015	306.5	22.8	668	5	BH87057	BH87057	1088	299.5	22.3	627	4	BG299397	BG299397	
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1019	306	22.8	692	6	CA168805	CA168805	1092	298.5	22.2	534	1	AI443130	AI443130	
1020	306	22.8	698	1	AW803239	AW803239	1093	298.5	22.2	590	5	BU577914	BU577914	
1021	306	22.8	727	6	CA219139	CA219139	1094	298.5	22.2	600	9	CK180853	CK180853	
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c1105	298	724	4	BJ572947	1178	290.5	21.6	820	7	CF443771	EST680116
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1114	297	673	4	BN371957	1187	289	21.5	890	7	CO529747	3530.1.19
c1115	297	927	7	CO480346	1188	289	21.5	650	2	BF260414	BF260414
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1117	296.5	537	7	BE490625	1190	289	21.5	702	7	CN123933	RHOH1.D
1118	296.5	586	7	CF419317	1191	289	21.5	732	3	CNS0A750	Arabi00ps
1119	296.5	664	1	AL820289	1192	289	21.5	826	7	CN128942	RHOH1.32
1120	296.5	687	6	CD820187	1193	288.5	21.5	540	4	BI779178	EBR001.SQ
1121	296.5	834	7	CO369560	1194	288.5	21.5	559	1	AU263008	AU263008
1122	296	646	2	AW695899	c1195	288.5	21.5	636	6	CD932185	GR45.117C
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c1160	292	647	6	CD899626	1233	285.5	21.3	555	4	BM885163	sa195f106.
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Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN	Alignment Scores:	Length:	889
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	Best Local Similarity:	99.03%	1
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	DB:		
US-10-017-407A-306 (1-262) x BM051236 (1-889)			
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QY	21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProTrpArgGly	40	
DB	73 CTGGCGCGCGCTTCCGCACTGGCTCTTCTGGGGAGCGGTGCCCGCCATGGAGGC	132	
QY	41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuSer	60	
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DB	193 CGCTCCATCGGGAGCACCGCGCTGCGAGCGCTGCTGACCTGGAGCAGCG	252	
QY	81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100	
DB	253 CAGGGGATTTATGATGACCTGCGAGCAGCGCGAGCTTGTGGCAACTGGCGGCTC	312	
QY	101 IleGlnAlaGlyAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120	
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QY	221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg	240	
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QY	241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeu-Alaph	260	
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BM051236 814 bp mRNA linear EST 07-NOV-2001  
 RESULT 2  
 BM051236  
 LOCUS

DEFINITION

603634191F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:5424766 5', mRNA sequence.

ACCESSION BM051236

VERSION BM051236.1 GI:16780503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 814)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1886 row: e column: 23

High quality sequence stop: 811.

Location/Qualifiers

1. 814

/organism="Homo sapiens"

/mol type="mRNA"

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/tissue\_type="normal pigmented retinal epithelium"

/lab\_host="NIH MGC\_43"

/notes="Organ: eye; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

FEATURES

source

1. 814

Location/Qualifiers

1. 814

Location/Qualifiers

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Location/Qualifiers

1. 814



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QY 163 AlaLeuGluThrLeuAspGluLeuLeuAlaGly-GluAla-GlyThrPheAspValA 182
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Db 664 CCTCGAAGGGGACGTGCGGCGCGAGTGTGTGCGAAACCTTAAACGACGCGATCCGGC 723

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QY 261 ysile 262
Db 784 AGATC 788

RESULT 3
LOCUS CR602194
DEFINITION full-length cDNA clone CS0D1073YH02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR602194
VERSION CR602194.1 GI:50483001
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1308)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
REMARK Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1308)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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FEATURES
source

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ORIGIN
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Best Local Similarity: 62.23% Mismatches: 0
Query Match: 91.44% Indels: 159
DB: 3 Gaps: 2

US-10-017-407A-306 (1-262) x CR602194 (1-1308)
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QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db 66 CTGGCGCGCGCTTCGCCCACTGGCCCTCTTCCTGGGTGAGCAGGACCTGGTCCCGGGGGC 125
QY 31 ----- 31
Db 126 GGGTGGCGGCGCAGAGTAGGGCGCGGTGGCTCAGGTTAATCCAACACCCCTCTCCCC 185
QY 32 ----GlyArgArgCysProTTPArgGlyArgArgGluGlnCysLeuLeuProProGln 50
Db 186 GTGAGGAGGCGGTGCCCCCATGCGCAGGCGCGGAGCAGTGCCTGCTTCCGCCCGCA 245
QY 50 uAspSerArgLeuTTPGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70
Db 246 GGACAGCGCGCTGTGGCAGTATCTTCTGAGCGCGTCCATGCGGGAGCACCGCGCGCTGG 305
QY 70 gSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluGln 90
Db 306 AAGCTGAGGCTGTGACCTTGAGCAGCGCGGCGGATTCATGATGACCTTCGAGCA 365
QY 90 nAlaGlnLeuAlaAlaLeuAlaArgLeuIleGlnAlaLysLysAlaLeuAspLeuGln 110
Db 366 GGCCAGCTCTTGGCCCAACCTTGGCGCGCTCATCCAGGCCAAGAGGCGCTGGACCTGGG 425
QY 110 YThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgVa 130
Db 426 CACCTTCACGGGCTACTCCGCCCTGGCCCTGGCCCTGGCGGCGGAGCGGCGGT 485
QY 130 lValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTTPArgGlnAl 150
Db 486 GGTGACCTGCGAGGTGGAGCGCGACGCCCGCGAGCTGGGACGGCCCTTGTGGAGGCGGC 545
QY 150 aGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLe 170
Db 546 CGAGCGGAGCACAAGATCGACCTCGGCTGAAGCCCGCTTGGAGACCTTCGACGAGCT 605
QY 170 uLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAs 190
Db 606 GCTGGCGGCGGCGAGCGCGCACCTTCGACGTGGCGCTGGTGGATGGGACCAAGAGAA 665
QY 190 nCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVa 210
Db 666 CTGCTCCGCCCTACTACGAGCGCTGCCTGCAGCTGCTGGACCCCGGAGGACATCTCGCGGT 725
QY 210 lLeuArg----- 212
Db 726 CCTCAGAGTAAGGATCCACTCGCGGGGAGGAGAAAGCACCTGTGCGGGCGGCTGCCCA 785
QY 212 ----- 212
Db 786 TCTTTTCCCTTGACTCCTCTTTATACCCCAAGCCCCACCCAGTCCAGTCAAGCTAGGTAC 845
QY 212 ----- 212
Db 846 ACCCCCTCGGGGCTCGGCCCGCGGTACCCAGGCTTTTCTCGGCTTTGTGTCTGTCTCCA 905

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QY 212 ----- 212
Db 906 GCTCTGGTCACTCTGCGCGGACCTCCCTCGAGGCGCGCTCCCGCCGACACAC 965
QY 212 ----- 212
Db 966 TCCCTCGAGACCGCGCTTCGGTCTGGGACCTCCCTCCAAGACCGCGCTCCGCGCG 1025
QY 212 ----- 212
Db 1026 GGCACCTCCCTCCAGTCCCGCGCTTCGCGCGGACACCTCCCTCGAAGCGCGCGCTC 1085
QY 213 ----- 213
Db 1086 CCAAGCGCGGTGGCGCGCGCTCCCGCGGAGTCTGTGGCGGGAAGGTGCTGCAACC 1145
QY 222 oProlyGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgileArgAs 242
Db 1146 TCCGAAGGGGACGTGGCGCGGAGTGTGCGAAACCTAAACGACATCCGCGCGGA 1205
QY 242 pValArgValTyrIleSerLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysII 262
Db 1206 CGTCAAGGTCTACATCAGCTCTGCGCGGATGACTCACCCTTGGGCTTCAAGAT 1265
QY 262 e 262
Db 1266 C 1266

RESULT 4
BF663323 1006 bp mRNA linear EST 21-DEC-2000
LOCUS 602144463F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5',
DEFINITION mRNA sequence.
ACCESSION BF663323
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1006)
AUTHORS NTH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: King Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI152 row: m column: 16
High quality sequence stop: 745.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297911"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by King
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NTH_MGC Library."

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ORIGIN
Alignment Scores: 2.43e-113 Length: 1006
Pred. No.: 1214.00 Matches: 251
Score: 1214.00 Conservative: 2
Percent Similarity: 96.56% Mismatches: 5
Best Local Similarity: 95.80% Indels: 5
Query Match: 90.39% Gaps: 0
DB: 2

US-10-017-407a-306 (1-262) x BF663323 (1-1006)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCGGCTGCCCGCGCTCTCCGTGCGCGCGCGCTGGCCCTGGGCTCAGCCGCA 66
QY 21 LeuGlyAlaAlaPheAlaThrClvLeuPheLeuGlyArgCysProProTrpArgGly 40
Db 67 CTGGCGCGCGCTTGGCCACTGGCCCTCTTCTGGGGAGGCGGTGCCCCCATGGCGAGGC 126
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrIleLeuSer 60
Db 127 CGCGGAGAGCAGTGCCTGCTTCCCGGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGC 186
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80
Db 187 CGCTCCATCGGAGACACCGCGCGCTGCCAAGCGCTGAGGCTGCTGACCTCCCTGGAGCAGCG 246
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 247 CAGGGGATTCATGATGACCTGCGAGGAGCGCGCTCTTGCGCAACCTGGCGCGGCTC 306
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 307 ATCCAGGCAAGAAGCGCTGGACCTTCCGGGCGCTTCCGGGCGCTTCCGGCCCTGGCCCTG 366
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 367 GCCCTGGCGCTGCGCGCGGCGCGCTGTGTCACCTGGCGAGGTGGACGCGGCGCGCG 426
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 427 GAGCTGGAGCGCGCTGTGGAGCGAGCGCGGAGCACAAGATCGACCTCCGGCTG 486
QY 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 487 AAGCCCGCTTGGAGACCCCTGGACAGCTGCTGGCGCGCGCGGAGCGCGCGCACCTTCGAC 546
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTrpGluArgCysLeuGln 200
Db 547 GTGGCGCTGTGGATGCGGACAGGAGAACTGCTCCGCTTACGAGCGCTGTCTCGAG 606
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal-LeuTrpArgGlyLysValle 220
Db 607 CTGCTGCGACCGCGAGGCGCATCTCGCGCTCTCAGAGTCTTGTGGCGGGAAGGTGCT 666
QY 220 uGlnProProLysGlyAspValAlaAlaAlaGluCysValArgAsnLeu-AsnGluArgIle 239
Db 667 GAACCT-CCGAAGGGGAGCGTGGCGCGCGGAGTGTGTGCGAAACCTAAACGAGACGCATC 725
QY 240 ArgArgAspValArgValTyrIleSerLeuLeu-ProLeuGlyAspGlyLeuThrLeu 258
Db 726 CGGCGGAGCGGAGGCTTACATCAGGCTTCTGGCGCGCTTGGCGCGATGAGATCACCCCTT 783

RESULT 5
BF664198 921 bp mRNA linear EST 21-DEC-2000
LOCUS 602145812F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4309298 5',
DEFINITION mRNA sequence.
ACCESSION BF664198
VERSION BF664198.1 GI:11938093
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI182 row: h column: 03
High quality sequence stop: 726.
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            /clone="IMAGE:4309298"
            /tissue_type="primary B-cells from tonsils (cell line)"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 48"
            /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 9.73e-111 Length: 921
Score: 1188.00 Matches: 244
Percent Similarity: 98.01% Conservative: 2
Best Local Similarity: 97.21% Mismatches: 5
Query Match: 88.46% Indels: 3
DB: 2 Gaps: 0

US-10-017-407A-306 (1-262) x BF664198 (1-921)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCGGTGCCCGGCTCTCCGTGCCCGCGGCTGGCCCTGGGCTCAGCGCA 66
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProThrArgGly 40
Db 67 CTGGGCGCGCGCTTCGCCACCTGGCTCTTCCTGGGAGCGGCTGCCCGCCATGCGAGGC 126
Qy 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60
Db 127 CGGCGAGAGCAGTGGCTCTTCCTCCCGGAGACAGCCCGCTGTGCGATATCTCTGAGC 186
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80
Db 187 CGCTCCATGCGGGAGCACCGCGCTGCGAAGCCTGAGGCTGCTGACCTTGGAGCAGCG 246
Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 247 CAGGCGGATTTCTATGATCACTTGCAGCAGGAGCCAGCTCTTGGCCAACTGGCGGGCTC 306
Qy 101 IleGlnAlaValLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 307 ATCAGGCCAGAGAGCGCTGACCTGGGACCTTCACGGGCTACTCGCCCTGGCCCTG 366
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAlaAspAlaGlnPro 140

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ORIGIN







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Db 635 CGCCCTGGGGCTTGGAGCCCGGCGAAGGTGGTGACCTGCATGGCTGGTCCACC 694
QY 75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetThrCysG1 89
Db 695 CTCTCTTTTACGCGAGCTGACCTGGAGCAGCGCGAGGGGATTCTATGATGACCTGCGA 754
QY 89 uclnalaglnleuAlaAenLeuAlaAglleuileGlnAlaLysLysAlaLeuAsp1e 109
Db 755 GAGGCCAGCTCTTGGCAACCTGGCGGGCTCATCCAGGCCAAGAGCGCTGACCT 814
QY 109 uGlyThrPheThrGlyTySerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 815 GGGACACTTTCAGGGCTACTCGCCCTGGCCCTGGCCCTGGCCCTGGCCGGAGCGGG 874
QY 129 gValValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArg-- 148
Db 875 COTGTGACCTGCGAGGTGGAGCGCAGCCCCCGAGCTGGGACGGCCCTGTGGAGGCA 934
QY 148 ----- 148
Db 935 GGTGAGCGCCCGCGCTAGCTCTGCAGCCCCAGCGGGGGCGCAACGCTGACCCGCTCC 994
QY 149 -----GlnAlaGluAlaGluHisLysLysLeuAspLeuArgLeuLysProAlaLeuGluThrL 167
Db 995 CTCCGCGCGCGAGCGGAGCACAGATCGACCTCGGCTGAGCCCGCCCTTGGAGACC 1054
QY 167 euAspGluLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaA 187
Db 1055 TGGACGAGCTGTGGCGGGCGGAGCGCGCACCTTCGACGTGGCGCTGGTGGATCGG 1114
QY 187 spLysGluAsnCySerAlaTyTyGluArgCysLeuGlnLeuArgProGlyGlyI 207
Db 1115 ACAAGGAGAACTGCTCCGCTACTACGAGCGCTGCTGAGCTGCTGGGACCCCGAGGCA 1174
QY 207 leLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspV 227
Db 1175 TCCTCGCGCTCTCAGAGTCTGTGGCGGGAGGTGCTGCAACTCCGAAAGGGAGC 1234
QY 227 alAlaAlaGluCysValArgAenLeuAenGluArgileArgArgAspValArgValTyri 247
Db 1235 TGGCGCGGAGTGTGTGCGAAACCTAAACGACGATCCGCGGGAGCTCAGGGTCTACA 1294
QY 247 leSerLeuLeuProLeuGlyAspGly 255
Db 1295 TCAGCTCTGCCCCCTGGGCGATGGA 1320

RESULT 8
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DEFINITION UI-CF-FN0-afl-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
ACCESSION CB852718
VERSION UI-CF-FN0-afl-p-08-0-UI 3', mRNA sequence.
KEYWORDS CB852718.1 GI:30047716
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 750)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=No.

Location/Qualifiers  
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/clone\_lib="UI-CF-FN0"  
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-CF-FN0 is a subtracted cDNA library derived from two  
normalized Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,79e-110 Length: 750  
Score: 1180.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 87.86% Indels: 0  
DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x CB852718 (1-750)

QY 32 GlyArgArgCysProProTrpArgGlyArgGluGlnCysLeuLeuProProGluAsp 51  
Db 30 GGGAGGCGTGCCTCCATGCGAGCGCGGAGGAGCAGTGCCTGCTTCCCCCGAGGAC 89  
QY 52 SerArgLeuTrpGlnTyLeuLeuSerArgSerMetArgGluHisProAlaLeuArgSer 71  
Db 90 AGCGCGCTGTGCAGTATCTTCTGAGCGCTCCATGCGGAGCACCCGCGCTGCGAAGC 149  
QY 72 LeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAla 91  
Db 150 CTGAGGCTGTGACCCCTGGAGCAGCGCGGGGATTTCTATGATGACCTGCGAGCAGGCC 209  
QY 92 GlnLeuLeuAlaAenLeuAlaAglleuileGlnAlaLysLysAlaLeuAspLeuGlyThr 111  
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QY 112 PheThrGlyTySerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValVal 131  
Db 270 TTACGCGGCTACTCGCCCTGCGCCCTGCGCTGCGCGCTGCCCGGAGCGCGCTGGTG 329  
QY 132 ThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGlu 151  
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QY 152 AlaGluHisLysLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeu 171  
Db 390 GCGGAGCACAGATCGACCTCCGCTGAGCCCGGCTTGGAGACCTTGGAGAGCTGTGTG 449  
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsn 191  
Db 450 GCGGCGGCGAGGCGGCGCACCTTCGACGTCGCGCTGGTGGATGCGGACAGGAGAACTGC 509  
QY 192 SerAlaTyTyGluArgCysLeuGlnLeuLeuArgProGlyGlyLysLeuAlaVal 211  
Db 510 TCCGCTACTACGAGCGCTGCTGAGCTGTGCGACCCCGAGGAGCATCTCTGCGCTCCTC 569



QY	212	ArgValLeuTrpArgGlyLysValLeuGlnProProProlysGlyAspValAlaAlaGluCys	231	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly	40
Db	570	AGAGTCTGTGGCGCGGAGGTCTGCTCAACCTCCGAAAGGGGACGTGGCGCGGAGTGT	629	CTGGCGCGCGCTTCGCACCTGGCCCTCTCTGGGGAGCGGTGCCCCCATGGCGAGGC	126
QY	232	ValArgAnLeuAanGluAqGileArgArgAspValArgValTyrileSerLeuLeuPro	251	ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer	60
Db	630	GTGGGAAACCTTAAACGACGATCCGGCGGACGTACAGGTCTACATCAGCCTCTTGCCC	689	CGCGAGAGCAGTGGCTGCTTCCCCCGAGGACGCCGCTGTGGCAGTAICTTCTGAGC	186
QY	252	LeuGlyAspGlyLeuThrLeuAla	259	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80
Db	690	CTGGCGGATGACTCACCCTTGCT	713	CGCTCATCGGGAGCACCCCGCGCTGCGAACCTGAGGCTGCTGACCTGAGCGAGCGG	246
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DEFINITION	mRNA sequence.				
ACCESSION	BF663695.1 GI:11937590				
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 779)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM181 row: 1 column: 03 High quality sequence stop: 761.				
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	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NIH MGC 48"				
	/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
ORIGIN					
Alignment Scores:					
Pred. No.:	1.02e-109	Length:	779		
Score:	1177.00	Matches:	249		
Percent Similarity:	95.06%	Conservative:	1		
Best Local Similarity:	94.68%	Mismatches:	5		
Query Match:	87.64%	Indels:	8		
DB:	2	Gaps:	0		
US-10-017-407A-306 (1-262) x BF663695 (1-779)					
QY	1	MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla	20	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly	40
Db	7	ATGACCCAGCGGTGCGCCGCGCTCTCCGTGGCGCGCGGTGGCCCTGGCGGTGAGCGCA	66	CTGGCGCGCGCTTCGCACCTGGCCCTCTCTGGGGAGCGGTGCCCCCATGGCGAGGC	126



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http://image.llnl.gov
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            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      3 56e-108      Length:      934
Score:          1163.00      Matches:     246
Percent Similarity: 94.36%      Conservative: 5
Best Local Similarity: 92.48%      Mismatches: 8
Query Match:      86.60%      Indels:      2
DB:                5          Gaps:          2

US-10-017-407A-306 (1-262) x BQ931589 (1-934)
Qy      2 ThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAlaLeu 21
Db      1 ACCAGCGGTGCTTCTCCGTGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 60
Qy      22 GlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGlyArg 41
Db      61 GCGCGCGCTTTCGACCTGCGCTTCTTCCTGCGGAGCGGTGCGCGCTGCGCGCGG 120
Qy      42 ArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSerArg 61
Db      121 CGAGAGCAGTGCTGCTTCCCGCGAGACAGCGCGCTGCGCTGCGCTGCGCTGCGCGC 180
Qy      62 SerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnProGln 81
Db      181 TCCATGCGGGAGCACCGCGCGCTGCGAGCGCTGAG---CTGACCTGAGCAGCGCGAG 236
Qy      82 GlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeu 101
Db      237 GCGGATTCATGATGACCTGCGAGCAGCGCGCGCTTTCGCGCAACCTGCGCGCGCTCATC 296
Qy      102 GlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAla 121
Db      297 CAGGCCAAGAAGCGCTGACCTGGACCTGGACCTTACGGGGCTACTCGCGCTGCGCTGCGCC 356
Qy      122 LeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProProGln 141
Db      357 CTGGCGCTGCGCGGAGCGCGCGTGTGCTGACCTGCGAGGTGGAGCGCGCGCGCGAG 416
Qy      142 LeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLys 161
Db      417 CTGGAGCGCGCGCTGCGAGCGCGCGCGCGCGCGAGCACAAGATCGACCTCGCGCTGAAG 476
Qy      162 ProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAspVal 181
Db      477 CCGCGCTTGGAGACCTCGAGAGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 536
Qy      182 AlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeu 201
Db      537 GCGGTGTGTGGATCGGACAGAGGAGACTGCTCCGCTACTACGAGCGCTGCTGCGAGTGTG 596
Qy      202 LeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGln 221

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|||||
597 CTGGACCCGGAGGAGCATCTCGCGTCTCAGAGTCTGTGCGCGGAGAGTGTGCAA 656
|||||
222 ProProLysGlyAspValAlaAlaGluCysVal---ArgAsnLeuAsnGluArg-IleArg 240
|||||
657 CCTCCCAAGGGGAACCTTGGCGCGCGGATTGTGTGCCAAACCTTAACGAGCCATCG 716
|||||
240 gArg-AspValArg-ValTyrIleSerLeu-LeuProLeuGlyAsp-GlyLeuThrLeuA 259
|||||
717 GCGGGAGCGTCAAGGGGTCTACATCAGCCTCCCGCGCGCGCGCGCGCGCGCGCGG 776
|||||
259 laPheLys 261
|||||
777 CCTTCA 784

RESULT 11
AK007659
LOCUS
DEFINITION
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
enriched library, clone:1810030M08 product:weakly similar to
PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus],
full insert sequence.
ACCESSION
AK007659
VERSION
AK007659.1 GI:12841341
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 919)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

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	GinglyAspSerMetThrCysGluClnIacInleuLeuAlaAenLeuAlaAArgLeu	100
QY	:	
	CAGGGGGATTCATGATCACTGTGAACAGGCCCRGCTTCTGGCCAACCTGGCGGGCTC	336
Db	:	
	iieGlnAlaLyseAlaLeuaspLeuGlyThrPheThrGlyTyrrSarAlaLeuAlaLeu	120
QY	:::::	
	ATTAAAGCCCAAGAAGCTCTGGACTGGGTACTTTTCAGGGGCTACTGGCCCCCTTA	396
Db	:	

	Qy	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp	180
		::::	::::	
	Db	517	CAGCCGCCCTCGACATTTGATGAGTCTCTAGCGGGCGGAGCCGGAACTTCGAC	576
		:	:	
	Qy	181	ValAlaValIleAspAlaAspLysGluAsnCysSerAlaTyrTrpGluArgCysLeuGln	200
		:::	::::	
	Db	577	ATAGCCGTGTGGACGGCGACAAGAAGAACTGTACCGCTACTACGAGCGTGCTGCAG	636
		:	:	
	Qy	201	LeuLeuArgProGlyIleLeuAlaValLeuArgValLeuTrpArgLysValLeu	220
		::::	::::	
	Db	637	CTCTCATGTCCTCCGAGCGTGTCTGTGTACTCAGAGTCTGTGGCGGAGAGTGTGTG	696
		:	:	
	Qy	221	GlnProLysGlyArgValAlaAlaAlaGluCysValArgAsnLeuAsnGlnUargIleArg	240
		::::	::::	

697	CAGCTTCAGCCCAAGAACAGACTGTTGATGTGTGCGGAACCTGAAACGAAGCATCTCTG	756
Db		
241	ArgaspValArgValTyrIleSerIleLeuProLeuGlyAspGlyLeuThrLeuAlaPhe	260
Qy		
757	AGGACGCCAGGGGTACATCAGCTCTCGCCCTGGATGATGGCTCTCCTTGGCCCTTT	816
Db		
261	LysIle	262
Qy		
817	AAGATC	822
Db		

**RESULT 12**

AK054334	AK054334	2243 bp	mRNA	linear	HTC 03-APR-2004
<b>LOCUS</b>	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E33001621 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.				
<b>DEFINITION</b>					

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AK054334	1	GI:26344156		
AK054334	1	GI:26344156		
		HTC; CAP trapper.		
		Mus musculus (house mouse)		
		Mus musculus		
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Murinae; Mus.		

REFERENCE	1	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Murini; Mus musculus
AUTHORS		Carninci, P. and Hayashizaki, Y.
TITLE		High-efficiency full-length cDNA cloning
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)
MEDLINE		99279253
PUBMED		10349636
REFERENCE	2	
AUTHORS		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL OF  
MEDICAL  
GENETICS  
1987, 24, 358

Genome Res. 10 (1997), 1027-1033

20493374  
PUBMED  
11042159

3

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,



Yanamoto, R., Mateumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

20530913  
11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6

(bases 1 to 2243)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

Location/Qualifiers

1. .2243

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM\_DB:E330016L21"

/db\_xref="taxon:10090"

/clone="E330016L21"

/sex="female"

/tissue type="ovary"

/clone\_libs="RIKEN full-length enriched mouse cDNA library"

/dev\_stages="2 days pregnant adult"

40. .828

/note="unnamed protein product; putative

weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT)

[Rhodothermus marinus] (SPTR|Q9XCB3, evidence: FASTY,

55.5%ID, 97.3%length, match=331)"

/protein\_id="BAC35735.1"

/codon\_start=1

/db\_xref="GI:26344157"

/translation="MAQPVPELSIPALALGSAALGAFATGLLLKRWPPWGSROE

RLLPENPLWQLLSRMSRHPALRSRLTLLEQPOGDSNMTCEQALANLARLIK

AKKALDLGTFGTYSALALALPAGRVVTCVDEAPPKLGRPMWQARVEQKIDRL

OPALQTLDELAAGEAGTFDIAVVDADKENCNTAYYERCLQLLRPGVGLVLRVLRGE

VLQPPRNKTVTCVNRNLNERILRDARVVISLLPLDDGLSLAFKI"

2223. .2228

/note="putative"

polyA\_signal

polyA\_site

2243

/note="putative"

ORIGIN

Alignment Scores:

Pred. NO.: 6.34e-107 Length: 2243

Score: 1156.00 Matches: 224

Percent Similarity: 92.37% Conservative: 18

Best Local Similarity: 85.50% Mismatches: 20

Query Match: 86.08% Indels: 0

DB: 3 Gaps: 0

US-10-017-407A-306 (1-262) x AK054334 (1-2243)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuGlySerAlaLeu 20  
Db 40 ATGGCTCAGCCCGTCCCTCGGCTATCTATCCAGCCGCTGGCCCTGGGCTGGCCGCG 99  
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrrArgGly 40  
Db 100 CTGGGCGCGCTTCGCTACTGCTCTCTTGTGGGGAACCGTGGCTCCATGGGGTCC 159  
Qy 41 ArgArgGlnCysLeuLeuProProGluAspSerArgLeuTrrGlnTrrLeuSer 60  
Db 160 AGCGCGCAAGAGCGCTGTGCCACCTGAGCAATCCCTGTGGCAGTACTTGTGAGC 219  
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGlnPro 80  
Db 220 CGCTCCATGAGAGACACCGCGCTCGGAGCTCGGACTGTGACCTGGAGCAGCG 279  
Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
Db 280 CAGGGGATTCATGATGATGCTGTGAACAGCCCGAGCTTCGGCCACCTGGCGCGGCTC 339  
Qy 101 IleglnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTrrSerAlaLeuAlaLeu 120  
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Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValThrCysGluValAspAlaGlnPro 140  
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Qy 141 GluLeuGlyArgProLeuTrrArgGlnAlaGluHisLysLysLysLysLysLysLys 160  
Db 460 AAGCTGGACCGCCCATGTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 519  
Qy 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
Db 520 CAGCCCGCTTCAGACATTTGGATGAGCTCTAGCGCGCGCGCGCGCGCGCGCGCGCG 579  
Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTrrTrrGluArgCysLeuGln 200  
Db 580 ATAGCCGTGGTGGACGGCGCAAGAGAACTGTATCCCGCTACTACGACGCGCTGTTCGAG 639  
Qy 201 LeuLeuArgProGlyGlyLysLeuAlaValLeuArgValLeuTrrArgGlyLysValLeu 220  
Db 640 CTCTCTAGCTCCGAGCGGCTCGCTCGCTACTAGAGTCTGTGGCGCGGAGAGTGTCTG 699  
Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLysArg 240  
Db 700 CAGCCTCAGCCCGCAAGACACTGTTGATGTGTGGGAACTTGAACGACCATCTCTG 759  
Qy 241 ArgAspValArgValTrrLysSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
Db 760 AGGACGCCAGGGTCTACATCAGCTCTGCGCCCTGGATGATGGCTCTCTCTTGGCCCTT 819  
Qy 261 LysIle 262  
Db 820 AAGATC 825



RESULT 13

BY707694

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY707694 910 bp mRNA linear EST 16-DEC-2002  
 BY707694 RIKEN full-length enriched, 10 day old male pancreas Mus  
 musculus cDNA clone 1810030M08 5', mRNA sequence.

BY707694.1 GI:27118872

EST.

BY707694 (house mouse)

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 910)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusica, V.,

Chothia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., Mckenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,

Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L.G., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozumi-Kishikawa, T., Kono, H., Nakamura, M.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozumi, K., Hori, F.,

Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,

Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Saito, R., Sakazume, N.,

Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

Location/Qualifiers

1..910

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="1810030M08"

/sex="male"

/tissue type="pancreas"

/dev stage="10 day old"

/clone lib="RIKEN full-length enriched, 10 day old male

pancreas"

pancreas

Alignment Scores:

2.07e-104 Length: 910

1126.00 Matches: 222

Score: 91.98% Conservative: 19

Percent Similarity: 84.73% Mismatches: 21

Best Local Similarity: 83.84% Indels: 1

Query Match: 6 Gaps: 0

DB:

US-10-017-407A-306 (1-262) x BY707694 (1-910)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20

Db 34 ATGGCTCAGCCCGCTCCCTGGCTATCTATCCACGCGCATCTGGCTGGGGTCGGCGCG 93

Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40

Db 94 CTGGCGC-SCCTTGGCTACTGCTCTTGTCTGGGAAACGGTGGCTCCATGGGGGTCC 152

Qy 41 ArgArgGlnGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60

Db 153 AGCGCGCAAGAGCGCTGCTGCCACCTTGAGACAACTCCCTCTGGCAGATATCTGTGAGC 212

Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80

Db 213 CGCTCCATGAGAGACACCGCGCGCTGCGAGCTGCGACTGTGACCTCTGGAGACGCC 272

Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuAlaAsnLeuAlaArgLeu 100

Db 273 CAGGGGATTCATGATGACCTGTGAACAGGCCCGAGCTTCTGGCCAACTTGGCGGGCTC 332

Qy 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120

Db 333 ATTAGGCCAAGAAGCTCTGGATCTGGTACTTTTCAGGGGTACTCGGCCCTGGCCCTA 392

Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140

Db 393 GCCTTGGCGCTTCCGAGGCTGGCGGCTGGTGTGACCTGCGAGGTGTACGACGAGCCCGC 452

Qy 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLysLeuAspLeu 160

Db 453 AAGCTGGGACCGCCCATGTGAAGCAGGCGAGAGTGTGAGCAGAGATCGACCTTCGGCTG 512

Qy 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180

Db 513 CAGCCCGCCCTCGACACATTTGATGAGCTCTTAGCGGGCGGCGGCGGAGACCTTCGAC 572

Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200

Db 573 ATAGCGGTGGTGGACCGGACAAAGAGAACTGTACCGCTACTACGACGCTGTCTGAG 632

Qy 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220

Db 633 CTCCTACGTCGCCGAGGGGTGCTCGCTGTACTCAGAGTCTGTGTGGCGGCGGAGAGTGCTG 692



QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgileArg 240  
 Db 693 CAGCCTCAGCCAGCAAGACTGTGAATGTGTGCGGAACCTGAACGACGATCTTG 752  
 QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
 Db 753 AGGAGCGCCAGGGTGTACATCAGCTCTCCCTCGATGATGGCGTCTCTTGGCCCTT 812

QY 261 Lysile 262  
 Db 813 AAGATC 818

## RESULT 14

BC019467

LOCUS

DEFINITION

Mus musculus catechol-O-methyltransferase domain containing 1, mRNA

(cDNA clone IMAGE:4036276), containing frame-shift errors.

ACCESSION

BC019467

VERSION

BC019467.1

KEYWORDS

Mus musculus

SOURCE

Mus musculus

ORGANISM

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 999)

Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klauser,R.D., Collins,F.S., Wagner,K.H., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Spatencko,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettnerman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalls,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.

human and mouse cDNA sequences

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 999)

Strausberg,R.

Direct Submission

Submitted (19-DEC-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Günaracne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 37 Row: a Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein  
 This clone has the following problem: frame shifted.

## FEATURES

source

1. 999

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:4036276"

/tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months

old, gross tissue."

/clone\_lib="NCI CGAP Mam5"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.: 8.06e-103

Score: 1111.00

Length: 999

Matches: 224

Percent Similarity: 83.97%

Conservative: 17

Best Local Similarity: 78.05%

Mismatches: 21

Query Match: 82.73%

Indels: 26

Gaps: 1

US-10-017-407a-306 (1-262) x BC019467 (1-999)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaGlySerAlaAla 20

Db 23 ATGGCTAGCCCGCTCCCTCGGCTATCTATCCAGCGCACCTGGCCCTCGGCTCGGCGCG 82

QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40

Db 83 CTGGCGCGCGCTTCGCTACTGGTCTCTTCTGGGGAACGGTGGCCCTCCATGGGGGTC 142

QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60

Db 143 AGGCGGCAAGACGCGCTGCTGCCACCTGAGGACCAATCCCTGTGGCAGTATCTGTGAGC 202

QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80

Db 203 CGCTCCATGAGAGACACCCCGCTGGAGCTTGGGAGCTTGCACCTGTGAGCAGCGCG 262

QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100

Db 263 CAGGGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 322

QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120

Db 323 ATTAAGGCCAAGAAAGCTCTGGATCTGGGTACTTTTACGGGCTACTTCGGCCCTCGCCCTA 382

QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140

Db 383 GCCTTGGCGCTTCCGAGGCTGGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 442

QY 141 GluLeuGlyArgProLeuTrpArg 148

Db 443 AAGCTGGGACGCGCCCATGTTGAA- GCAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501

QY 149 -----GlnAlaGluAlaGluHisLys 155

Db 502 CCGGCTCGGGGGCGTGGCGGCTGACCGGCTCTCTTCGCGAGGAGAGAGAGAGAGAGAGAG 561

QY 156 IleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAlaAlaGluGlu 175

Db 562 ATCCAGCTTCGGCTGCGAGCGCGCCCTGCAGACATTTGGATGAGCTTCTTAGCGCGCGCGAG 621

QY 176 AlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyr 195

Db 622 GCCGGAACCTTCGACATAGCGCTGGTGGAGCGGAGCAAGAGAACTGTACCGCTACTACTAC 681

QY 196 GluArgCysLeuGlnLeuLeuArgProGlyGlyLeuAlaValLeuArgValLeuTrp 215







GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 CompuGen Ltd.  
 OM protein - nucleic search, using frame\_plus p2n model  
 Run on: January 12, 2005, 22:41:53 ; Search time 421 Seconds  
 (without alignments)  
 3266.861 Million cell updates/sec

Title: US-10-017-407A-306  
 Perfect score: 1343  
 Sequence: 1 MTQVPRLSVPAALALGSA.....VRVYISLLPLGDTLAFKI 262  
 Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0  
 4134886 seqs, 2624710521 residues  
 Total number of hits satisfying chosen parameters: 8269772  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Command line parameters:  
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 -DB=N\_Geneseq\_23Sep04 -QNT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
 -LIST=1500 -DICALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1500  
 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
 -USER=US10017407 @CGN 1 1 708 @runat\_11012005\_135153\_22529 -NCPU=6 -ICPU=3  
 -NO\_MMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
 -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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 634: geneseq2004ws:  
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 636: geneseq2004ys:  
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 638: geneseq2004as:



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ID ACD68458 standard; cDNA; 989 BP.  
DE Novel human secreted and transmembrane protein PRO1558 cDNA.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 8  
ID ACH04560 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 9  
ID ACD68104 standard; cDNA; 989 BP.  
DE Novel human secreted and transmembrane protein PRO1558 cDNA.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 10  
ID ADC18174 standard; cDNA; 989 BP.  
DE Human PRO polynucleotide #86.  
PN US2003084925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 11  
ID ADD70820 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 12  
ID ADD39897 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 13  
ID ADD70343 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 14  
ID ADD38464 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 15  
ID ADD39420 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 16  
ID ADD38943 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 17  
ID ADD40374 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 18  
ID ADE50595 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 19  
ID ADE20207 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 20  
ID ADE50118 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 21  
ID ADE21676 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 22  
ID ADF30101 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 23  
ID ADF55994 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.



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PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 24
ID ADH99498 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 25
ID ADJ37302 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 26
ID ADE96678 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 27
ID ADE25989 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 28
ID ADF24888 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 29
ID ADF29624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 30
ID ADE97155 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 31
ID ADH03193 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003216562-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 32
ID ADH04147 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 33
ID ADH03670 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 34
ID ADG68226 standard; cDNA; 989 BP.
DE Human PRO polypeptide cDNA #11.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 35
ID ADH04624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 36
ID ADH61625 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 37
ID ADL94824 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 38
ID ADO42276 standard; cDNA; 989 BP.
DE Human NOVX polynucleotide #63.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIP/) DIPPEO V A.
PA (EDIN/) EDINGER S R.
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PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HER/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPVT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 39
ID ABA05419 standard; cDNA; 1037 BP.
DE Human O-methyltransferase family member 25692 encoding cDNA.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 40
ID ABO61039 standard; cDNA; 1100 BP.
DE Human PRO1558 protein encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 41
ID AAH33455 standard; cDNA; 967 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Conservative: 0
Mismatch: 3
Indels: 0
Percent Similarity: 98.85%
Best Local Similarity: 98.85%
Query Match: 98.59%
RESULT 42
ID AAC76634 standard; cDNA; 812 BP.
DE Human ORFX ORF2189 polynucleotide sequence SEQ ID NO:4377.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Conservative: 0
Mismatch: 2
Indels: 0
Percent Similarity: 99.14%
Best Local Similarity: 99.14%
Query Match: 87.79%
RESULT 43
ID AAD56372 standard; DNA; 876 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Conservative: 0
Mismatch: 1
Indels: 46
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
RESULT 44
ID AAD56361 standard; DNA; 885 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Conservative: 0
Mismatch: 1
Indels: 46
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
RESULT 45
ID ADO42274 standard; cDNA; 787 BP.
DE Human NOVX polynucleotide #62.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGES C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPP/) DIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPVT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 70.23%
Best Local Similarity: 70.23%
Query Match: 65.82%
RESULT 46
ID ADD34178 standard; DNA; 770 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEN-) UNIV EMORY.
```



Percent Similarity: 92.49% Conservative: 13  
 Best Local Similarity: 84.97% Mismatches: 13  
 Query Match: 56.22% Indels: 0  
 RESULT 47  
 ID ACH35890 standard; cDNA; 458 BP.  
 DE Human endothelial cell cDNA #4023.  
 PD 17-APR-2003.  
 PA (DRMA//) DRMANAC R T.  
 PA (LABA//) LABAT I.  
 PA (STAC//) STACHE-CHAIN B.  
 PA (DICK//) DICKSON M C.  
 PA (JONE//) JONES L W.  
 Percent Similarity: 99.02% Conservative: 1  
 Best Local Similarity: 98.04% Mismatches: 1  
 Query Match: 37.90% Indels: 0  
 RESULT 48  
 ID ACH35195 standard; cDNA; 474 BP.  
 DE Human endothelial cell cDNA #3328.  
 PD 17-APR-2003.  
 PA (DRMA//) DRMANAC R T.  
 PA (LABA//) LABAT I.  
 PA (STAC//) STACHE-CHAIN B.  
 PA (DICK//) DICKSON M C.  
 PA (JONE//) JONES L W.  
 Percent Similarity: 99.02% Conservative: 1  
 Best Local Similarity: 98.04% Mismatches: 1  
 Query Match: 37.90% Indels: 0  
 RESULT 49  
 ID ADM80035 standard; DNA; 11171 BP.  
 DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS.  
 Percent Similarity: 50.49% Conservative: 35  
 Best Local Similarity: 39.09% Mismatches: 96  
 Query Match: 33.73% Indels: 56  
 RESULT 50  
 ID ADM97551 standard; DNA; 11171 BP.  
 DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
 PN WO2004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS.  
 Percent Similarity: 50.49% Conservative: 35  
 Best Local Similarity: 39.09% Mismatches: 96  
 Query Match: 33.73% Indels: 56  
 RESULT 51  
 ID AAA81501 standard; DNA; 48275 BP.  
 DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR ) CHIRON CORP.  
 Percent Similarity: 53.45% Conservative: 48  
 Best Local Similarity: 36.90% Mismatches: 98  
 Query Match: 33.54% Indels: 37  
 RESULT 52  
 ID AAA81489 standard; DNA; 837096 BP.  
 DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR ) CHIRON CORP.  
 Percent Similarity: 53.45% Conservative: 48  
 Best Local Similarity: 36.90% Mismatches: 98  
 Query Match: 33.54% Indels: 37  
 RESULT 53  
 ID AAP21610 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR ) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 53.45% Conservative: 48  
 Best Local Similarity: 36.90% Mismatches: 98  
 Query Match: 33.54% Indels: 37  
 RESULT 54  
 ID AB240101 standard; DNA; 666 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 62.15% Conservative: 42  
 Best Local Similarity: 42.52% Mismatches: 71  
 Query Match: 32.69% Indels: 10  
 RESULT 55  
 ID ADM80044 standard; DNA; 675 BP.  
 DE Spiramycin biosynthesis orf5\*, SEQ ID 11.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Percent Similarity: 60.99% Conservative: 33  
 Best Local Similarity: 46.19% Mismatches: 80  
 Query Match: 32.61% Indels: 8  
 RESULT 56  
 ID ADM97560 standard; DNA; 675 BP.  
 DE S ambofaciens spiramycin biosynthetic gene ORF5\*.  
 PN WO2004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS.  
 Percent Similarity: 60.99% Conservative: 33  
 Best Local Similarity: 46.19% Mismatches: 80  
 Query Match: 32.61% Indels: 8  
 RESULT 57  
 ID ABD04592 standard; DNA; 846 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3196.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 55.19% Conservative: 31  
 Best Local Similarity: 42.32% Mismatches: 82  
 Query Match: 31.94% Indels: 26  
 RESULT 58  
 ID AAQ44449 standard; DNA; 2381 BP.  
 DE 3-acylating enzyme coding sequence.  
 PN JP06038750-A.  
 PD 15-FEB-1994.  
 PA (MEIJ ) MEIJI SEIKA KAISHA.  
 Percent Similarity: 54.12% Conservative: 37  
 Best Local Similarity: 39.61% Mismatches: 94  
 Query Match: 31.68% Indels: 24  
 RESULT 59  
 ID ADM45913 standard; DNA; 84428 BP.  
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
 PN JP2004049100-A.  
 PD 19-FEB-2004.  
 PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
 Percent Similarity: 54.12% Conservative: 37  
 Best Local Similarity: 39.61% Mismatches: 94  
 Query Match: 31.68% Indels: 24  
 RESULT 60  
 ID AAX25215 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 56.59% Conservative: 45  
 Best Local Similarity: 39.15% Mismatches: 97  
 Query Match: 30.75% Indels: 15  
 RESULT 61  
 ID AAD05742 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA-3-O-methyltransferase (cCoA-OMT) cDNA.  
 PN WO200134817-A2.



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RESULT 76
ID ADC68544 standard; cDNA; 1059 BP.
DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.
PN WO2003040306-A2.
PD 15-MAY-2003.
PA (GENE-) WRIGHTSON SEEDS LTD.
PA (WRIG-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 56.43%
Best Local Similarity: 39.00%
Query Match: 29.23%
Conservative: 42
Mismatch: 87
Indels: 18
RESULT 77
ID ADN74200 standard; cDNA; 780 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Percent Similarity: 58.85%
Best Local Similarity: 37.61%
Query Match: 29.15%
Conservative: 48
Mismatch: 82
Indels: 11
RESULT 78
ID ADN73162 standard; cDNA; 780 BP.
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Percent Similarity: 58.85%
Best Local Similarity: 37.61%
Query Match: 29.15%
Conservative: 48
Mismatch: 82
Indels: 11
RESULT 79
ID AAC42559 standard; DNA; 1033 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (ANY/) AN Y.
Percent Similarity: 58.85%
Best Local Similarity: 37.61%
Query Match: 29.15%
Conservative: 48
Mismatch: 82
Indels: 11
RESULT 80
ID ABN98364 standard; DNA; 1072 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Percent Similarity: 58.85%
Best Local Similarity: 37.61%
Query Match: 29.15%
Conservative: 48
Mismatch: 82
Indels: 11
RESULT 81
ID AAC4172 standard; DNA; 1180 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (ANY/) AN Y.
Percent Similarity: 58.85%
Best Local Similarity: 37.61%
Query Match: 29.15%
Conservative: 48
Mismatch: 82
Indels: 11
RESULT 82
ID AAC45547 standard; DNA; 1032 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (ANY/) AN Y.
Percent Similarity: 55.14%
Best Local Similarity: 34.98%
Query Match: 29.00%
Conservative: 49
Mismatch: 88
Indels: 21
RESULT 83
ID ABS63413 standard; cDNA; 997 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Percent Similarity: 57.47%
Best Local Similarity: 39.37%
Query Match: 28.97%
Conservative: 40
Mismatch: 82
Indels: 12
RESULT 84
ID ABS63429 standard; cDNA; 953 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Percent Similarity: 55.51%
Best Local Similarity: 38.60%
Query Match: 28.82%
Conservative: 46
Mismatch: 104
Indels: 18
RESULT 85
ID ABS54115 standard; DNA; 967 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-9 (COAOMT-9) cDNA.
PN US6441272-B1.
PD 27-AUG-2002.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Percent Similarity: 58.56%
Best Local Similarity: 36.94%
Query Match: 28.78%
Conservative: 48
Mismatch: 83
Indels: 9
RESULT 86
ID ADM49212 standard; DNA; 798 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000506-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 55.56%
Best Local Similarity: 37.16%
Query Match: 28.74%
Conservative: 48
Mismatch: 91
Indels: 25
RESULT 87
ID AAG68001 standard; DNA; 1012 BP.
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 57.56%
Best Local Similarity: 36.13%
Query Match: 28.74%
Conservative: 51
Mismatch: 88
Indels: 13
RESULT 88
ID ADD41751 standard; DNA; 1012 BP.
DE O-methyl transferase DNA #9.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 57.56%
Best Local Similarity: 36.13%
Query Match: 28.74%
Conservative: 51
Mismatch: 88
Indels: 13
RESULT 89
ID AAV23912 standard; DNA; 1026 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

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Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%   Mismatches: 88
Query Match: 28.74%            Indels: 13
RESULT 90
ID AA206875 standard; cDNA; 1026 BP.
DE Pine O-methyl transferase (OMT) partial cDNA 1.
PD US952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%   Mismatches: 88
Query Match: 28.74%            Indels: 13
RESULT 91
ID AAA67913 standard; DNA; 1026 BP.
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.
PD WO2000202099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%   Mismatches: 88
Query Match: 28.74%            Indels: 13
RESULT 92
ID ADD41663 standard; DNA; 1026 BP.
DE O-methyl transferase DNA #1.
PD US200311373-A1.
PD 10-JUL-2003.
PA (BLOK-) BLOKSBERG L N.
PA (HAVU-) HAVUKKALA I.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%   Mismatches: 88
Query Match: 28.74%            Indels: 13
RESULT 93
ID ABS63425 standard; cDNA; 1118 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%   Mismatches: 91
Query Match: 28.74%            Indels: 25
RESULT 94
ID ABS63408 standard; cDNA; 1146 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%   Mismatches: 91
Query Match: 28.74%            Indels: 25
RESULT 95
ID AAX25208 standard; cDNA; 1160 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PD WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%   Mismatches: 91
Query Match: 28.74%            Indels: 25
RESULT 96
ID ABS63415 standard; cDNA; 931 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 47
Best Local Similarity: 37.16%   Mismatches: 95
Query Match: 28.74%            Indels: 10
RESULT 97
ID ADC68545 standard; cDNA; 1063 BP.
DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.
PD WO2003040306-A2.
PD 15-MAY-2003.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Percent Similarity: 54.85%      Conservative: 46
Best Local Similarity: 37.69%   Mismatches: 101
Query Match: 28.70%            Indels: 21
RESULT 98
ID ADA71075 standard; DNA; 783 BP.
DE Rice gene, SEQ ID 4398.
PD WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 52.73%      Conservative: 36
Best Local Similarity: 38.67%   Mismatches: 94
Query Match: 28.59%            Indels: 27
RESULT 99
ID AAX25210 standard; cDNA; 1003 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PD WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 52.55%      Conservative: 44
Best Local Similarity: 36.50%   Mismatches: 101
Query Match: 28.56%            Indels: 30
RESULT 100
ID ABS63409 standard; cDNA; 1057 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 52.55%      Conservative: 44
Best Local Similarity: 36.50%   Mismatches: 101
Query Match: 28.56%            Indels: 30
RESULT 101
ID ABS63416 standard; cDNA; 929 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 56.43%      Conservative: 47
Best Local Similarity: 36.93%   Mismatches: 95
Query Match: 28.48%            Indels: 10
RESULT 102
ID ABS63428 standard; cDNA; 1049 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO-) CAHOON R E.
PA (FADE-) FADER G M.
PA (RAFA-) RAFALSKI J A.
Percent Similarity: 55.15%      Conservative: 46
Best Local Similarity: 38.24%   Mismatches: 105
Query Match: 28.37%            Indels: 18
RESULT 103
ID ABS54114 standard; DNA; 845 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.
PD US6441272-B1.
PD 27-AUG-2002.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 57.66%      Conservative: 47
Best Local Similarity: 36.49%   Mismatches: 85
Query Match: 28.26%            Indels: 9
RESULT 104

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ID ADA49019 standard; DNA; 1112 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 53.59%  
 Best Local Similarity: 38.43%  
 Query Match: 28.22%  
 Indels: 22  
 RESULT 105  
 ID AAX25209 standard; cDNA; 944 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PTON) PIONEER HI-BRED INT INC.  
 Percent Similarity: 52.42%  
 Best Local Similarity: 36.80%  
 Query Match: 28.15%  
 Indels: 15  
 RESULT 106  
 ID ABN87108 standard; cDNA; 1113 BP.  
 DE Lolium perenne LpCCOAMTA nucleotide sequence SEQ ID NO:1.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 56.02%  
 Best Local Similarity: 37.76%  
 Query Match: 28.11%  
 Indels: 18  
 RESULT 107  
 ID ABN87245 standard; cDNA; 1161 BP.  
 DE Lolium perenne CCOAOWT1 cDNA sequence SEQ ID NO:168.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 56.41%  
 Best Local Similarity: 38.03%  
 Query Match: 28.03%  
 Indels: 14  
 RESULT 108  
 ID AAQ32259 standard; cDNA; 1258 BP.  
 DE Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).  
 PN DE4117747-A.  
 PD 03-DEC-1992.  
 PA (FARB) BAYER AG.  
 Percent Similarity: 57.21%  
 Best Local Similarity: 36.94%  
 Query Match: 28.03%  
 Indels: 9  
 RESULT 109  
 ID ABS63410 standard; cDNA; 923 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 53.10%  
 Best Local Similarity: 37.21%  
 Query Match: 28.00%  
 Indels: 13  
 RESULT 110  
 ID ABN87246 standard; cDNA; 1199 BP.  
 DE Lolium perenne CCOAOWT2 cDNA sequence SEQ ID NO:170.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 56.36%  
 Best Local Similarity: 38.56%  
 Query Match: 27.89%  
 Indels: 18  
 RESULT 111  
 ID ABS54112 standard; DNA; 870 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Percent Similarity: 58.11%  
 Best Local Similarity: 35.59%  
 Query Match: 27.81%  
 Indels: 9  
 RESULT 112  
 ID ABS54113 standard; DNA; 811 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAMT-2) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Percent Similarity: 58.72%  
 Best Local Similarity: 36.24%  
 Query Match: 27.74%  
 Indels: 9  
 RESULT 113  
 ID AAC45004 standard; DNA; 917 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Percent Similarity: 56.64%  
 Best Local Similarity: 38.94%  
 Query Match: 27.48%  
 Indels: 12  
 RESULT 114  
 ID ABS63424 standard; cDNA; 1018 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 50.55%  
 Best Local Similarity: 35.06%  
 Query Match: 27.44%  
 Indels: 50  
 RESULT 115  
 ID ADA48371 standard; DNA; 835 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 56.76%  
 Best Local Similarity: 39.00%  
 Query Match: 27.36%  
 Indels: 24  
 RESULT 116  
 ID ABN94134 standard; DNA; 326 BP.  
 DE Gene #632 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 98.65%  
 Best Local Similarity: 98.85%  
 Query Match: 27.25%  
 Indels: 1  
 RESULT 117  
 ID ABN87118 standard; cDNA; 1103 BP.  
 DE Lolium perenne LpCCOAMTB nucleotide sequence SEQ ID NO:12.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 54.23%  
 Best Local Similarity: 35.00%  
 Query Match: 26.99%  
 Indels: 19  
 RESULT 118  
 ID ABZ14595 standard; DNA; 729 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI) SCRIPPS RES INST.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 56.28%  
 Best Local Similarity: 39.07%  
 Query Match: 26.81%  
 Indels: 10  
 RESULT 119  
 ID AAC42096 standard; DNA; 1186 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
 PN EP1033405-A2.



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PD 06-SEP-2000.
Percent Similarity: 60.66%
Best Local Similarity: 37.91%
Query Match: 26.58%
Conservative: 48
Mismatch: 76
Indels: 7
RESULT 120
ID ADH02852 standard; cDNA; 1006 BP.
DE Torenia TMT5.nt cDNA #SEQ ID 11.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Percent Similarity: 56.58%
Best Local Similarity: 36.40%
Query Match: 26.40%
Conservative: 46
Mismatch: 84
Indels: 15
RESULT 121
ID ABS63420 standard; cDNA; 912 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAPALSKI J A.
Percent Similarity: 53.71%
Best Local Similarity: 36.68%
Query Match: 26.36%
Conservative: 39
Mismatch: 96
Indels: 10
RESULT 122
ID ADK69931 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #10.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.57%
Best Local Similarity: 32.50%
Query Match: 26.32%
Conservative: 45
Mismatch: 71
Indels: 73
RESULT 123
ID ADK69906 standard; DNA; 1180 BP.
DE Maize F4 CCoAOMT2 gene, seq id 3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 41.83%
Best Local Similarity: 29.36%
Query Match: 26.28%
Conservative: 45
Mismatch: 98
Indels: 112
RESULT 124
ID ADK69932 standard; DNA; 1199 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 42.90%
Best Local Similarity: 30.11%
Query Match: 26.21%
Conservative: 45
Mismatch: 97
Indels: 104
RESULT 125
ID ADK69927 standard; DNA; 1178 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.39%
Best Local Similarity: 32.62%
Query Match: 26.14%
Conservative: 44
Mismatch: 72
Indels: 72
RESULT 126
ID ADK69925 standard; DNA; 1196 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 46.67%
Best Local Similarity: 33.33%
Query Match: 26.14%
Conservative: 38
Mismatch: 74
Indels: 78
RESULT 127
ID ADK69918 standard; DNA; 1172 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 128
ID ADK69919 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 129
ID ADK69920 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 130
ID ADK69928 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #7.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 131
ID ADK69923 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 132
ID ADK69904 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene, seq id 1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 133
ID ADK69922 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #4.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 134
ID ADK69924 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #6.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 135
ID ADK69929 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #8.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73

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PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21%  
 Best Local Similarity: 32.50%  
 Query Match: 26.10%  
 RESULT 136  
 ID ADK69921 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21%  
 Best Local Similarity: 32.50%  
 Query Match: 26.10%  
 RESULT 137  
 ID ADK69930 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #9.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21%  
 Best Local Similarity: 32.50%  
 Query Match: 26.10%  
 RESULT 138  
 ID ADK69917 standard; DNA; 1186 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21%  
 Best Local Similarity: 32.50%  
 Query Match: 26.10%  
 RESULT 139  
 ID ADH02845 standard; cDNA; 888 BP.  
 DE Petunia E20 cDNA #SEQ ID 4.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39%  
 Best Local Similarity: 37.66%  
 Query Match: 25.99%  
 RESULT 140  
 ID ADH02842 standard; cDNA; 969 BP.  
 DE Petunia dife cDNA #SEQ ID 1.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39%  
 Best Local Similarity: 37.66%  
 Query Match: 25.99%  
 RESULT 141  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 Percent Similarity: 51.97%  
 Best Local Similarity: 38.43%  
 Query Match: 25.91%  
 RESULT 142  
 ID ADK69926 standard; DNA; 1199 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 47.20%  
 Best Local Similarity: 31.82%  
 Query Match: 25.87%  
 RESULT 143  
 ID ABS63422 standard; cDNA; 982 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.14%  
 Conservative: 37

Best Local Similarity: 37.85%  
 Query Match: 25.39%  
 RESULT 144  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum anasmitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Percent Similarity: 52.63%  
 Best Local Similarity: 40.35%  
 Query Match: 25.32%  
 RESULT 145  
 ID ADH02867 standard; cDNA; 1079 BP.  
 DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 57.59%  
 Best Local Similarity: 36.61%  
 Query Match: 25.28%  
 RESULT 146  
 ID ABN87110 standard; cDNA; 758 BP.  
 DE Lolium perenne LpCCoAMT2 partial nucleotide sequence SEQ ID NO:4.  
 PN WO200326994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 51.82%  
 Best Local Similarity: 34.82%  
 Query Match: 25.17%  
 RESULT 147  
 ID ABN87115 standard; cDNA; 793 BP.  
 DE Lolium perenne LpCCoAMT2 partial nucleotide sequence SEQ ID NO:9.  
 PN WO200326994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 55.56%  
 Best Local Similarity: 37.04%  
 Query Match: 24.91%  
 RESULT 148  
 ID ABN87126 standard; cDNA; 689 BP.  
 DE Lolium perenne LpCCoAMT2 partial nucleotide sequence SEQ ID NO:21.  
 PN WO200326994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 55.94%  
 Best Local Similarity: 41.09%  
 Query Match: 24.80%  
 RESULT 149  
 ID ABN87112 standard; cDNA; 765 BP.  
 DE Lolium perenne LpCCoAMT2 partial nucleotide sequence SEQ ID NO:6.  
 PN WO200326994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 58.33%  
 Best Local Similarity: 39.06%  
 Query Match: 24.46%  
 RESULT 150  
 ID ADH02847 standard; cDNA; 1077 BP.  
 DE Petunia E33 cDNA #SEQ ID 5.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 56.70%  
 Best Local Similarity: 36.16%  
 Query Match: 24.42%  
 RESULT 151  
 ID ADH02884 standard; cDNA; 943 BP.  
 DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
 PN WO2003062428-A1.



PD	31-JUL-2003.	Conservative: 48	
PA	(ITFL-) INT FLOWER DEV PTY LTD.	Mismatches: 82	
	Percent Similarity: 57.47%	Indels: 12	
	Best Local Similarity: 24.35%		
Query Match:			
RESULT 152			
ID	ADH02882 standard; cDNA; 841 BP.		
DE	Fuchsia FMT (3282) cDNA #SEQ ID 41.		
PD	WO20003062428-A1.		
PD	31-JUL-2003.		
PA	(ITFL-) INT FLOWER DEV PTY LTD.	Conservative: 44	
	Percent Similarity: 58.82%	Mismatches: 74	
	Best Local Similarity: 37.25%	Indels: 10	
Query Match:			
RESULT 153			
ID	AAC47161 standard; DNA; 738 BP.		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.		
PD	EP1033405-A2.	Conservative: 44	
PD	06-SEP-2000.	Mismatches: 85	
	Percent Similarity: 56.42%	Indels: 10	
	Best Local Similarity: 36.24%		
Query Match:			
RESULT 154			
ID	AAC47930 standard; DNA; 833 BP.		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.		
PD	EP1033405-A2.	Conservative: 44	
PD	06-SEP-2000.	Mismatches: 85	
	Percent Similarity: 56.42%	Indels: 10	
	Best Local Similarity: 36.24%		
Query Match:			
RESULT 155			
ID	ABN87111 standard; cDNA; 774 BP.		
DE	Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:5.		
PD	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.	Conservative: 37	
	Percent Similarity: 57.81%	Mismatches: 73	
	Best Local Similarity: 38.54%	Indels: 8	
Query Match:			
RESULT 156			
ID	ABN87113 standard; cDNA; 777 BP.		
DE	Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:7.		
PD	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.	Conservative: 40	
	Percent Similarity: 54.63%	Mismatches: 78	
	Best Local Similarity: 36.11%	Indels: 20	
Query Match:			
RESULT 157			
ID	ABN87114 standard; cDNA; 792 BP.		
DE	Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:8.		
PD	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.	Conservative: 40	
	Percent Similarity: 54.63%	Mismatches: 78	
	Best Local Similarity: 36.11%	Indels: 20	
Query Match:			
RESULT 158			
ID	ABN87122 standard; cDNA; 789 BP.		
DE	Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.		
PD	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.	Conservative: 37	
	Percent Similarity: 52.77%	Mismatches: 94	
	Best Local Similarity: 37.02%	Indels: 18	
Query Match:			
RESULT 159			
ID	ABN87121 standard; cDNA; 773 BP.		
DE	Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.		
PD	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.	Conservative: 37	
	Percent Similarity: 52.77%	Mismatches: 94	
	Best Local Similarity: 37.02%	Indels: 18	
Query Match:			
RESULT 160			
ID	ABZ13934 standard; DNA; 699 BP.		
DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.		
PD	WO200216655-A2.		
PD	28-FEB-2002.		
PA	(SCRI ) SCRIPPS RES INST.	Conservative: 46	
	Percent Similarity: 55.00%	Mismatches: 84	
	Best Local Similarity: 34.09%	Indels: 15	
Query Match:			
RESULT 161			
ID	ADG87603 standard; cDNA; 699 BP.		
DE	A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.		
PD	WO200222675-A2.		
PD	21-MAR-2002.		
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.	Conservative: 46	
	Percent Similarity: 55.00%	Mismatches: 84	
	Best Local Similarity: 34.09%	Indels: 15	
Query Match:			
RESULT 162			
ID	ADG87604 standard; cDNA; 699 BP.		
DE	A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.		
PD	WO200222675-A2.		
PD	21-MAR-2002.		
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.	Conservative: 46	
	Percent Similarity: 55.00%	Mismatches: 84	
	Best Local Similarity: 34.09%	Indels: 15	
Query Match:			
RESULT 163			
ID	ADA67907 standard; DNA; 699 BP.		
DE	Arabidopsis thaliana gene, SEQ ID 151.		
PD	WO2003000898-A1.		
PD	03-JAN-2003.		
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.	Conservative: 46	
	Percent Similarity: 55.00%	Mismatches: 84	
	Best Local Similarity: 34.09%	Indels: 15	
Query Match:			



Best Local Similarity: 31.30% Mismatches: 99  
Query Match: 22.23% Indels: 23  
RESULT 166  
ID AA206878 standard; cDNA; 1075 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 4.  
PN US5952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 50.41% Conservative: 47  
Best Local Similarity: 31.30% Mismatches: 99  
Query Match: 22.23% Indels: 23  
RESULT 167  
ID AA67962 standard; DNA; 1075 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
PN WO20022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 50.41% Conservative: 47  
Best Local Similarity: 31.30% Mismatches: 99  
Query Match: 22.23% Indels: 23  
RESULT 168  
ID ADD41712 standard; DNA; 1075 BP.  
DE O-methyl transferase DNA #8.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 50.41% Conservative: 47  
Best Local Similarity: 31.30% Mismatches: 99  
Query Match: 22.23% Indels: 23  
RESULT 169  
ID AAX28142 standard; DNA; 3072 BP.  
DE CCoAOMT promoter, PtCCoAOMT2.  
PN WO9909188-A2.  
PD 25-FEB-1999.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 43.80% Conservative: 41  
Best Local Similarity: 27.91% Mismatches: 63  
Query Match: 22.15% Indels: 82  
RESULT 170  
ID AC23248 standard; DNA; 509 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13239.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Percent Similarity: 57.23% Conservative: 29  
Best Local Similarity: 39.76% Mismatches: 64  
Query Match: 22.15% Indels: 7  
RESULT 171  
ID AAQ14978 standard; DNA; 1810 BP.  
DE ACYA gene.  
PN EP459525-A.  
PD 04-DEC-1991.  
PA (SAOC) MERCIAN CORP.  
Percent Similarity: 49.76% Conservative: 22  
Best Local Similarity: 39.02% Mismatches: 69  
Query Match: 21.89% Indels: 34  
RESULT 172  
ID AAV23874 standard; DNA; 1074 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 53.15% Conservative: 46  
Best Local Similarity: 32.43% Mismatches: 92  
Query Match: 21.67% Indels: 12  
RESULT 173  
ID AA206877 standard; cDNA; 1074 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 3.  
PN US5952486-A.

PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 53.15% Conservative: 46  
Best Local Similarity: 32.43% Mismatches: 92  
Query Match: 21.67% Indels: 12  
RESULT 174  
ID AA67961 standard; DNA; 1074 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
PN WO20022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 53.15% Conservative: 46  
Best Local Similarity: 32.43% Mismatches: 92  
Query Match: 21.67% Indels: 12  
RESULT 175  
ID ADD41711 standard; DNA; 1074 BP.  
DE O-methyl transferase DNA #7.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 53.15% Conservative: 46  
Best Local Similarity: 32.43% Mismatches: 92  
Query Match: 21.67% Indels: 12  
RESULT 176  
ID ABN87120 standard; cDNA; 693 BP.  
DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:15.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.15% Conservative: 32  
Best Local Similarity: 38.54% Mismatches: 81  
Query Match: 21.37% Indels: 14  
RESULT 177  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.  
Percent Similarity: 47.60% Conservative: 39  
Best Local Similarity: 33.21% Mismatches: 111  
Query Match: 21.33% Indels: 31  
RESULT 178  
ID AA260809 standard; DNA; 2983 BP.  
DE Nucleotide sequence of promoter of coffeyl-CoA-O-methyltransferase.  
PN WO200006752-A1.  
PD 10-FEB-2000.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 43.63% Conservative: 41  
Best Local Similarity: 27.80% Mismatches: 63  
Query Match: 21.22% Indels: 83  
RESULT 179  
ID ABN90073 standard; DNA; 792 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAM/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHEW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.



PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Percent Similarity: 56.35%  
Best Local Similarity: 34.25%  
Conservative: 40  
Mismatches: 68  
Indels: 11  
Query Match:  
RESULT 180  
ID AAX28141 standard; DNA; 3800 BP.  
DE CCoAOMT promoter, PCCOAOOMT1.  
PN WO9909188-A2.  
PD 25-FEB-1999.  
PA (VLA-A-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 40.79%  
Best Local Similarity: 25.27%  
Conservative: 43  
Mismatches: 63  
Indels: 101  
Query Match:  
RESULT 181  
ID AAZ60808 standard; DNA; 3800 BP.  
DE Nucleotide sequence of promoter of caffeoyl-CoA-O-methyltransferase.  
PN WO200006752-A1.  
PD 10-FEB-2000.  
PA (VLA-A-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 40.79%  
Best Local Similarity: 25.27%  
Conservative: 43  
Mismatches: 63  
Indels: 101  
Query Match:  
RESULT 182  
ID ABK2368 standard; cDNA; 343 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #275.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 60.00%  
Best Local Similarity: 55.65%  
Conservative: 5  
Mismatches: 6  
Indels: 40  
Query Match:  
RESULT 183  
ID ADB55662 standard; DNA; 343 BP.  
DE Toxicity-related gene, SEQ ID 688.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 60.00%  
Best Local Similarity: 55.65%  
Conservative: 5  
Mismatches: 6  
Indels: 40  
Query Match:  
RESULT 184  
ID ABT40596 standard; DNA; 343 BP.  
DE Toxicity modelling related rat gene SEQ ID No 298.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 60.00%  
Best Local Similarity: 55.65%  
Conservative: 5  
Mismatches: 6  
Indels: 40  
Query Match:  
RESULT 185  
ID ADH02862 standard; cDNA; 780 BP.  
DE Fuchsia PMT. cDNA #SEQ ID 21.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITEL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 57.50%  
Best Local Similarity: 38.12%  
Conservative: 31  
Mismatches: 60  
Indels: 8  
Query Match:  
RESULT 186  
ID ABD00975 standard; DNA; 675 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 6750.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 53.33%  
Best Local Similarity: 35.56%  
Conservative: 32  
Mismatches: 76  
Indels: 8  
Query Match:  
RESULT 187  
ID ADD34177 standard; DNA; 407 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
PN WO2003020220-A2.  
PD 13-MAR-2003.

PA (UYEM-) UNIV EMORY.  
Percent Similarity: 85.71%  
Best Local Similarity: 79.37%  
Conservative: 4  
Mismatches: 9  
Indels: 0  
Query Match:  
RESULT 188  
ID AAV23845 standard; DNA; 760 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Conservative: 29  
Mismatches: 52  
Indels: 3  
Query Match:  
RESULT 189  
ID AAZ06846 standard; cDNA; 760 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
PN US952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Conservative: 29  
Mismatches: 52  
Indels: 3  
Query Match:  
RESULT 190  
ID AAB69584 standard; cDNA; 760 BP.  
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Conservative: 29  
Mismatches: 52  
Indels: 3  
Query Match:  
RESULT 191  
ID AAB67932 standard; DNA; 760 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Conservative: 29  
Mismatches: 52  
Indels: 3  
Query Match:  
RESULT 192  
ID ADD41682 standard; DNA; 760 BP.  
DE O-methyl transferase DNA #5.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Conservative: 29  
Mismatches: 52  
Indels: 3  
Query Match:  
RESULT 193  
ID ABS63430 standard; cDNA; 534 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAPALSKI J A.  
Percent Similarity: 58.71%  
Best Local Similarity: 36.13%  
Conservative: 35  
Mismatches: 56  
Indels: 8  
Query Match:  
RESULT 194  
ID ABN87119 standard; cDNA; 628 BP.  
DE Lolium perenne LpCCOAMTb partial nucleotide sequence SEQ ID NO:14.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 51.93%  
Conservative: 30



Best Local Similarity: 35.36% Mismatches: 75  
Query Match: 16.46% Indels: 13  
RESULT 195  
ID AC123249 standard; DNA; 542 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13240.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Percent Similarity: 55.70% Conservative: 28  
Best Local Similarity: 37.97% Mismatches: 59  
Query Match: 15.82% Indels: 13  
RESULT 196  
ID ABS63423 standard; cDNA; 528 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAPALSKI J A.  
Percent Similarity: 59.52% Conservative: 27  
Best Local Similarity: 38.10% Mismatches: 45  
Query Match: 15.41% Indels: 6  
RESULT 197  
Percent Similarity: 54.29% Conservative: 37  
Best Local Similarity: 33.14% Mismatches: 69  
Query Match: 15.08% Indels: 11  
RESULT 198  
Percent Similarity: 54.29% Conservative: 37  
Best Local Similarity: 33.14% Mismatches: 69  
Query Match: 15.08% Indels: 11  
RESULT 199  
ID AAA68101 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 62.93% Conservative: 27  
Best Local Similarity: 39.66% Mismatches: 33  
Query Match: 15.04% Indels: 11  
RESULT 200  
ID ADD41851 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #2.  
PN US200313173-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 62.93% Conservative: 27  
Best Local Similarity: 39.66% Mismatches: 33  
Query Match: 15.04% Indels: 11  
RESULT 201  
ID ADA31006 standard; DNA; 588 BP.  
DE DNA encoding Acinetobacter baumannii protein #2293.  
PN US652958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 50.24% Conservative: 34  
Best Local Similarity: 33.66% Mismatches: 65  
Query Match: 15.00% Indels: 37  
RESULT 202  
ID ABN87109 standard; cDNA; 557 BP.  
DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:3.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.35% Conservative: 28  
Best Local Similarity: 34.06% Mismatches: 52  
Query Match: 14.30% Indels: 11  
RESULT 203  
ID AAS96694 standard; DNA; 8580 BP.  
DE Arabidopsis DMT4 (1DMT4) DNA.  
PN WO200180626-A1.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PD 01-NOV-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 39.59% Conservative: 27  
Best Local Similarity: 25.89% Mismatches: 51  
Query Match: 14.11% Indels: 69  
RESULT 204  
ID ADM39547 standard; DNA; 8580 BP.  
DE DMT polynucleotide #9.  
PN US2003135890-A1.  
PD 17-JUL-2003.  
PA (FISC/) FISCHER R.  
PA (CHOI/) CHOI Y.  
PA (HANN/) HANNON M.  
PA (OKAM/) OKAMURO J.  
PA (TATA/) TATARINOVA T.  
Percent Similarity: 39.59% Conservative: 27  
Best Local Similarity: 25.89% Mismatches: 51  
Query Match: 14.11% Indels: 69  
RESULT 205  
ID AAA68012 standard; DNA; 594 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.17% Conservative: 25  
Best Local Similarity: 36.89% Mismatches: 38  
Query Match: 13.63% Indels: 2  
RESULT 206  
ID ADD41762 standard; DNA; 594 BP.  
DE O-methyl transferase DNA #11.  
PN US200313173-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 61.17% Conservative: 25  
Best Local Similarity: 36.89% Mismatches: 38  
Query Match: 13.63% Indels: 2  
RESULT 207  
ID ADB06101 standard; DNA; 798 BP.  
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:41.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Percent Similarity: 47.98% Conservative: 31  
Best Local Similarity: 32.32% Mismatches: 72  
Query Match: 13.55% Indels: 31  
RESULT 208  
ID ADB12064 standard; DNA; 1754382 BP.  
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Percent Similarity: 47.98% Conservative: 31  
Best Local Similarity: 32.32% Mismatches: 72  
Query Match: 13.55% Indels: 31  
RESULT 209  
ID ABS63421 standard; cDNA; 505 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAPALSKI J A.  
Percent Similarity: 51.92% Conservative: 30  
Best Local Similarity: 32.69% Mismatches: 56  
Query Match: 13.51% Indels: 19  
RESULT 210  
ID AAV23843 standard; DNA; 607 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.



Thu Jan 13 11:25:08 2005

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22% Conservative: 23  
Best Local Similarity: 37.76% Mismatches: 36  
Indels: 2  
Query Match:  
RESULT 211  
ID AAZ06844 standard; cDNA; 607 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.  
PN US9592486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22% Conservative: 23  
Best Local Similarity: 37.76% Mismatches: 36  
Indels: 2  
Query Match:  
RESULT 212  
ID AAA69594 standard; cDNA; 607 BP.  
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22% Conservative: 23  
Best Local Similarity: 37.76% Mismatches: 36  
Indels: 2  
Query Match:  
RESULT 213  
ID AAA67930 standard; DNA; 607 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.22% Conservative: 23  
Best Local Similarity: 37.76% Mismatches: 36  
Indels: 2  
Query Match:  
RESULT 214  
ID ADD41680 standard; DNA; 607 BP.  
DE O-methyl transferase DNA #3.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 61.22% Conservative: 23  
Best Local Similarity: 37.76% Mismatches: 36  
Indels: 2  
Query Match:  
RESULT 215  
ID AAS59516 standard; DNA; 29255 BP.  
DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 45.54% Conservative: 38  
Best Local Similarity: 28.57% Mismatches: 91  
Indels: 32  
Query Match:  
RESULT 216  
ID ACF64445 standard; DNA; 29255 BP.  
DE Propionibacterium acnes DNA contig sequence #11.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 45.54% Conservative: 38  
Best Local Similarity: 28.57% Mismatches: 91  
Indels: 32  
Query Match:  
RESULT 217  
ID ADA4866 standard; DNA; 584 BP.  
DE Banana gene conferring disease resistance in plants.  
PN WO2003000906-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 46.67% Conservative: 18  
Best Local Similarity: 33.33% Mismatches: 38  
Indels: 34  
Query Match:  
RESULT 218  
ID ABS63411 standard; cDNA; 510 BP.

DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 54.93% Conservative: 27  
Best Local Similarity: 35.92% Mismatches: 45  
Indels: 20  
Query Match:  
RESULT 219  
ID ABS63426 standard; cDNA; 600 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 48.84% Conservative: 21  
Best Local Similarity: 36.63% Mismatches: 57  
Indels: 32  
Query Match:  
RESULT 220  
ID AAA31496 standard; DNA; 451 BP.  
DE Plant microsatellite marker #457.  
PN WO9967421-A1.  
PD 29-DEC-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 59.18% Conservative: 21  
Best Local Similarity: 37.76% Mismatches: 38  
Indels: 2  
Query Match:  
RESULT 221  
ID AAA68102 standard; DNA; 296 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 62.89% Conservative: 23  
Best Local Similarity: 39.18% Mismatches: 32  
Indels: 4  
Query Match:  
RESULT 222  
ID ADD41852 standard; DNA; 296 BP.  
DE Caffeoyl CoA methyl transferase DNA #3.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 62.89% Conservative: 23  
Best Local Similarity: 39.18% Mismatches: 32  
Indels: 4  
Query Match:  
RESULT 223  
ID ABQ81846 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Percent Similarity: 42.31% Conservative: 39  
Best Local Similarity: 27.31% Mismatches: 137  
Indels: 13  
Query Match:  
RESULT 224  
ID AAV23873 standard; DNA; 562 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.26% Conservative: 29  
Best Local Similarity: 33.04% Mismatches: 42  
Indels: 6  
Query Match:  
RESULT 225  
ID AAZ06876 standard; cDNA; 562 BP.  
DE Fine O-methyl transferase (OMT) partial cDNA 2.  
PN US95952486-A.



PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.26% Conservative: 29  
Best Local Similarity: 33.04% Mismatches: 42  
Query Match: 12.77% Indels: 6  
RESULT 226  
ID AA69580 standard; cDNA; 562 BP.  
DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.26% Conservative: 29  
Best Local Similarity: 33.04% Mismatches: 42  
Query Match: 12.77% Indels: 6  
RESULT 227  
ID AA67960 standard; DNA; 562 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.26% Conservative: 29  
Best Local Similarity: 33.04% Mismatches: 42  
Query Match: 12.77% Indels: 6  
RESULT 228  
ID AD41710 standard; DNA; 562 BP.  
DE O-methyl transferase DNA #6.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 58.26% Conservative: 29  
Best Local Similarity: 33.04% Mismatches: 42  
Query Match: 12.77% Indels: 6  
RESULT 229  
ID ADP95323 standard; cDNA; 447 BP.  
DE Cotton expressed sequence tag, EST, #4334.  
PN US2004123338-A1.  
PD 24-JUN-2004.  
PA (FINC/) FINCHER K L.  
Percent Similarity: 60.42% Conservative: 22  
Best Local Similarity: 37.50% Mismatches: 36  
Query Match: 12.66% Indels: 2  
RESULT 230  
ID ABX09141 standard; DNA; 75216 BP.  
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV230.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP) INST PASTEUR.  
Percent Similarity: 41.32% Conservative: 33  
Best Local Similarity: 29.86% Mismatches: 134  
Query Match: 12.66% Indels: 37  
RESULT 231  
Percent Similarity: 41.32% Conservative: 33  
Best Local Similarity: 29.86% Mismatches: 134  
Query Match: 12.66% Indels: 37  
RESULT 232  
Percent Similarity: 41.32% Conservative: 33  
Best Local Similarity: 29.86% Mismatches: 134  
Query Match: 12.66% Indels: 37  
RESULT 233  
ID ABO68900 standard; DNA; 1289 BP.  
DE Listeria monocytogenes 4b contig DNA sequence #1666.  
PN WO200228891-A2.  
PD 11-APR-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Percent Similarity: 43.93% Conservative: 36  
Best Local Similarity: 27.10% Mismatches: 96  
Query Match: 12.58% Indels: 24  
RESULT 234

Percent Similarity: 44.95% Conservative: 37  
Best Local Similarity: 27.98% Mismatches: 88  
Query Match: 12.58% Indels: 32  
RESULT 235  
ID ABO70732 standard; DNA; 2233 BP.  
DE Listeria monocytogenes 4b contig DNA sequence #674.  
PN WO200228891-A2.  
PD 11-APR-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Percent Similarity: 43.93% Conservative: 36  
Best Local Similarity: 27.10% Mismatches: 96  
Query Match: 12.51% Indels: 24  
RESULT 236  
ID AA668100 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 61.86% Conservative: 21  
Best Local Similarity: 40.21% Mismatches: 27  
Query Match: 12.21% Indels: 11  
RESULT 237  
ID AD41850 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #1.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 61.86% Conservative: 21  
Best Local Similarity: 40.21% Mismatches: 27  
Query Match: 12.21% Indels: 11  
RESULT 238  
Percent Similarity: 41.84% Conservative: 37  
Best Local Similarity: 26.36% Mismatches: 93  
Query Match: 12.21% Indels: 46  
RESULT 239  
Percent Similarity: 41.84% Conservative: 37  
Best Local Similarity: 26.36% Mismatches: 93  
Query Match: 12.21% Indels: 46  
RESULT 240  
ID ADA31376 standard; DNA; 702 BP.  
DE DNA encoding Acinetobacter baumannii protein #2663.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 42.92% Conservative: 37  
Best Local Similarity: 26.03% Mismatches: 104  
Query Match: 12.10% Indels: 21  
RESULT 241  
Percent Similarity: 51.18% Conservative: 38  
Best Local Similarity: 28.82% Mismatches: 72  
Query Match: 12.10% Indels: 11  
RESULT 242  
ID ABX62366 standard; DNA; 415 BP.  
DE Arabidopsis thaliana expressed sequence related polynucleotide #481.  
PN US2002040490-A1.  
PD 04-APR-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.



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PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 46.11%  
Best Local Similarity: 43.28%  
Best Local Similarity: 23.95%  
Query Match: 9.34%  
RESULT 258  
Conservative: 46  
Mismatch: 84  
Indels: 51  
Percent Similarity: 43.28%  
Best Local Similarity: 23.95%  
Query Match: 9.34%  
RESULT 259  
Conservative: 46  
Mismatch: 84  
Indels: 51  
ID ABN87123 standard; cDNA; 532 BP.  
DE Loliu perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:18.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRERESEARCH LTD.  
Percent Similarity: 52.69%  
Best Local Similarity: 32.26%  
Query Match: 9.23%  
RESULT 260  
Conservative: 19  
Mismatch: 38  
Indels: 7  
ID ABN87124 standard; cDNA; 532 BP.  
DE Loliu perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:19.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRERESEARCH LTD.  
Percent Similarity: 52.69%  
Best Local Similarity: 32.26%  
Query Match: 9.23%  
RESULT 261  
Conservative: 19  
Mismatch: 38  
Indels: 7  
ID ADC92983 standard; DNA; 498 BP.  
DE E. faecium DNA sequence SEQ ID 2610.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 45.78%  
Best Local Similarity: 28.31%  
Query Match: 9.16%  
RESULT 262  
Conservative: 29  
Mismatch: 74  
Indels: 16  
ID ABN91349 standard; DNA; 699 BP.  
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:812.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 44.83%  
Best Local Similarity: 22.99%  
Query Match: 9.16%  
RESULT 263  
Conservative: 38  
Mismatch: 86  
Indels: 10  
ID AAH54424 standard; DNA; 3673 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3788.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX) GLAXO GROUP LTD.  
Percent Similarity: 44.83%  
Best Local Similarity: 22.99%  
Query Match: 9.16%  
RESULT 264  
Conservative: 38  
Mismatch: 86  
Indels: 10  
ID AAA31117 standard; DNA; 402 BP.  
DE Plant microsatellite marker #78.  
PN WO9967421-A1.  
PD 29-DEC-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
Percent Similarity: 57.32%  
Best Local Similarity: 39.02%  
Query Match: 9.08%  
RESULT 265  
Conservative: 15  
Mismatch: 32  
Indels: 3  
ID ABX06678 standard; DNA; 711 BP.  
DE S. pneumoniae type 4 strain coding region #966.  
PN WO200272021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 46.11%  
Best Local Similarity: 26.11%  
Query Match: 9.05%  
RESULT 266  
Conservative: 36  
Mismatch: 66  
Indels: 31  
ID AA552241 standard; DNA; 11309 BP.  
DE Streptococcus pneumoniae genome fragment SEQ ID NO:108.  
PN WO9918931-A2.  
PD 07-MAY-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 46.11%  
Best Local Similarity: 26.11%  
Query Match: 9.05%  
RESULT 267  
Conservative: 36  
Mismatch: 66  
Indels: 31  
Percent Similarity: 46.11%  
Best Local Similarity: 26.11%  
Query Match: 9.05%  
RESULT 268  
Conservative: 36  
Mismatch: 66  
Indels: 31  
ID AA254186 standard; DNA; 918 BP.  
DE Neisseria gonorrhoeae ORF 695 partial DNA sequence SEQ ID NO:2321.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 60.00%  
Best Local Similarity: 35.71%  
Query Match: 8.94%  
RESULT 269  
Conservative: 17  
Mismatch: 18  
Indels: 10  
ID AA254188 standard; DNA; 921 BP.  
DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2325.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 60.61%  
Best Local Similarity: 36.36%  
Query Match: 8.94%  
RESULT 270  
Conservative: 16  
Mismatch: 24  
Indels: 2  
ID ABX17318 standard; cDNA; 2712 BP.  
DE Human cancer promoting protein PP7517.  
PN CN1351082-A.  
PD 29-MAY-2002.  
PA (SHAN-) SHANGHAI INST ONCOLOGY.  
Percent Similarity: 40.19%  
Best Local Similarity: 28.50%  
Query Match: 8.90%  
RESULT 271  
Conservative: 25  
Mismatch: 81  
Indels: 47  
ID AAD13477 standard; cDNA; 507 BP.  
DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #2.  
PN WO200157220-A2.  
PD 09-AUG-2001.  
PA (LEXI-) LEXICON GENETICS INC.  
Percent Similarity: 45.52%  
Best Local Similarity: 32.84%  
Query Match: 8.79%  
RESULT 272  
Conservative: 17  
Mismatch: 53  
Indels: 20  
ID AA254187 standard; DNA; 918 BP.  
DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2323.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 60.61%  
Best Local Similarity: 36.36%  
Query Match: 8.79%  
RESULT 273  
Conservative: 16  
Mismatch: 24  
Indels: 2  
ID AAH66205 standard; DNA; 639 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 1240.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 39.70%  
Best Local Similarity: 25.63%  
Conservative: 28  
Mismatch: 82



Query Match: 8.56% Indels: 38  
RESULT 274  
ID ACA00413 standard; DNA: 639 BP.  
DE C. glutamicum derived ORF SEQ ID 404.  
PN DE10128510-A1.  
PD 19-DEC-2002.  
PA (DEGS) DEGUSSA AG.  
Percent Similarity: 39.70%  
Best Local Similarity: 25.63%  
Conservative: 28  
Mismatches: 82  
Indels: 38  
Query Match: 8.56%  
RESULT 275  
ID ADD13690 standard; DNA: 769 BP.  
DE C. glutamicum homeostasis and adaptation associated DNA SEQ ID 91.  
PN WO2003040290-A2.  
PD 15-MAY-2003.  
PA (BADI) BASF AG.  
Percent Similarity: 39.70%  
Best Local Similarity: 25.63%  
Conservative: 28  
Mismatches: 82  
Indels: 38  
Query Match: 8.56%  
RESULT 276  
ID AAF68527 standard; DNA: 349980 BP.  
DE C. glutamicum coding sequence fragment SEQ ID NO: 7062.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 39.70%  
Best Local Similarity: 25.63%  
Conservative: 28  
Mismatches: 82  
Indels: 38  
Query Match: 8.56%  
RESULT 277  
ID ACF72506 standard; DNA: 636 BP.  
DE Staphylococcus aureus DNA #186.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 42.01%  
Best Local Similarity: 21.92%  
Conservative: 44  
Mismatches: 99  
Indels: 28  
Query Match: 8.49%  
RESULT 278  
ID ABL12193 standard; cDNA: 5514 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Percent Similarity: 42.33%  
Best Local Similarity: 29.63%  
Conservative: 24  
Mismatches: 70  
Indels: 39  
Query Match: 8.49%  
RESULT 279  
ID ABL12193 standard; cDNA: 5514 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Percent Similarity: 42.33%  
Best Local Similarity: 29.63%  
Conservative: 24  
Mismatches: 70  
Indels: 39  
Query Match: 8.49%  
RESULT 280  
ID ABL12193 standard; cDNA: 5514 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Percent Similarity: 42.33%  
Best Local Similarity: 29.63%  
Conservative: 24  
Mismatches: 70  
Indels: 39  
Query Match: 8.49%  
RESULT 281  
ID AAC89765 standard; cDNA: 178 BP.  
DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
PN WO200007334-A2.  
PD 07-DEC-2000.  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 8.41%  
RESULT 282  
ID ABN91116 standard; cDNA: 457 BP.  
DE Lolium perenne lpCCOAM7a partial nucleotide sequence SEQ ID NO:10.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
Percent Similarity: 54.93%  
Best Local Similarity: 35.21%  
Conservative: 14  
Mismatches: 26  
Indels: 6  
Query Match: 8.41%

RESULT 283  
ID AAD35115 standard; DNA: 2086 BP.  
DE Corynebacterium glutamicum sigE gene.  
PN WO200218428-A2.  
PD 07-MAR-2002.  
PA (DEGS) DEGUSSA AG.  
Percent Similarity: 39.80%  
Best Local Similarity: 25.51%  
Conservative: 28  
Mismatches: 80  
Indels: 38  
Query Match: 8.34%  
RESULT 284  
ID ABQ90300 standard; DNA: 4029 BP.  
DE M. capsulatus gene #285 for DNA array.  
PN WO200255655-A2.  
PD 18-JUL-2002.  
PA (UNIF-) UNIFOB STIFTTELSEN UNIV BERGEN.  
Percent Similarity: 37.63%  
Best Local Similarity: 25.44%  
Conservative: 35  
Mismatches: 98  
Indels: 83  
Query Match: 8.30%  
RESULT 285  
ID AAH53823 standard; DNA: 495 BP.  
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3039.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX) GLAXO GROUP LTD.  
Percent Similarity: 44.24%  
Best Local Similarity: 22.42%  
Conservative: 36  
Mismatches: 82  
Indels: 10  
Query Match: 8.27%  
RESULT 286  
ID ADB74275 standard; DNA: 38494 BP.  
DE Mycobacterium leprae DNA #2.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 50.00%  
Best Local Similarity: 33.33%  
Conservative: 14  
Mismatches: 42  
Indels: 0  
Query Match: 8.27%  
RESULT 287  
ID AAA68082 standard; DNA: 236 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:175.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 54.55%  
Best Local Similarity: 29.87%  
Conservative: 19  
Mismatches: 27  
Indels: 8  
Query Match: 8.19%  
RESULT 288  
ID ADD41832 standard; DNA: 236 BP.  
DE O-methyl transferase DNA #16.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK-) BLOKBERG L N.  
Percent Similarity: 54.55%  
Best Local Similarity: 29.87%  
Conservative: 19  
Mismatches: 27  
Indels: 8  
Query Match: 8.19%  
RESULT 289  
ID AAQ13306 standard; DNA: 1107 BP.  
DE Human catechol-O-methyltransferase gene.  
PN WO9111513-A.  
PD 08-AUG-1991.  
PA (ORIN) ORION YHTVMAE OY.  
Percent Similarity: 38.72%  
Best Local Similarity: 23.31%  
Conservative: 41  
Mismatches: 118  
Indels: 45  
Query Match: 8.08%  
RESULT 290  
ID ADP45594 standard; DNA: 133100 BP.  
DE Human NUMA1/FLJ20625/LOC220074 region gDNA.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
Percent Similarity: 41.83%  
Best Local Similarity: 28.37%  
Conservative: 28  
Mismatches: 81  
Indels: 41  
Query Match: 8.04%  
RESULT 291



ID AB283278 standard; cDNA; 1024 BP.  
 DE Toxicologically relevant human nucleotide sequence #437.  
 PN WO2003016500-A2.  
 PD 27-FEB-2003.  
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Indels: 45  
 Query Match: 8.00%  
 RESULT 292  
 ID ADE84973 standard; DNA; 1206 BP.  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
 PN WO2003038129-A2.  
 PD 08-MAY-2003.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Indels: 45  
 Query Match: 8.00%  
 RESULT 293  
 ID ABX63642 standard; cDNA; 1327 BP.  
 DE Human cDNA #642 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND//) BANDMAN O.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Indels: 45  
 Query Match: 8.00%  
 RESULT 294  
 ID AB251068 standard; cDNA; 836 BP.  
 DE Aspergillus oryzae polynucleotide SEQ ID NO 181.  
 PN WO200279476-A1.  
 PD 10-OCT-2002.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 Percent Similarity: 40.96% Conservative: 21  
 Best Local Similarity: 28.31% Mismatches: 57  
 Indels: 41  
 Query Match: 7.97%  
 RESULT 295  
 ID AAC77872 standard; cDNA; 1350 BP.  
 DE Human cancer associated gene sequence SEQ ID NO:266.  
 PN WO200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.84% Conservative: 38  
 Best Local Similarity: 24.70% Mismatches: 116  
 Indels: 35  
 Query Match: 7.89%  
 RESULT 296  
 ID AAA31195 standard; DNA; 356 BP.  
 DE Plant microsatellite marker #156.  
 PN WO9967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Percent Similarity: 52.87% Conservative: 16  
 Best Local Similarity: 34.48% Mismatches: 33  
 Indels: 9  
 Query Match: 7.82%  
 RESULT 297  
 ID AAB35116 standard; DNA; 457 BP.  
 DE Corynebacterium glutamicum sigE gene upstream region DNA.  
 PN WO200218428-A2.  
 PD 07-MAR-2002.  
 PA (DEGS) DEGUSA AG.  
 Percent Similarity: 44.37% Conservative: 26  
 Best Local Similarity: 26.06% Mismatches: 59  
 Indels: 20  
 Query Match: 7.82%  
 RESULT 298  
 ID ACA51621 standard; DNA; 834 BP.  
 DE Prokaryotic essential gene #33278.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.11% Conservative: 33  
 Best Local Similarity: 26.57% Mismatches: 95

Query Match: 7.71% Indels: 82  
 RESULT 299  
 ID ADB58045 standard; DNA; 1531 BP.  
 DE Toxicity-related gene, SEQ ID 3071.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Indels: 31  
 Query Match: 7.71%  
 RESULT 300  
 ID ADB52519 standard; DNA; 1531 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Indels: 31  
 Query Match: 7.71%  
 RESULT 301  
 ID ADK16023 standard; DNA; 64492 BP.  
 DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
 PN US2004053274-A1.  
 PD 18-MAR-2004.  
 PA (TOKD) TOKYO INST TECHNOLOGY.  
 Percent Similarity: 30.15% Conservative: 24  
 Best Local Similarity: 22.77% Mismatches: 85  
 Indels: 142  
 Query Match: 7.67%  
 RESULT 302  
 ID AAQ13305 standard; DNA; 1591 BP.  
 DE Rat catechol-O-methyltransferase gene.  
 PN WO9111513-A.  
 PD 08-AUG-1991.  
 PA (ORIN) ORION YHTYMAE OY.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Indels: 31  
 Query Match: 7.63%  
 RESULT 303  
 ID AAS83954 standard; cDNA; 4083 BP.  
 DE DNA encoding novel human diagnostic protein #19758.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 37.29% Conservative: 18  
 Best Local Similarity: 27.12% Mismatches: 66  
 Indels: 45  
 Query Match: 7.63%  
 RESULT 304  
 ID AAQ88760 standard; DNA; 1813 BP.  
 DE Human ubiquitous nuclear receptor protein DNA.  
 PN WO9513373-A1.  
 PD 18-MAY-1995.  
 PA (ARCH-) ARCH DEV CORP.  
 Percent Similarity: 34.41% Conservative: 30  
 Best Local Similarity: 25.59% Mismatches: 122  
 Indels: 101  
 Query Match: 7.59%  
 RESULT 305  
 ID AAT79634 standard; DNA; 1898 BP.  
 DE DNA encoding human ubiquitous nuclear receptor polypeptide.  
 PN US5639616-A.  
 PD 17-JUN-1997.  
 PA (ARCH-) ARCH DEV CORP.  
 Percent Similarity: 34.21% Conservative: 29  
 Best Local Similarity: 25.73% Mismatches: 120  
 Indels: 105  
 Query Match: 7.59%  
 RESULT 306  
 ID AAT27617 standard; cDNA to mRNA; 1688 BP.  
 DE Steroid hormone receptor analogue ECDN small mol. variant cDNA.  
 PN WO9609324-A1.  
 PD 28-MAR-1996.  
 PA (CANC-) CANCER INST.  
 Percent Similarity: 37.41% Conservative: 32  
 Best Local Similarity: 25.90% Mismatches: 106



Query Match: 7.56% Indels: 68

RESULT 307

ID ACC85541 standard; DNA; 2505 BP.

DE T thermophilus strain GK24 DNA polymerase gene SEQ ID NO: 1.

PN WO2003048309-A2.

PD 12-JUN-2003.

PA (APPL-) APPLERA CORP.

Percent Similarity: 36.73%

Best Local Similarity: 26.19%

Query Match: 7.56%

RESULT 308

ID ACC85544 standard; DNA; 2505 BP.

DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 4.

PN WO2003048309-A2.

PD 12-JUN-2003.

PA (APPL-) APPLERA CORP.

Percent Similarity: 36.73%

Best Local Similarity: 26.19%

Query Match: 7.56%

RESULT 309

ID AB211775 standard; cDNA; 1564 BP.

DE Human polynucleotide SEQ ID NO 657.

PN WO200270539-A2.

PD 12-SEP-2002.

PA (HYSE-) HYSEQ INC.

Percent Similarity: 31.96%

Best Local Similarity: 24.63%

Query Match: 7.52%

RESULT 310

ID ADM44293 standard; cDNA; 1786 BP.

DE Novel human arginine-rich protein cDNA #657.

PN US2004053250-A1.

PD 18-MAR-2004.

PA (TANG/) TANG Y T.

PA (XUEA/) XUE A.

PA (DRMA/) DRMANAC R T.

Percent Similarity: 31.96%

Best Local Similarity: 24.63%

Query Match: 7.52%

RESULT 311

ID ADC30127 standard; cDNA; 3298 BP.

DE Human novel cDNA sequence, SEQ ID NO:209.

PN WO2003029271-A2.

PD 10-APR-2003.

PA (HYSE-) HYSEQ INC.

Percent Similarity: 37.09%

Best Local Similarity: 28.17%

Query Match: 7.52%

RESULT 312

ID ACF36088 standard; DNA; 1815 BP.

DE Human LXR beta polypeptide encoding DNA.

PN WO2003059884-A1.

PD 24-JUL-2003.

PA (XCEP-) X-CEPTOR THERAPEUTICS INC.

Percent Similarity: 37.68%

Best Local Similarity: 27.90%

Query Match: 7.48%

RESULT 313

ID ACF04414 standard; DNA; 1815 BP.

DE Human liver X receptor LXR beta coding sequence.

PN WO2003060078-A2.

PD 24-JUL-2003.

PA (XCEP-) X-CEPTOR THERAPEUTICS INC.

Percent Similarity: 37.68%

Best Local Similarity: 27.90%

Query Match: 7.48%

RESULT 314

ID ADL12925 standard; cDNA; 1987 BP.

DE Human steroid-induced C3A liver cell cDNA #654.

PN US6673549-B1.

PD 06-JAN-2004.

PA (INCY-) INCYTE CORP.

Percent Similarity: 37.68%

Conservative: 27

Mismatches: 108

Indels: 64

Best Local Similarity: 27.90%

Query Match: 7.48%

RESULT 315

ID AAT88206 standard; cDNA; 8460 BP.

DE cDNA for protein (OA-519) cross-reactive with hpr gene product.

PN US5665874-A.

PD 09-SEP-1997.

PA (UYJO ) UNIV JOHNS HOPKINS.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 316

ID ACC49471 standard; cDNA; 8460 BP.

DE Human fatty acid synthase encoding cDNA.

PN WO2003023355-A2.

PD 20-MAR-2003.

PA (BURN-) BURNHAM INST.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 317

ID ACA64923 standard; DNA; 8460 BP.

DE Human breast carcinoma fatty acid synthase DNA corresponding to U29344.

PN DE10127572-A1.

PD 05-DEC-2002.

PA (PATH-) PATHOARRAY GMBH.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 318

ID ACF63393 standard; DNA; 8460 BP.

DE Human fatty acid synthase gene SEQ ID NO:115.

PN WO2003006478-A1.

PD 23-JAN-2003.

PA (OLIG-) OLIGOS ETC INC.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 319

ID ADO21281 standard; cDNA; 8460 BP.

DE DNA encoding human fatty acid synthase.

PN US2004077570-A1.

PD 22-APR-2004.

PA (FREI/) FREIER S M.

PA (DOBI/) DOBIE K W.

PA (BHAN/) BHANOT S.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 320

ID ADP13456 standard; DNA; 8460 BP.

DE Renal cell carcinoma differentially expressed gene #192.

PN WO2004048933-A2.

PD 10-JUN-2004.

PA (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 321

ID AAV74506 standard; DNA; 13715 BP.

DE Staphylococcus aureus contig SEQ ID #195.

PN EP786519-A2.

PD 30-JUL-1997.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 39.27%

Best Local Similarity: 21.46%

Query Match: 7.45%

Conservative: 39

Mismatches: 105

Indels: 28



RESULT 322  
 ID ABD07304 standard; DNA; 2469 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5908.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.37%  
 Best Local Similarity: 27.40%  
 Query Match: 7.41%  
 Indels: 69  
 Conservative: 28  
 Mismatches: 107  
 RESULT 323  
 ID ABD11218 standard; DNA; 636 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9822.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 43.88%  
 Best Local Similarity: 28.78%  
 Query Match: 7.37%  
 Indels: 20  
 Conservative: 21  
 Mismatches: 58  
 RESULT 324  
 ID ABD11311 standard; DNA; 1275 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9915.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 43.88%  
 Best Local Similarity: 28.78%  
 Query Match: 7.37%  
 Indels: 20  
 Conservative: 21  
 Mismatches: 58  
 RESULT 325  
 ID ABD11556 standard; DNA; 1443 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10160.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 43.88%  
 Best Local Similarity: 28.78%  
 Query Match: 7.37%  
 Indels: 20  
 Conservative: 21  
 Mismatches: 58  
 RESULT 326  
 ID AAQ24322 standard; DNA; 1635 BP.  
 DE Mutant thermostable DNA polymerase p205A292.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98%  
 Best Local Similarity: 25.09%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 37  
 Mismatches: 112  
 RESULT 327  
 ID AAQ24321 standard; DNA; 1899 BP.  
 DE Mutant thermostable DNA polymerase p205d2-203.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98%  
 Best Local Similarity: 25.09%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 37  
 Mismatches: 112  
 RESULT 328  
 ID ABX84201 standard; cDNA; 2010 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #772.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 27.62%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 329  
 ID ADJ14181 standard; DNA; 2010 BP.  
 DE DNA encoding human liver X receptor LXR beta.  
 PN US2004018560-A1.  
 PD 29-JAN-2004.  
 PA (BLED/) BLED SOE R K.  
 PA (MILL/) MILLER A.  
 PA (MOOR/) MOORE J T.  
 PA (WILL/) WILLIAMS S P.  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 330  
 ID ADJ14181 standard; DNA; 2010 BP.  
 DE Human liver X receptor beta gene.  
 PN EPI398032-A1.  
 PD 17-MAR-2004.  
 PA (PHEN-) PHENEX PHARM AG.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 27.62%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 331  
 ID AAQ63134 standard; cDNA; 2030 BP.  
 DE Human recombinant steroid hormone receptor NERI cDNA.  
 PN WO9407916-A1.  
 PD 14-APR-1994.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 27.62%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 332  
 ID AAT18996 standard; DNA; 2030 BP.  
 DE Human steroid receptor NER gene.  
 PN WO9613519-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 27.62%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 333  
 ID AAT30031 standard; DNA; 2030 BP.  
 DE NER receptor potentiator DNA.  
 PN WO9613257-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MEDICAL COLLEGE PENNSYLVANIA.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 27.62%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 29  
 Mismatches: 111  
 RESULT 334  
 ID AAQ24320 standard; DNA; 2043 BP.  
 DE Mutant thermostable DNA polymerase p205d2-155.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98%  
 Best Local Similarity: 25.09%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 37  
 Mismatches: 112  
 RESULT 335  
 ID AAQ24013 standard; DNA; 2277 BP.  
 DE Mutant thermostable DNA polymerase p205d2-77.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98%  
 Best Local Similarity: 25.09%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 37  
 Mismatches: 112  
 RESULT 336  
 ID AAQ24012 standard; DNA; 2370 BP.  
 DE Mutant thermostable DNA polymerase p205d2-46.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98%  
 Best Local Similarity: 25.09%  
 Query Match: 7.37%  
 Indels: 67  
 Conservative: 37  
 Mismatches: 112  
 RESULT 337  
 ID AAQ24011 standard; DNA; 2505 BP.  
 DE Mutant thermostable DNA polymerase from Thermus species Z05.  
 PN WO9206200-A.



Query Match:	7.33%	Indels:	58
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Conservative:	24		
Mismatches:	58		
Indels:	58		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			
PA (HOF) ROCHE DIAGNOSTICS GMBH.			
Conservative:	37		
Mismatches:	112		
Indels:	67		
Query Match:			
PD 08-OCT-2003.			



DE Pseudomonas aeruginosa polynucleotide #109.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.16%  
Best Local Similarity: 26.57%  
Query Match: 7.30%  
Indels: 101  
RESULT 355  
ID AAH16078 standard; cDNA; 1782 BP.  
DE Human cDNA sequence SEQ ID NO:14776.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 31.67%  
Best Local Similarity: 24.63%  
Query Match: 7.30%  
Indels: 108  
RESULT 356  
ID ACC78000 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 37.37%  
Best Local Similarity: 25.61%  
Query Match: 7.30%  
Indels: 68  
RESULT 357  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Percent Similarity: 32.34%  
Best Local Similarity: 21.66%  
Query Match: 7.30%  
Indels: 149  
RESULT 358  
ID ABD10747 standard; DNA; 657 BP.  
DE Pseudomonas aeruginosa polynucleotide #9351.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.50%  
Best Local Similarity: 28.32%  
Query Match: 7.26%  
Indels: 56  
RESULT 359  
ID AA291260 standard; DNA; 1632 BP.  
DE Acetohydroxyacid synthase nucleotide sequence SEQ ID NO:14.  
PN WO200004158-A2.  
PD 27-JAN-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Percent Similarity: 38.33%  
Best Local Similarity: 26.48%  
Query Match: 7.26%  
Indels: 53  
RESULT 360  
ID AA127616 standard; cDNA to mRNA; 1979 BP.  
DE Human foetal lung steroid hormone receptor analogue BCDN cDNA.  
PN WO9609324-A1.  
PD 28-MAR-1996.  
PA (CANC-) CANCER INST.  
PA (EISA) EISAI CO LTD.  
Percent Similarity: 37.77%  
Best Local Similarity: 28.42%  
Query Match: 7.26%  
Indels: 68  
RESULT 361  
ID ABD13152 standard; DNA; 2232 BP.  
DE Pseudomonas aeruginosa polynucleotide #11756.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.11%  
Best Local Similarity: 28.32%  
Query Match: 7.26%  
Indels: 67  
RESULT 362  
ID ABD13005 standard; DNA; 2274 BP.

DE Pseudomonas aeruginosa polynucleotide #11609.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.11%  
Best Local Similarity: 28.32%  
Query Match: 7.28%  
Indels: 67  
RESULT 363  
ID ACC85543 standard; DNA; 2505 BP.  
DE T thermophilus strain 1b21 DNA polymerase gene SEQ ID NO: 3.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 37.33%  
Best Local Similarity: 25.68%  
Query Match: 7.26%  
Indels: 74  
RESULT 364  
ID ACC85542 standard; DNA; 2505 BP.  
DE T thermophilus strain RQ-1 DNA polymerase gene SEQ ID NO: 2.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.68%  
Query Match: 7.26%  
Indels: 74  
RESULT 365  
ID ACC85547 standard; DNA; 2505 BP.  
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 7.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.39%  
Best Local Similarity: 26.19%  
Query Match: 7.26%  
Indels: 78  
RESULT 366  
ID ACC85545 standard; DNA; 2505 BP.  
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 5.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.68%  
Query Match: 7.26%  
Indels: 74  
RESULT 367  
ID ACC85550 standard; DNA; 2505 BP.  
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 10.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.39%  
Best Local Similarity: 26.19%  
Query Match: 7.26%  
Indels: 78  
RESULT 368  
ID ACC85546 standard; DNA; 2505 BP.  
DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 6.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 37.33%  
Best Local Similarity: 25.68%  
Query Match: 7.26%  
Indels: 74  
RESULT 369  
ID ABD13232 standard; DNA; 2613 BP.  
DE Pseudomonas aeruginosa polynucleotide #11836.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.11%  
Best Local Similarity: 28.32%  
Query Match: 7.26%  
Indels: 67  
RESULT 370  
ID ACC77974 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.



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PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 371
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 34
Mismatches: 112
Indels: 74
RESULT 372
ID AAZ31253 standard; DNA; 24494 BP.
DE Bacterium 2412.1 fumonis-catabolising gene cluster.
PN WO200004158-A2.
PD 27-JAN-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 38.33%
Best Local Similarity: 26.48%
Query Match: 7.26%
Conservative: 34
Mismatches: 124
Indels: 53
RESULT 373
ID AAQ46806 standard; DNA; 29879 BP.
DE eryA region of S. erythraea chromosome.
PN WO9313663-A1.
PD 22-JUL-1993.
PA (ABBO-) ABBOTT LAB.
Percent Similarity: 33.03%
Best Local Similarity: 24.62%
Query Match: 7.26%
Conservative: 28
Mismatches: 93
Indels: 130
RESULT 374
ID ABD11655 standard; DNA; 1086 BP.
DE Pseudomonas aeruginosa polynucleotide #10259.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Conservative: 40
Mismatches: 122
Indels: 49
RESULT 375
ID ABD11993 standard; DNA; 1101 BP.
DE Pseudomonas aeruginosa polynucleotide #10597.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Conservative: 40
Mismatches: 122
Indels: 49
RESULT 376
ID ACA45703 standard; DNA; 1104 BP.
DE Prokaryotic essential gene #27360.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 44.22%
Best Local Similarity: 26.63%
Query Match: 7.22%
Conservative: 35
Mismatches: 72
Indels: 39
RESULT 377
ID AA81453 standard; DNA; 36471 BP.
DE N. meningitidis partial DNA sequence gnm_1 SEQ ID NO:1.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Conservative: 36
Mismatches: 103
Indels: 92
RESULT 378
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 379
ID AAF21611 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Conservative: 36
Mismatches: 103
Indels: 92
RESULT 380
ID ABD13494 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #12098.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%
Conservative: 24
Mismatches: 93
Indels: 71
RESULT 381
ID ABD13569 standard; DNA; 984 BP.
DE Pseudomonas aeruginosa polynucleotide #12173.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%
Conservative: 24
Mismatches: 93
Indels: 71
RESULT 382
ID ABD13816 standard; DNA; 1254 BP.
DE Pseudomonas aeruginosa polynucleotide #12420.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.03%
Best Local Similarity: 27.57%
Query Match: 7.19%
Conservative: 23
Mismatches: 125
Indels: 50
RESULT 383
ID ACC77992 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.19%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 384
ID ABD07318 standard; DNA; 3135 BP.
DE Pseudomonas aeruginosa polynucleotide #5922.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.17%
Best Local Similarity: 27.14%
Query Match: 7.15%
Conservative: 27
Mismatches: 101
Indels: 68
RESULT 385
ID ADC59447 standard; cDNA; 15534 BP.
DE Human epiplakin-encoding cDNA.
PN JP2003047469-A.
PD 18-FEB-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Percent Similarity: 34.68%
Best Local Similarity: 25.25%
Query Match: 7.15%
Conservative: 28
Mismatches: 101
Indels: 93
RESULT 386
ID ADJ75047 standard; DNA; 15534 BP.
DE Marker gene SEQ ID NO:299.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 34.68%
Best Local Similarity: 25.25%
Query Match: 7.15%
Conservative: 28
Mismatches: 101
Indels: 93

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RESULT 387  
 ID ACF12853 standard; cDNA; 15952 BP.  
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:51.  
 PN WO2002101075-A2.  
 PD 19-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.11% Indels: 93  
 RESULT 388  
 ID ABD09003 standard; DNA; 852 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7607.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.39% Conservative: 20  
 Best Local Similarity: 27.27% Mismatches: 71  
 Query Match: 7.11% Indels: 29  
 RESULT 389  
 ID ABD05329 standard; DNA; 1452 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3933.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89% Conservative: 34  
 Best Local Similarity: 26.30% Mismatches: 95  
 Query Match: 7.11% Indels: 70  
 RESULT 390  
 ID AAT27255 standard; DNA; 1794 BP.  
 DE DNA polymerase I exonuclease-free fragment.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74  
 RESULT 391  
 ID AAT732327 standard; DNA; 1794 BP.  
 DE Thermus flavus DNA polymerase I exonuclease free fragment.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74  
 RESULT 392  
 ID ADN96193 standard; cDNA; 1837 BP.  
 DE Human NOVX polynucleotide #124.  
 PN US2004067490-A1.  
 PD 08-APR-2004.  
 PA (ZHON/) ZHONG M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (SPYT/) SPYTEK K A.  
 PA (KEKU/) KEKUDA R.  
 PA (TAUP/) TAUPIER R J.  
 PA (ANDE/) ANDERSON D W.  
 PA (VERN/) VERNET C A M.  
 PA (CATT/) CATTERTON E.  
 PA (MILL/) MILLER C E.  
 PA (SHEN/) SHENOY S G.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (TCHE/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (GUSE/) GUSEV V Y.  
 PA (MALY/) MALYANKAR U M.  
 PA (BURG/) BURGESS C E.  
 PA (GERL/) GERLACH V.  
 PA (CASM/) CASMAN S J.  
 PA (RIEG/) RIEGER D K.  
 PA (GROS/) GROSSE W M.  
 PA (SMIT/) SMITHSON G.

PA (PEYM/) PEYMAN J A.  
 PA (STAR/) STARLING G.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LARO/) LAROCHELLE W J.  
 PA (SHIM/) SHIMKETS R A.  
 PA (CRAB/) CRABTREE J.  
 PA (RAST/) RASTELLI L.  
 PA (VOSS/) VOSS E Z.  
 PA (BOLD/) BOLDOG F L.  
 PA (EDIN/) EDINGER S R.  
 PA (MILL/) MILLET I.  
 PA (MACD/) MACDOUGALL J R.  
 PA (ELLE/) ELLERMAN K.  
 PA (CHAP/) CHAPOVAL A.  
 Percent Similarity: 32.99% Conservative: 25  
 Best Local Similarity: 24.40% Mismatches: 93  
 Query Match: 7.11% Indels: 102  
 RESULT 393  
 ID AAS4053 standard; DNA; 2553 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #184.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26% Conservative: 24  
 Best Local Similarity: 27.47% Mismatches: 99  
 Query Match: 7.11% Indels: 76  
 RESULT 394  
 ID ACA42124 standard; DNA; 2553 BP.  
 DE Prokaryotic essential gene #23781.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26% Conservative: 24  
 Best Local Similarity: 27.47% Mismatches: 99  
 Query Match: 7.11% Indels: 76  
 RESULT 395  
 ID AA448661 standard; DNA; 2942 BP.  
 DE L. mycophilus chitinase gene, N4-7 ch1a.  
 PN WO9955833-A2.  
 PD 04-NOV-1999.  
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.  
 Percent Similarity: 35.89% Conservative: 21  
 Best Local Similarity: 27.42% Mismatches: 92  
 Query Match: 7.11% Indels: 68  
 RESULT 396  
 ID AAT27254 standard; DNA; 3048 BP.  
 DE DNA polymerase I holoenzyme coding sequence.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74  
 RESULT 397  
 ID ACC78014 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.11% Indels: 74  
 RESULT 398  
 ID ACC78011 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.11% Indels: 74  
 RESULT 399  
 ID ACC77998 standard; DNA; 3221 BP.



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DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.68%
Query Match: 7.11%
Indels: 74
Conservative: 33
Mismatch: 112
Indels: 74
RESULT 400
ID ABD05402 standard; DNA; 4284 BP.
DE Pseudomonas aeruginosa polynucleotide #4006.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.89%
Best Local Similarity: 26.30%
Query Match: 7.11%
Indels: 70
Conservative: 34
Mismatch: 95
Indels: 70
RESULT 401
ID ABO55289 standard; cDNA; 553 BP.
DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.66%
Best Local Similarity: 25.00%
Query Match: 7.07%
Indels: 4
Conservative: 24
Mismatch: 59
Indels: 4
RESULT 402
ID AAH13983 standard; cDNA; 1416 BP.
DE Human cDNA sequence SEQ ID NO:11048.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.13%
Best Local Similarity: 24.89%
Query Match: 7.07%
Indels: 55
Conservative: 29
Mismatch: 94
Indels: 55
RESULT 403
ID ACA27231 standard; DNA; 1948 BP.
DE Prokaryotic essential gene #8888.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 29.66%
Best Local Similarity: 22.57%
Query Match: 7.07%
Indels: 172
Conservative: 27
Mismatch: 96
Indels: 172
RESULT 404
ID ADA52678 standard; cDNA; 2597 BP.
DE Human coding sequence, SEQ ID 246.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.13%
Best Local Similarity: 24.89%
Query Match: 7.07%
Indels: 55
Conservative: 29
Mismatch: 94
Indels: 55
RESULT 405
ID ADD69665 standard; cDNA; 3153 BP.
DE Human REMAP cDNA - SEQ ID 94.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 39.81%
Best Local Similarity: 26.07%
Query Match: 7.07%
Indels: 55
Conservative: 29
Mismatch: 72
Indels: 55
RESULT 406
ID ADD24914 standard; DNA; 4184 BP.
DE DNA encoding Escherichia coli intracellular protease #6.
PN US2003036176-A1.
PD 20-FEB-2003.
PA (BOWE/) BOWEN S G.
Percent Similarity: 36.84%
Best Local Similarity: 25.39%
Query Match: 7.07%
Indels: 97
Conservative: 37
Mismatch: 109
Indels: 97
RESULT 407
ID AAF86431 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #1.
PN FR2792851-A1.
PD 27-OCT-2000.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Percent Similarity: 36.00%
Best Local Similarity: 20.36%
Query Match: 7.07%
Indels: 76
Conservative: 43
Mismatch: 100
Indels: 76
RESULT 408
ID AAQ14176 standard; cDNA; 2304 BP.
DE Clone pXR2C8 encoding insect steroid receptor XR2C.
PN WO9114695-A.
PD 03-OCT-1991.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Indels: 85
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 409
ID AAQ55374 standard; DNA; 2304 BP.
DE pXR2C8 DNA.
PN WO9401558-A2.
PD 20-JAN-1994.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Indels: 85
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 410
ID AAT76787 standard; DNA; 2304 BP.
DE Insect XR2C receptor coding sequence.
PN US5641652-A.
PD 24-JUN-1997.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Indels: 85
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 411
ID AAT89959 standard; DNA; 2304 BP.
DE D. melanogaster XR2C retinoid-like receptor DNA.
PN US5688691-A.
PD 18-NOV-1997.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Indels: 85
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 412
ID ABL07559 standard; cDNA; 2483 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17159.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Indels: 85
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 413
ID ACC77970 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.04%
Indels: 74
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 414
ID ACC77978 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.04%
Indels: 74
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 415
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ID ACC77991 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%      Conservative: 33  
Best Local Similarity: 25.34%      Mismatches: 113  
Query Match: 7.04%      Indels: 74  
RESULT 416  
ID ACC77984 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%      Conservative: 33  
Best Local Similarity: 25.34%      Mismatches: 113  
Query Match: 7.04%      Indels: 74  
RESULT 417  
ID ABL07558 standard; cDNA; 4483 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17156.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.46%      Conservative: 28  
Best Local Similarity: 25.00%      Mismatches: 109  
Query Match: 7.04%      Indels: 85  
RESULT 418  
ID ABL07492 standard; cDNA; 18737 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16958.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.46%      Conservative: 28  
Best Local Similarity: 25.00%      Mismatches: 109  
Query Match: 7.04%      Indels: 85  
RESULT 419  
ID ABL07530 standard; cDNA; 18737 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17072.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.46%      Conservative: 28  
Best Local Similarity: 25.00%      Mismatches: 109  
Query Match: 7.04%      Indels: 85  
RESULT 420  
ID ACA43915 standard; DNA; 717 BP.  
DE Prokaryotic essential gene #25572.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Percent Similarity: 34.08%      Conservative: 22  
Best Local Similarity: 25.84%      Mismatches: 84  
Query Match: 7.00%      Indels: 93  
RESULT 421  
ID AAB65542 standard; cDNA; 825 BP.  
DE DNA encoding novel human diagnostic protein #1346.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 44.79%      Conservative: 11  
Best Local Similarity: 33.33%      Mismatches: 33  
Query Match: 7.00%      Indels: 20  
RESULT 422  
ID AAO80524 standard; DNA; 1410 BP.  
DE Oxidoreducing avermectin DNA from S. avermetilis ATCC31271.  
PN JP06189774-A.  
PD 12-JUL-1994.  
PA (KITA) KITASATO KENKYUSHO SH.  
Percent Similarity: 35.48%      Conservative: 32  
Best Local Similarity: 24.01%      Mismatches: 104  
Query Match: 7.00%      Indels: 76  
RESULT 423  
ID ABD13438 standard; DNA; 1527 BP.

DE Pseudomonas aeruginosa polynucleotide #12042.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 37.62%      Conservative: 23  
Best Local Similarity: 26.67%      Mismatches: 78  
Query Match: 7.00%      Indels: 53  
RESULT 424  
ID ABD01627 standard; DNA; 1962 BP.  
DE Pseudomonas aeruginosa polynucleotide #231.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.64%      Conservative: 24  
Best Local Similarity: 28.42%      Mismatches: 118  
Query Match: 7.00%      Indels: 67  
RESULT 425  
ID ABD13335 standard; DNA; 2313 BP.  
DE Pseudomonas aeruginosa polynucleotide #11939.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 37.62%      Conservative: 23  
Best Local Similarity: 26.67%      Mismatches: 78  
Query Match: 7.00%      Indels: 53  
RESULT 426  
ID ADQ22115 standard; DNA; 4618 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4935.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 37.33%      Conservative: 22  
Best Local Similarity: 27.19%      Mismatches: 79  
Query Match: 7.00%      Indels: 57  
RESULT 427  
ID ABD10637 standard; DNA; 1233 BP.  
DE Pseudomonas aeruginosa polynucleotide #9241.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.86%      Conservative: 26  
Best Local Similarity: 24.65%      Mismatches: 100  
Query Match: 6.96%      Indels: 147  
RESULT 428  
ID ABD10108 standard; DNA; 1980 BP.  
DE Pseudomonas aeruginosa polynucleotide #8712.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 30.93%      Conservative: 17  
Best Local Similarity: 25.09%      Mismatches: 78  
Query Match: 6.96%      Indels: 123  
RESULT 429  
ID ACC85548 standard; DNA; 2505 BP.  
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 8.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.30%      Conservative: 31  
Best Local Similarity: 25.68%      Mismatches: 114  
Query Match: 6.96%      Indels: 74  
RESULT 430  
ID ACC85552 standard; DNA; 2505 BP.  
DE T thermophilus strain lb21 variant DNA polymerase gene SEQ ID NO: 12.  
PN WO2003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.99%      Conservative: 33  
Best Local Similarity: 25.68%      Mismatches: 112  
Query Match: 6.96%      Indels: 74  
RESULT 431  
ID ACC85549 standard; DNA; 2505 BP.  
DE T thermophilus strain lb21 variant DNA polymerase gene SEQ ID NO: 9.



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PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Conservative: 33
Percent Similarity: 36.99%
Mismatches: 112
Indels: 74
Best Local Similarity: 25.68%
Query Match: 6.96%
RESULT 432
ID ACC85551 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 11.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Conservative: 31
Percent Similarity: 36.30%
Mismatches: 114
Indels: 74
Best Local Similarity: 25.68%
Query Match: 6.96%
RESULT 433
ID ACC78001 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 434
ID ACC78002 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 435
ID ACC77983 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 436
ID ACC77987 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 437
ID ACC77996 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 438
ID ACC78013 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Conservative: 33
Percent Similarity: 36.64%
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.96%
RESULT 439
ID AAV62176 standard; DNA; 117213 BP.
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.
Conservative: 22
Percent Similarity: 34.46%

Best Local Similarity: 27.03%
Query Match: 6.96%
Mismatches: 109
Indels: 86
RESULT 440
ID AAD25519 standard; DNA; 154746 BP.
DE Human herpesvirus 2 complete DNA genome.
PN WO200176643-A1.
PD 18-OCT-2001.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
Conservative: 22
Percent Similarity: 34.46%
Mismatches: 109
Indels: 86
Best Local Similarity: 27.03%
Query Match: 6.96%
RESULT 441
ID ABD03356 standard; DNA; 1701 BP.
DE Pseudomonas aeruginosa polynucleotide #1960.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Conservative: 36
Percent Similarity: 37.13%
Mismatches: 119
Indels: 75
Best Local Similarity: 25.41%
Query Match: 6.92%
RESULT 442
ID ABD10467 standard; DNA; 1848 BP.
DE Pseudomonas aeruginosa polynucleotide #9071.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Conservative: 16
Percent Similarity: 32.06%
Mismatches: 68
Indels: 110
Best Local Similarity: 25.95%
Query Match: 6.92%
RESULT 443
ID AAV39834 standard; cDNA; 1898 BP.
DE Mouse protein phosphatase 2A subunit encoding cDNA.
PN WO9824915-A1.
PD 11-JUN-1998.
PA (VEHE-) VER HET NEDERLANDS KANKER INST.
Conservative: 18
Percent Similarity: 36.02%
Mismatches: 81
Indels: 70
Best Local Similarity: 28.39%
Query Match: 6.92%
RESULT 444
ID AAV39835 standard; cDNA; 1988 BP.
DE Mouse protein phosphatase 2A subunit variant encoding cDNA.
PN WO9824915-A1.
PD 11-JUN-1998.
PA (VEHE-) VER HET NEDERLANDS KANKER INST.
Conservative: 18
Percent Similarity: 36.02%
Mismatches: 81
Indels: 70
Best Local Similarity: 28.39%
Query Match: 6.92%
RESULT 445
ID ABD03306 standard; DNA; 2169 BP.
DE Pseudomonas aeruginosa polynucleotide #1910.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Conservative: 36
Percent Similarity: 37.13%
Mismatches: 119
Indels: 75
Best Local Similarity: 25.41%
Query Match: 6.92%
RESULT 446
ID ABA97187 standard; DNA; 2326 BP.
DE Goat lactoferrin-associated DNA.
PN KR98043944-A.
PD 05-SEP-1998.
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
Conservative: 28
Percent Similarity: 37.01%
Mismatches: 103
Indels: 75
Best Local Similarity: 27.05%
Query Match: 6.92%
RESULT 447
ID ABD03441 standard; DNA; 2946 BP.
DE Pseudomonas aeruginosa polynucleotide #2045.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
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Percent Similarity: 37.13% Conservative: 36  
 Best Local Similarity: 25.41% Mismatches: 119  
 Query Match: 6.92% Indels: 75  
 RESULT 448  
 ID AAQ53954 standard; DNA; 3221 BP.  
 DE Heat stable DNA polymerase coding sequence.  
 PN JP05317058-A.  
 PD 03-DEC-1993.  
 PA (TOYO) TOYOBO KK.  
 Percent Similarity: 35.64% Conservative: 34  
 Best Local Similarity: 23.27% Mismatches: 101  
 Query Match: 6.92% Indels: 77  
 RESULT 449  
 ID ACCT7985 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99% Conservative: 34  
 Best Local Similarity: 25.34% Mismatches: 112  
 Query Match: 6.92% Indels: 74  
 RESULT 450  
 ID ACCT7994 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99% Conservative: 34  
 Best Local Similarity: 25.34% Mismatches: 112  
 Query Match: 6.92% Indels: 74  
 RESULT 451  
 ID ACCT7979 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.92% Indels: 74  
 RESULT 452  
 ID AB211703 standard; cDNA; 3744 BP.  
 DE Human polynucleotide SEQ ID NO 585.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 40.00% Conservative: 16  
 Best Local Similarity: 30.00% Mismatches: 65  
 Query Match: 6.92% Indels: 31  
 RESULT 453  
 ID ADM44221 standard; cDNA; 3744 BP.  
 DE Novel human arginine-rich protein cDNA #585.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Percent Similarity: 40.00% Conservative: 16  
 Best Local Similarity: 30.00% Mismatches: 65  
 Query Match: 6.92% Indels: 31  
 RESULT 454  
 ID ABQ83861 standard; DNA; 5032 BP.  
 DE Human MDTF-3 encoding cDNA SEQ ID NO:26.  
 PN WO200278420-A2.  
 PD 10-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 40.00% Conservative: 16  
 Best Local Similarity: 30.00% Mismatches: 65  
 Query Match: 6.92% Indels: 31  
 RESULT 455  
 ID ABV77879 standard; DNA; 5591 BP.  
 DE Hypoxia-induced protein coding sequence #7.  
 PN WO200246465-A2.  
 PD 13-JUN-2002.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 Percent Similarity: 40.00% Conservative: 16  
 Best Local Similarity: 30.00% Mismatches: 65  
 Query Match: 6.92% Indels: 31  
 RESULT 456  
 ID AD182477 standard; DNA; 5592 BP.  
 DE Human modifier of p21 (MP21) gene sequence SeqID43.  
 PN WO2004005486-A2.  
 PD 15-JAN-2004.  
 PA (EXEL-) EXELIXIS INC.  
 Percent Similarity: 40.00% Conservative: 16  
 Best Local Similarity: 30.00% Mismatches: 65  
 Query Match: 6.92% Indels: 31  
 RESULT 457  
 ID AD123894 standard; DNA; 7788 BP.  
 DE Streptomyces fradiae A541 locus ORF3.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 36.24% Conservative: 33  
 Best Local Similarity: 24.74% Mismatches: 114  
 Query Match: 6.92% Indels: 70  
 RESULT 458  
 ID AD123892 standard; DNA; 37360 BP.  
 DE Streptomyces fradiae A541 locus contig 2.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 36.24% Conservative: 33  
 Best Local Similarity: 24.74% Mismatches: 114  
 Query Match: 6.92% Indels: 70  
 RESULT 459  
 Percent Similarity: 30.90% Conservative: 12  
 Best Local Similarity: 25.75% Mismatches: 73  
 Query Match: 6.92% Indels: 88  
 RESULT 460  
 Percent Similarity: 30.90% Conservative: 12  
 Best Local Similarity: 25.75% Mismatches: 73  
 Query Match: 6.92% Indels: 88  
 RESULT 461  
 Percent Similarity: 30.90% Conservative: 12  
 Best Local Similarity: 25.75% Mismatches: 73  
 Query Match: 6.92% Indels: 88  
 RESULT 462  
 Percent Similarity: 30.90% Conservative: 12  
 Best Local Similarity: 25.75% Mismatches: 73  
 Query Match: 6.92% Indels: 88  
 RESULT 463  
 ID AD122710 standard; DNA; 1052 BP.  
 DE S. pristinaespiralis papM gene C658T mutant.  
 PN WO2004003012-A2.  
 PD 08-JAN-2004.  
 PA (AVET-) AVENTIS PHARMA SA.  
 Percent Similarity: 32.23% Conservative: 26  
 Best Local Similarity: 22.71% Mismatches: 120  
 Query Match: 6.89% Indels: 65  
 RESULT 464  
 ID AD122712 standard; DNA; 1052 BP.  
 DE S. pristinaespiralis papM gene C658T/G828A mutant.  
 PN WO2004003012-A2.  
 PD 08-JAN-2004.  
 PA (AVET-) AVENTIS PHARMA SA.  
 Percent Similarity: 32.23% Conservative: 26  
 Best Local Similarity: 22.71% Mismatches: 120  
 Query Match: 6.89% Indels: 65  
 RESULT 465  
 ID ABD01646 standard; DNA; 1200 BP.  
 DE Pseudomonas aeruginosa polynucleotide #250.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.17% Conservative: 23  
 Best Local Similarity: 28.01% Mismatches: 114



Query Match: 6.89% Indels: 66  
RESULT 466  
ID ABS05045 standard; DNA; 1311 BP.  
DE Pseudomonas aeruginosa polynucleotide #3649.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 37.06% Conservative: 33  
Best Local Similarity: 25.52% Mismatches: 95  
Query Match: 6.89% Indels: 86  
RESULT 467  
ID ADK56578 standard; DNA; 1828 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #3961.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DMC) DOW CHEM CO.  
PA (DMC) DOW AGROSCIENCES LLC.  
Percent Similarity: 34.20% Conservative: 38  
Best Local Similarity: 21.82% Mismatches: 102  
Query Match: 6.89% Indels: 100  
RESULT 468  
ID AAV53995 standard; DNA; 2511 BP.  
DE Nucleotide sequence of the structure specific endonuclease 2.  
PN WO9823774-A1.  
PD 04-JUN-1998.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 469  
ID ABS68749 standard; DNA; 2511 BP.  
DE DNA encoding Thermus thermophilus mutant DNA polymerase #2.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 470  
ID ADE53076 standard; DNA; 2511 BP.  
DE PEN-1 related DNA used within the scope of the invention, #231.  
PN WO200270755-A2.  
PD 12-SEP-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 471  
ID ABS68757 standard; DNA; 2526 BP.  
DE DNA encoding Thermus thermophilus mutant DNA polymerase #4.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 472  
ID ABS68759 standard; DNA; 2526 BP.  
DE DNA encoding Thermus thermophilus mutant DNA polymerase #5.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.68% Conservative: 34  
Best Local Similarity: 24.91% Mismatches: 111  
Query Match: 6.89% Indels: 74  
RESULT 473  
ID ABS68751 standard; DNA; 2526 BP.  
DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113

Query Match: 6.89% Indels: 74  
RESULT 474  
ID ABS68755 standard; DNA; 2526 BP.  
DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 475  
ID ACC77865 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 476  
ID ACC77880 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74  
RESULT 477  
ID ACC77960 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 478  
ID ACC77936 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 37.89% Conservative: 36  
Best Local Similarity: 25.26% Mismatches: 119  
Query Match: 6.89% Indels: 60  
RESULT 479  
ID ACC77975 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 480  
ID ACC78006 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.89% Indels: 74  
RESULT 481  
ID ACC77873 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.49% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 116  
Query Match: 6.89% Indels: 74



RESULT 482  
ID ACC77961 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 483  
ID ACC77990 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 484  
ID ACC78009 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 485  
ID ACC77999 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 486  
ID ACC77993 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 487  
ID ACC77883 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 116  
Indels: 74  
Query Match: 6.89%  
RESULT 488  
ID ACC77966 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 489  
ID ACC78012 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 490  
ID ACC77935 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 37.89%  
Best Local Similarity: 25.26%  
Conservative: 36  
Mismatches: 119  
Indels: 60  
Query Match: 6.89%  
RESULT 491  
ID ACC78003 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 492  
ID ACC77976 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
Query Match: 6.89%  
RESULT 493  
ID AAP26352 standard; DNA; 1035 BP.  
DE P. putida oxygenase encoding DNA ORF04472.  
PN WO200107629-A2.  
PD 01-FEB-2001.  
PA (TIGR-) TIGR INST GENOMIC RES.  
PA (QUIA-) QUIAGEN GMBH.  
PA (GBFB) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
Percent Similarity: 33.21%  
Best Local Similarity: 24.91%  
Conservative: 22  
Mismatches: 100  
Indels: 77  
Query Match: 6.85%  
RESULT 494  
ID ACA31567 standard; DNA; 1130 BP.  
DE Prokaryotic essential gene #13224.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 37.62%  
Best Local Similarity: 24.76%  
Conservative: 27  
Mismatches: 89  
Indels: 42  
Query Match: 6.85%  
RESULT 495  
ID AAS72289 standard; cDNA; 1390 BP.  
DE DNA encoding novel human diagnostic protein #8093.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.03%  
Best Local Similarity: 23.83%  
Conservative: 21  
Mismatches: 75  
Indels: 100  
Query Match: 6.85%  
RESULT 496  
ID ABD14414 standard; DNA; 1407 BP.  
DE Pseudomonas aeruginosa polynucleotide #13018.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.41%  
Best Local Similarity: 28.15%  
Conservative: 31  
Mismatches: 96  
Indels: 90  
Query Match: 6.85%  
RESULT 497  
ID ADO07762 standard; cDNA; 1932 BP.  
DE Fly polynucleotide #43.  
PN US2004071700-A1.  
PD 15-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Percent Similarity: 33.33%  
Conservative: 29



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Best Local Similarity: 23.05%	Mismatches: 101		
Query Match: 6.85%	Indels: 87		
RESULT 498			
ID AAS94512 standard; cDNA; 2305 BP.			
DE DNA encoding novel human diagnostic protein #30316.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 31.54%	Conservative: 19		
Best Local Similarity: 23.65%	Mismatches: 94		
Indels: 71			
Query Match: 6.85%			
RESULT 499			
ID ABL08195 standard; cDNA; 2396 BP.			
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19067.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE-) PE CORP NY.			
Percent Similarity: 33.33%	Conservative: 29		
Best Local Similarity: 23.03%	Mismatches: 101		
Indels: 87			
Query Match: 6.85%			
RESULT 500			
ID ABL20321 standard; DNA; 2590 BP.			
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12436.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE-) PE CORP NY.			
Percent Similarity: 33.33%	Conservative: 29		
Best Local Similarity: 23.05%	Mismatches: 101		
Indels: 87			
Query Match: 6.85%			
RESULT 501			
ID ABL20331 standard; DNA; 2894 BP.			
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12466.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE-) PE CORP NY.			
Percent Similarity: 33.33%	Conservative: 29		
Best Local Similarity: 23.05%	Mismatches: 101		
Indels: 87			
Query Match: 6.85%			
RESULT 502			
ID ACC77995 standard; DNA; 3221 BP.			
DE Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN WO2003025132-A2.			
PD 27-MAR-2003.			
PA (INVI-) INVITROGEN CORP.			
Percent Similarity: 36.99%	Conservative: 34		
Best Local Similarity: 25.34%	Mismatches: 112		
Indels: 74			
Query Match: 6.85%			
RESULT 503			
ID AAS84829 standard; cDNA; 3451 BP.			
DE DNA encoding novel human diagnostic protein #20633.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 42.95%	Conservative: 25		
Best Local Similarity: 26.92%	Mismatches: 58		
Indels: 32			
Query Match: 6.85%			
RESULT 504			
ID ACA44278 standard; DNA; 1116 BP.			
DE Prokaryotic essential gene #25935.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity: 37.45%	Conservative: 31		
Best Local Similarity: 25.10%	Mismatches: 76		
Indels: 81			
Query Match: 6.81%			
RESULT 505			
ID ABD08133 standard; DNA; 1197 BP.			
DE Pseudomonas aeruginosa polynucleotide #6737.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 38.19%	Conservative: 31		
Best Local Similarity: 25.98%	Mismatches: 107		
Indels: 51			
Query Match: 6.81%			
RESULT 506			
ID ABD08348 standard; DNA; 1272 BP.			
DE Pseudomonas aeruginosa polynucleotide #6952.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 38.19%	Conservative: 31		
Best Local Similarity: 25.98%	Mismatches: 107		
Indels: 51			
Query Match: 6.81%			
RESULT 507			
ID ABZ38701 standard; DNA; 1560 BP.			
DE N. gonorrhoeae nucleotide sequence SEQ ID 1991.			
PN WO200279243-A2.			
PD 10-OCT-2002.			
PA (CHIR-) CHIRON SPA.			
Percent Similarity: 38.21%	Conservative: 33		
Best Local Similarity: 24.80%	Mismatches: 91		
Indels: 61			
Query Match: 6.81%			
RESULT 508			
ID AAQ24328 standard; DNA; 1635 BP.			
DE Mutant thermostable DNA polymerase pTTHA292.			
PN WO9206200-A.			
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Percent Similarity: 36.64%	Conservative: 33		
Best Local Similarity: 25.34%	Mismatches: 113		
Indels: 74			
Query Match: 6.81%			
RESULT 509			
ID AAQ24327 standard; DNA; 1899 BP.			
DE Mutant thermostable DNA polymerase pTTHd2-203.			
PN WO9206200-A.			
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Percent Similarity: 36.64%	Conservative: 33		
Best Local Similarity: 25.34%	Mismatches: 113		
Indels: 74			
Query Match: 6.81%			
RESULT 510			
ID AAQ24326 standard; DNA; 2043 BP.			
DE Mutant thermostable DNA polymerase pTTHd2-155.			
PN WO9206200-A.			
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Percent Similarity: 36.64%	Conservative: 33		
Best Local Similarity: 25.34%	Mismatches: 113		
Indels: 74			
Query Match: 6.81%			
RESULT 511			
ID ACA42740 standard; DNA; 2253 BP.			
DE Prokaryotic essential gene #24397.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity: 37.85%	Conservative: 27		
Best Local Similarity: 27.09%	Mismatches: 101		
Indels: 55			
Query Match: 6.81%			
RESULT 512			
ID AAQ24325 standard; DNA; 2277 BP.			
DE Mutant thermostable DNA polymerase pTTHd2-77.			
PN WO9206200-A.			
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Percent Similarity: 36.64%	Conservative: 33		
Best Local Similarity: 25.34%	Mismatches: 113		
Indels: 74			
Query Match: 6.81%			
RESULT 513			
ID ABD08178 standard; DNA; 2346 BP.			
DE Pseudomonas aeruginosa polynucleotide #6782.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 38.19%	Conservative: 31		
Best Local Similarity: 25.98%	Mismatches: 107		
Indels: 51			
Query Match: 6.81%			



RESULT 514  
ID AAQ24324 standard; DNA; 2370 BP.  
DE Mutant thermostable DNA polymerase pTthd2-46.  
PN WO9206200-A.  
PD 16-APR-1992.  
PA (CETU) CETUS CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 515  
ID AAQ24323 standard; DNA; 2505 BP.  
DE Mutant thermostable DNA polymerase from Thermus thermophilus.  
PN WO9206200-A.  
PD 16-APR-1992.  
PA (CETU) CETUS CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 516  
ID AAV5393 standard; DNA; 2505 BP.  
DE Nucleotide sequence of the nucleic acid 6.  
PN WO9823774-A1.  
PD 04-JUN-1998.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 517  
ID AAV5394 standard; DNA; 2511 BP.  
DE Nucleotide sequence of the structure specific endonuclease 1.  
PN WO9823774-A1.  
PD 04-JUN-1998.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 518  
ID ABS68747 standard; DNA; 2511 BP.  
DE Thermus thermophilus DNA polymerase, PCR primer #4.  
PN WO200263030-A2.  
PD 15-AUG-2002.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 519  
ID AAQ12748 standard; DNA; 2640 BP.  
DE T. thermophilus DNA polymerase I.  
PN WO9109950-A.  
PD 11-JUL-1991.  
PA (CETU) CETUS CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 520  
ID AAH14004 standard; cDNA; 2653 BP.  
DE Human cDNA sequence SEQ ID NO:11090.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 33.23%  
Best Local Similarity: 25.16%  
Query Match: 6.81%  
Conservative: 25  
Mismatches: 98  
Indels: 109  
RESULT 521  
ID AAD45690 standard; DNA; 2653 BP.  
DE Human LBDS4 DNA.  
PN WO200270560-A2.  
PD 12-SEP-2002.  
PA (INPH-) INPHARMATICA LTD.  
Percent Similarity: 33.23%  
Best Local Similarity: 25.16%  
Query Match: 6.81%  
Conservative: 25  
Mismatches: 98  
Indels: 109  
RESULT 522

ID AAA30241 standard; DNA; 2943 BP.  
DE Chimaeric Pfu/T. thermophilus DNA polymerase coding sequence.  
PN GB2344591-A.  
PD 14-JUN-2000.  
PA (BIOL-) BIOLINE LTD.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 523  
ID ABD11116 standard; DNA; 3006 BP.  
DE Pseudomonas aeruginosa polynucleotide #9720.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.97%  
Best Local Similarity: 22.45%  
Query Match: 6.81%  
Conservative: 28  
Mismatches: 80  
Indels: 120  
RESULT 524  
ID ACC78016 standard; DNA; 3210 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 525  
ID AAO96261 standard; DNA; 3221 BP.  
DE Thermus thermophilus thermostable DNA polymerase genomic DNA.  
PN JP07163343-A.  
PD 27-JUN-1995.  
PA (TOYM) TOYOBO KK.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 526  
ID ACC77892 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 527  
ID ACC77919 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 528  
ID ACC77962 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 529  
ID ACC77972 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatches: 113  
Indels: 74  
RESULT 530  
ID ACC77874 standard; DNA; 3221 BP.



RESULTS 358  
ID ACC77909 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.







Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 563				
ID	ACC77934 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	38.11%	Conservative:	34	
Best Local Similarity:	26.22%	Mismatches:	117	
Query Match:	6.81%	Indels:	62	
RESULT 564				
ID	ACC77875 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 565				
ID	ACC77895 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 566				
ID	ACC77868 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 567				
ID	ACC77869 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 568				
ID	ACC77887 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 569				
ID	ACC77897 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 570				
ID	ACC77922 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 571				
ID	ACC77925 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 572				
ID	ACC77940 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	
RESULT 573				
ID	ACC77878 standard; DNA; 3221 BP.			
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.			
PN	WO2003025132-A2.			
PD	27-MAR-2003.			
PA	(INVI-) INVITROGEN CORP.			
Percent Similarity:	36.64%	Conservative:	33	
Best Local Similarity:	25.34%	Mismatches:	113	
Query Match:	6.81%	Indels:	74	







[illegible]



PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 38.11%  
Best Local Similarity: 26.22%  
Query Match: 6.81%  
Conservative: 34  
Mismatch: 117  
Indels: 62  
RESULT 612  
ID ACCT77938 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 26.64%  
Best Local Similarity: 25.34%  
Query Match: 6.81%  
Conservative: 33  
Mismatch: 113  
Indels: 74  
RESULT 613  
ID ABD13665 standard; DNA; 3660 BP.  
DE Pseudomonas aeruginosa polynucleotide #12269.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.90%  
Best Local Similarity: 26.92%  
Query Match: 6.81%  
Conservative: 21  
Mismatch: 83  
Indels: 68  
RESULT 614  
ID ADD48688 standard; DNA; 5352 BP.  
DE Rat gene M34384, SEQ ID NO 14397.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
Percent Similarity: 36.32%  
Best Local Similarity: 28.25%  
Query Match: 6.81%  
Conservative: 18  
Mismatch: 96  
Indels: 47  
RESULT 615  
ID ACA35857 standard; DNA; 846 BP.  
DE Prokaryotic essential gene #17514.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.74%  
Best Local Similarity: 26.02%  
Query Match: 6.78%  
Conservative: 19  
Mismatch: 74  
Indels: 90  
RESULT 616  
ID AC97285 standard; DNA; 906 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 3080.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.25%  
Best Local Similarity: 24.26%  
Query Match: 6.78%  
Conservative: 19  
Mismatch: 70  
Indels: 118  
RESULT 617  
ID ABD14669 standard; DNA; 966 BP.  
DE Pseudomonas aeruginosa polynucleotide #13273.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.55%  
Best Local Similarity: 28.43%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 86  
Indels: 39  
RESULT 618  
ID ABD08723 standard; DNA; 1083 BP.  
DE Pseudomonas aeruginosa polynucleotide #7327.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.72%  
Best Local Similarity: 27.73%  
Query Match: 6.78%  
Conservative: 23  
Mismatch: 101  
Indels: 62  
RESULT 619  
ID ABD16105 standard; DNA; 1200 BP.  
DE Pseudomonas aeruginosa polynucleotide #14709.

PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
Conservative: 29  
Mismatch: 91  
Indels: 49  
RESULT 620  
ID ABD16436 standard; DNA; 1290 BP.  
DE Pseudomonas aeruginosa polynucleotide #15040.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
Conservative: 29  
Mismatch: 91  
Indels: 49  
RESULT 621  
ID ABD15673 standard; DNA; 1299 BP.  
DE Pseudomonas aeruginosa polynucleotide #14277.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.00%  
Best Local Similarity: 27.31%  
Query Match: 6.78%  
Conservative: 20  
Mismatch: 108  
Indels: 61  
RESULT 622  
ID ABD14522 standard; DNA; 1428 BP.  
DE Pseudomonas aeruginosa polynucleotide #13126.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86%  
Best Local Similarity: 30.86%  
Query Match: 6.78%  
Conservative: 14  
Mismatch: 77  
Indels: 31  
RESULT 623  
ID ABD16317 standard; DNA; 1449 BP.  
DE Pseudomonas aeruginosa polynucleotide #14921.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60%  
Best Local Similarity: 25.88%  
Query Match: 6.78%  
Conservative: 29  
Mismatch: 91  
Indels: 49  
RESULT 624  
ID ACF39359 standard; DNA; 1509 BP.  
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:96.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Percent Similarity: 37.84%  
Best Local Similarity: 29.19%  
Query Match: 6.78%  
Conservative: 16  
Mismatch: 83  
Indels: 32  
RESULT 625  
ID ABD14362 standard; DNA; 1515 BP.  
DE Pseudomonas aeruginosa polynucleotide #12966.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86%  
Best Local Similarity: 30.86%  
Query Match: 6.78%  
Conservative: 14  
Mismatch: 77  
Indels: 31  
RESULT 626  
ID ACA53421 standard; DNA; 1590 BP.  
DE 'Prokaryotic essential gene #35078.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 34.89%  
Best Local Similarity: 24.82%  
Query Match: 6.78%  
Conservative: 28  
Mismatch: 74  
Indels: 107  
RESULT 627  
ID ABD15703 standard; DNA; 1824 BP.  
DE Pseudomonas aeruginosa polynucleotide #14307.  
PN US6551795-B1.



PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 20  
 Percent Similarity: 35.00% Mismatches: 108  
 Best Local Similarity: 27.31% Indels: 61  
 Query Match:  
 RESULT 628  
 ID AAN70306 standard; DNA; 1906 BP.  
 DE Sequence encoding bovine mullerian inhibiting substance (MIS)-like  
 DE polypeptide and the promoter region based on genomic/cDNA fusion.  
 PN EP221761-A.  
 PD 13-MAY-1987.  
 PA (BIO) BIOGEN NV.  
 PA (GENO) GEN HOSPITAL CORP.  
 Percent Similarity: 32.72% Conservative: 25  
 Mismatches: 111  
 Best Local Similarity: 25.00% Indels: 107  
 Query Match:  
 RESULT 629  
 ID AAF60989 standard; DNA; 2085 BP.  
 DE P. putida KT2440-associated DNA ORF01994.  
 PN DE19935088-A1.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUILA-) QUIAGEN GMBH.  
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MED1-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Percent Similarity: 34.39% Conservative: 22  
 Mismatches: 116  
 Best Local Similarity: 26.67% Indels: 71  
 Query Match:  
 RESULT 630  
 ID ABS51351 standard; cDNA; 2299 BP.  
 DE cDNA encoding human secretory protein #49.  
 PN WO200257304-A2.  
 PD 25-JUL-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.30% Conservative: 32  
 Mismatches: 77  
 Best Local Similarity: 24.18% Indels: 76  
 Query Match:  
 RESULT 631  
 ID AAZ34073 standard; cDNA; 2748 BP.  
 DE Human PRO846 nucleotide sequence.  
 PN WO9946281-A2.  
 PD 16-SEP-1999.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 632  
 ID AAA99905 standard; cDNA; 2749 BP.  
 DE cDNA encoding human protein PRO846.  
 PN WO200053757-A2.  
 PD 14-SEP-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 633  
 ID AAC88517 standard; cDNA; 2749 BP.  
 DE Human PRO846 cDNA clone DNA44196-1353.  
 PN WO200053760-A2.  
 PD 14-SEP-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 634  
 ID AAC78503 standard; cDNA; 2749 BP.  
 DE Human PRO846 (UNQ422) nucleotide sequence SEQ ID NO:215.  
 PN WO200053756-A2.  
 PD 14-SEP-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 72  
 Query Match:  
 RESULT 635  
 ID AAS21436 standard; cDNA; 2749 BP.  
 DE Human cDNA sequence encoding for PRO846 polypeptide.  
 PN WO200140466-A2.  
 PD 07-JUN-2001.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 636  
 ID AAF44269 standard; cDNA; 2749 BP.  
 DE Human PRO846 nucleotide sequence SEQ ID NO:516.  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 637  
 ID ABL88101 standard; cDNA; 2749 BP.  
 DE Human PRO846 cDNA sequence SEQ ID NO:59.  
 PN WO20020690-A2.  
 PD 03-JAN-2002.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 638  
 ID ABL95590 standard; cDNA; 2749 BP.  
 DE Human angiogenesis related cDNA PRO846 SEQ ID NO: 59.  
 PN WO200208284-A2.  
 PD 31-JAN-2002.  
 PA (GETH) GENENTECH INC.  
 PA (BAKE) BAKER K P.  
 PA (FERR) FERRARA N.  
 PA (GERB) GERBER H.  
 PA (GERR) GERRITSEN M E.  
 PA (GODD) GODDARD A.  
 PA (GODO) GODOWSKI P J.  
 PA (GURN) GURNEY A L.  
 PA (HILL) HILLAN K J.  
 PA (MARS) MARSTERS S A.  
 PA (PANJ) PAN J.  
 PA (PAON) PAONI N F.  
 PA (STEP) STEPHAN J F.  
 PA (WATA) WATANABE C K.  
 PA (WILL) WILLIAMS P M.  
 PA (WOOD) WOOD W I.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 639  
 ID ACAG3641 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002192706-A1.  
 PD 19-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 640  
 ID ACA44520 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003003531-A1.  
 PD 02-JAN-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Mismatches: 72  
 Best Local Similarity: 19.92% Indels: 100  
 Query Match:  
 RESULT 641  
 ID ACA03795 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.



PN US2003036180-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 642  
 ID ACA71805 standard; cDNA; 2749 BP.  
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.  
 PN US2002177553-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 643  
 ID ABX89333 standard; cDNA; 2749 BP.  
 DE DNA encoding novel secreted and transmembrane protein PRO846.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 644  
 ID ABX92445 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2002169284-A1.  
 PD 14-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 645  
 ID ABX80979 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein cDNA, #183.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 646  
 ID ACD4488 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 647  
 ID ACD1987 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #193.  
 PN US2003036179-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 648  
 ID ACA66186 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003004102-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 649  
 ID ABX79659 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein cDNA, #183.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.

PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 650  
 ID ACA93680 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003022187-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 651  
 ID ABX81362 standard; DNA; 2749 BP.  
 DE Human secreted or transmembrane protein related PCR primer #149.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 652  
 ID ACA04216 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 385.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 653  
 ID ACA93178 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003017476-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 654  
 ID ABX17262 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 655  
 ID ACA68117 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 656  
 ID ACA88566 standard; cDNA; 2749 BP.  
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.  
 PN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 657  
 ID ACD82073 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO846 polypeptide.  
 PN US2003017981-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Query Match: 6.78%  
 RESULT 658  
 ID ABX79659 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane protein cDNA, #183.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.



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ID ADA45904 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003023238-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 659
ID ADA76335 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 660
ID ADA18985 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 661
ID ADA61608 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 662
ID ADB19393 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 663
ID ADB27934 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 664
ID ADA86413 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 665
ID ADB15977 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 666
ID ADA38027 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 667
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 668
ID ADA21713 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 669
ID ADA10500 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 670
ID ADA67558 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 671
ID ADB30565 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 672
ID ADA85861 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 673
ID ADA18044 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 674
ID ADA97073 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100

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Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 675  
ID ADA79377 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 676  
ID ADA87516 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 677  
ID ADB16718 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 678  
ID ADA28152 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 679  
ID ADA91810 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 680  
ID ADB14873 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 681  
ID ADA24754 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 682  
ID ADB18834 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72

Query Match: 6.78%      Indels: 100  
RESULT 683  
ID ADA94049 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 684  
ID ADB19945 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 685  
ID ADB13257 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 686  
ID ACD98616 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 687  
ID ACD29787 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 688  
ID ADA12415 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 689  
ID ADA94732 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 690  
ID ADA74511 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%      Conservative: 25  
Best Local Similarity: 19.92%      Mismatches: 72  
Query Match: 6.78%      Indels: 100  
RESULT 691



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ID ADB24744 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 692
ID ADB2268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 693
ID ADA75231 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 694
ID ADA85309 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 695
ID ADA84757 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 696
ID ADB30013 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 697
ID ADA80541 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 698
ID ADA75783 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 699
ID ADA38957 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 700
ID ADA47008 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 701
ID ADB25304 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 702
ID ADA93480 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 703
ID ADB26830 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 704
ID ADB31117 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 705
ID ADA93078 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 706
ID ADA61045 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 707
ID ADB24192 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077714-A1.
PD 24-APR-2003.

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ID ADA8620 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003073213-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 725
ID ADA97625 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082686-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 726
ID ADB27382 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 727
ID ADB22315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 728
ID ACD39624 standard; DNA; 2749 BP.
DE Human PRO 846 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 729
ID ADA06805 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #147.
PN US2003049638-A1.
PD 13-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 730
ID ADA39498 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059782-A1.
PD 27-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 731
ID ADA67006 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068793-A1.
PD 10-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 732
ID ADB22867 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077711-A1.
PD 24-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 733
ID ADB23640 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077712-A1.
PD 24-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 734
ID ADA92362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 735
ID ADB15425 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087352-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 736
ID ADB38677 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 737
ID ADB96524 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003054403-A1.
PD 20-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 738
ID ADB38125 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 739
ID ADB66597 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 740
ID ADB89677 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082698-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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RESULT 741  
 ID ADB90409 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082762-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 742  
 ID ADB39510 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082764-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 743  
 ID ADB73721 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide sequence #46.  
 PN US2003045462-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 744  
 ID ADB47133 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082687-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 745  
 ID ADB86740 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082697-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 746  
 ID ADB76437 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide sequence #46.  
 PN US2003083248-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 747  
 ID ADB77345 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082696-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 748  
 ID ADB34502 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077717-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 749  
 ID ADB12227 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003049681-A1.

ID ADB35606 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077719-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 750  
 ID ADB33950 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077716-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 751  
 ID ADB35054 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077718-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 752  
 ID ADB36158 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077720-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 753  
 ID ADB46553 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082692-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 754  
 ID ADC43863 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003054986-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 755  
 ID ADC57996 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003027754-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 756  
 ID ADC53360 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003045463-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 757  
 ID ADC12227 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003049681-A1.



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PD 13-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 758
ID ADC61623 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 759
ID ADC63587 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 760
ID ADC66687 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 761
ID ADC56649 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 762
ID ADC68811 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 763
ID ADC62871 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 764
ID ADC67936 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 765
ID ADC11694 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 766
ID ADC41256 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 767
ID ADC67311 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 768
ID ADC62247 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 769
ID ADC41880 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 770
ID ADC50426 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 771
ID ADC71973 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 772
ID ADC59952 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 773
ID ADC52959 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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ID	ADC58536 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein cDNA Seq ID385.				
PN	US2003087346-A1.				
PD	08-MAY-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 783					
ID	ADC14816 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003082546-A1.				
PD	01-MAY-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 784					
ID	AD08348 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003068623-A1.				
PD	10-APR-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 785					
ID	AD03210 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003092104-A1.				
PD	15-MAY-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 786					
ID	AC90202 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003087348-A1.				
PD	08-MAY-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 787					
ID	ADC82173 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #147.				
PN	US2003083461-A1.				
PD	01-MAY-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 788					
ID	ADC69621 standard; cDNA; 2749 BP.				
DE	cDNA encoding human PRO polypeptide #193.				
PN	US2003194770-A1.				
PD	16-OCT-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 789					
ID	ADC48510 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003194773-A1.				
PD	16-OCT-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 790					
ID	ADD10039 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003194776-A1.				
PD	16-OCT-2003.				
PA	( GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		



Query Match:	6.78%	Indels:	100
RESULT 799			
ID	ADC80018 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003087358-A1.		
PD	08-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 800			
ID	ADD07135 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2002193300-A1.		
PD	19-DEC-2002.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 801			
ID	ADD11308 standard; cDNA; 2749 BP.		
DE	Human secreted/transmembrane PRO polypeptide cDNA #30.		
PN	US2003105013-A1.		
PD	05-JUN-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 802			
ID	ADD09487 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
PN	US2003194775-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 803			
ID	ADC83382 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #147.		
PN	US2003059783-A1.		
PD	27-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 804			
ID	ADD41200 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003203438-A1.		
PD	30-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 805			
ID	ADD52339 standard; cDNA; 2749 BP.		
DE	cDNA encoding human PRO polypeptide #193.		
PN	US2003194769-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 806			
ID	ADD53079 standard; cDNA; 2749 BP.		
DE	cDNA encoding human PRO polypeptide #193.		
PN	US2003194792-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 807			
ID	ADD53079 standard; cDNA; 2749 BP.		
DE	cDNA encoding human PRO polypeptide #193.		
PN	US2003194792-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100



ID ADD53631 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203437-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 808  
 ID ADD55489 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003077593-A1.  
 PD 24-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 809  
 ID ADD37101 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
 PN US2003105012-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 810  
 ID ADD56447 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003077594-A1.  
 PD 24-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 811  
 ID ADD51787 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003194779-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 812  
 ID ADD2586 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003203431-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 813  
 ID ADD2020 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003203430-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 814  
 ID ADD54202 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203432-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 815  
 ID ADD54885 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2002132253-A1.

PD 19-SEP-2002.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 816  
 ID ADE49249 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003096744-A1.  
 PD 22-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 817  
 ID ADD92519 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199030-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 818  
 ID ADD91415 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199055-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 819  
 ID ADE04029 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199057-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 820  
 ID ADE31904 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003068647-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 821  
 ID ADE27039 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087304-A1.  
 PD 08-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 822  
 ID ADE32326 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003194765-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 823  
 ID ADE22258 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199056-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 824  
 ID ADD54885 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2002132253-A1.



	Best Local Similarity:	19.92%	Mismatches:	72	
	Query Match:	6.78%	Indels:	100	
RESULT 824	ID ADE33982 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003194791-A1.				
PD	16-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 825	ID ADD79482 standard; cDNA; 2749 BP.				
DE	cDNA encoding human PRO polypeptide #193.				
PN	US2003203428-A1.				
PD	30-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 826	ID ADE33303 standard; cDNA; 2749 BP.				
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.				
PN	US2003203434-A1.				
PD	30-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 827	ID ADI61417 standard; cDNA; 2749 BP.				
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.				
PN	US2003203435-A1.				
PD	30-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 828	ID ADE42018 standard; cDNA; 2749 BP.				
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.				
PN	US2003203436-A1.				
PD	30-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 829	ID ADE17835 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003199023-A1.				
PD	23-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 830	ID ADE43135 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003199033-A1.				
PD	23-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 831	ID ADD91967 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003199053-A1.				
PD	23-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 832	ID ADE33982 standard; cDNA; 2749 BP.				
DE	Novel human secreted and transmembrane protein PRO846 cDNA.				
PN	US2003194791-A1.				
PD	16-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 833	ID ADD80034 standard; cDNA; 2749 BP.				
DE	cDNA encoding human PRO polypeptide #193.				
PN	US2003207417-A1.				
PD	06-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 834	ID ADD93071 standard; cDNA; 2749 BP.				
DE	Human PRO polynucleotide #193.				
PN	US2003194768-A1.				
PD	16-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 835	ID ADD72390 standard; cDNA; 2749 BP.				
DE					



RESULT 840  
ID ADE22810 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 841  
ID ADD78928 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 842  
ID ADE26506 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 843  
ID ADE32878 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 844  
ID AD42570 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 845  
ID ADE17041 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 846  
ID ADB80586 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 847  
ID ADD89614 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 848  
ID ADE40898 standard; cDNA; 2749 BP.

DE Human PRO polynucleotide #193.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 849  
ID ADE04697 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 850  
ID ADE92826 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 851  
ID ADF47055 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 852  
ID ADP67443 standard; cDNA; 2749 BP.  
DE Human PRO846 nucleotide sequence SEQ ID NO:516.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 853  
ID ADG21535 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 854  
ID ADG23176 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 855  
ID ADF97511 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
RESULT 856  
ID ADG80575 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.



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PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 857
ID ADG52812 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 858
ID ADG60132 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 859
ID ADG80023 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 860
ID ADH55315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 861
ID ADH5867 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 862
ID ADI35697 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 863
ID ADI60892 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 864
ID ADI64086 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 865
ID ADI65035 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 866
ID ADH81948 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 867
ID ADI00190 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 868
ID ADH81396 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 869
ID ABX78063 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 870
ID ABX80475 standard; cDNA; 2749 BP.
DE Human secreted or transmembrane protein related PCR primer #149.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 871
ID ACA69381 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 872
ID ACD24045 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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RESULT 873
ID ABX30452 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane protein cDNA, #183.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 874
ID ACDA4266 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 875
ID ABX64298 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 876
ID ACA67186 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 877
ID ADM82565 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 878
ID ADN15964 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 879
ID ADN16593 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 880
ID ADN15412 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 881
ID ADN15412 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 882
ID ADC81122 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 883
ID ADD76570 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 884
ID ADD87934 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 885
ID ADD86338 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 886
ID ADS75786 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 887
ID ADS48549 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 888
ID ADS41309 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #30.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 889
ID ADE23362 standard; cDNA; 2749 BP.
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DE cDNA encoding human PRO polypeptide #193.
PN US2003092108-A1.
PA (GAOW//) FONG S.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GIRM//) GIRMALDI J C.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (KLJA//) KLJAVIN I J.
PA (KOOS//) KUO S S.
PA (NAPI//) NAPIER M A.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (ROYM//) ROY M A.
PA (SHEL//) SHELTON D L.
PA (STEW//) STEWART T A.
PA (TUMA//) TUMAS D.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 897
ID ADF61290 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195345-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 898
ID ADF39982 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003198994-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 899
ID ADF45778 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195148-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 900
ID ADE94716 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199027-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 901
ID ADE91127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199061-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 902
ID ADF35642 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003194760-A1.
PN 16-OCT-2003.

DE cDNA encoding human PRO polypeptide #193.
PN US2003092108-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 890
ID ADE23914 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092110-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 891
ID ADE24557 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092111-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 892
ID ADD87382 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203439-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 893
ID ADE89248 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199062-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 894
ID ADE18387 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194794-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 895
ID ADE88696 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199054-A1.
PA (GETH//) GENENTECH INC.
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 896
ID ADE89650 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003130181-A1.
PA (ASHK//) ASHKENAZI A J.
PA (BAKE//) BAKER K P.
PA (BOTS//) BOTSTEIN D.
PA (DESN//) DESNOVERS L.
PA (EATO//) EATON D L.
PA (FERR//) FERRARA N.
PA (FILV//) FILVAROFF E.

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Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 903  
 ID ADE95268 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199052-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 904  
 ID ADE93378 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199060-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 905  
 ID ADP24174 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003204055-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 906  
 ID ADF40606 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199021-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 907  
 ID ADF23550 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003203402-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 908  
 ID ADF33533 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003194780-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 909  
 ID ADF34959 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199029-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 910  
 ID ADF27000 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199436-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25

Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 911  
 ID ADF27636 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199437-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 912  
 ID ADE92274 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003199051-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 913  
 ID ADE90575 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199063-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 914  
 ID ADF41230 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199435-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 915  
 ID ADF32909 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003211091-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 916  
 ID ADF25275 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003211092-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 917  
 ID ADF26376 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199674-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 918  
 ID ADF34165 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003194410-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 919  
 ID ADF27000 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199436-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25



Query Match: 6.78% Indels: 100

RESULT 919  
ID ADF46402 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 920  
ID ADE91722 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 921  
ID ADG11892 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 922  
ID ADG02301 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 923  
ID ADG22087 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 924  
ID ADG20157 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 925  
ID ADF98063 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 926  
ID ADG24280 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 927  
ID ADF98634 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 927  
ID ADF98634 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 928  
ID ADG03465 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 929  
ID ADF99186 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 930  
ID ADG16771 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 931  
ID ADG05230 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 932  
ID ADG19497 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 933  
ID ADG13334 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 934  
ID ADG08391 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100

RESULT 935  
ID ADG16771 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Indels: 100

Conservative: 25  
Mismatches: 72  
Indels: 100



ID ADG15561 standard; cDNA; 2749 BP.  
DE CDNA encoding human PRO polypeptide #193.4  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 936

ID ADF96959 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 937

ID ADG06144 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 938

ID ADG23728 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 939

ID ADG04017 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 940

ID ADG24918 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 941

ID ADG07215 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 942

ID ADG07767 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 943

ID ADG55262 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 944

ID ADG60926 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 945

ID ADG62030 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 946

ID ADG82231 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 947

ID ADG57470 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 948

ID ADG56918 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 949

ID ADG55814 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 950

ID ADG58574 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 951

ID ADG70940 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 952



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PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 952
ID ADG58022 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 953
ID ADG51636 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 954
ID ADG52430 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 955
ID ADG50388 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 956
ID ADG81679 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 957
ID ADH19762 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 958
ID ADH30641 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 959
ID ADH12008 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 960
ID ADG49764 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 961
ID ADG51636 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 962
ID ADG52430 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 963
ID ADG54158 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 964
ID ADG49140 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 965
ID ADG81127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 966
ID ADG56366 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 967
ID ADH12632 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100

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Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 968  
 ID ADG48516 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003216560-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 969  
 ID ADH21255 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003224358-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 970  
 ID ADG61478 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207429-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 971  
 ID ADH20295 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003219856-A1.  
 PD 27-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 972  
 ID ADH28565 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003022331-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 973  
 ID ADG54710 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207367-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 974  
 ID ADG59750 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207369-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 975  
 ID ADG51012 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100

Query Match: 6.78% Indels: 100  
 RESULT 976  
 ID ADH43492 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #30.  
 PN US2003224984-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 977  
 ID ADG58956 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005657-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 978  
 ID ADG62412 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004006219-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 979  
 ID ADI81174 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003207361-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 980  
 ID ADH25437 standard; cDNA; 2749 BP.  
 DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:215.  
 PN EPI386931-A1.  
 PD 04-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 981  
 ID ADG09917 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004009548-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 982  
 ID ADI15388 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207382-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 983  
 ID ADG09265 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004009547-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100



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RESULT 984
ID ADL14720 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004063921-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 993
ID ADM42473 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004058424-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 994
ID ADM28335 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004077064-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 995
ID ACC77620 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 996
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 997
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 998
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 999
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 1000
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 1001
ID ADJ40534 standard; cDNA; 1611 BP.
DE Plant cDNA #1534.
PN US2004016025-A1.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.

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PA (PROV/) PROVART N.  
 PA (RICK/) RICK E D.  
 PA (ZHUT/) ZHU T.  
 Percent Similarity: 38.91% Conservative: 24  
 Best Local Similarity: 28.87% Mismatches: 87  
 Query Match: 6.74% Indels: 60  
 RESULT 1002  
 ID AD057711 standard; DNA; 1950 BP.  
 DE Actinobacillus actinomycetemcomitans immunogenic polypeptide gene #81.  
 PN WO2004045499-A2.  
 PD 03-JUN-2004.  
 PA (UYEL) UNIV FLORIDA.  
 Percent Similarity: 37.25% Conservative: 35  
 Best Local Similarity: 23.08% Mismatches: 127  
 Query Match: 6.74% Indels: 28  
 RESULT 1003  
 ID ABD14922 standard; DNA; 2496 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13526.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.91% Conservative: 25  
 Best Local Similarity: 26.25% Mismatches: 90  
 Query Match: 6.74% Indels: 77  
 RESULT 1004  
 ID ABD15329 standard; DNA; 2622 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13933.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.91% Conservative: 25  
 Best Local Similarity: 26.25% Mismatches: 90  
 Query Match: 6.74% Indels: 77  
 RESULT 1005  
 ID ABD15222 standard; DNA; 2685 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13826.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.91% Conservative: 25  
 Best Local Similarity: 26.25% Mismatches: 90  
 Query Match: 6.74% Indels: 77  
 RESULT 1006  
 ID AAV02312 standard; DNA; 3065 BP.  
 DE C16N gene for promoting neuron survival and type 1 collagen production.  
 PN WO9740150-A1.  
 PD 30-OCT-1997.  
 PA (SUMU) SUMITOMO PHARM CO LTD.  
 Percent Similarity: 30.84% Conservative: 30  
 Best Local Similarity: 22.19% Mismatches: 95  
 Query Match: 6.74% Indels: 146  
 RESULT 1007  
 ID ACCT7988 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.74% Indels: 74  
 RESULT 1008  
 ID ACCT7981 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.74% Indels: 74  
 RESULT 1009  
 ID ACCT7805 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.

PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.74% Indels: 74  
 RESULT 1010  
 ID ACCT7997 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.74% Indels: 74  
 RESULT 1011  
 ID AA240178 standard; cDNA; 3337 BP.  
 DE Mouse C16N-2 coding sequence.  
 PN JP11308995-A.  
 PD 09-NOV-1999.  
 PA (SUMU) SUMITOMO SEIYAKU KK.  
 Percent Similarity: 30.84% Conservative: 30  
 Best Local Similarity: 22.19% Mismatches: 95  
 Query Match: 6.74% Indels: 146  
 RESULT 1012  
 ID AA244729 standard; cDNA; 3337 BP.  
 DE Murine C16N-2 cDNA.  
 PN WO200001405-A1.  
 PD 13-JAN-2000.  
 PA (SUMU) SUMITOMO PHARM CO LTD.  
 Percent Similarity: 30.84% Conservative: 30  
 Best Local Similarity: 22.19% Mismatches: 95  
 Query Match: 6.74% Indels: 146  
 RESULT 1013  
 ID AA240177 standard; cDNA; 3674 BP.  
 DE Mouse C16N-1 coding sequence.  
 PN JP11308995-A.  
 PD 09-NOV-1999.  
 PA (SUMU) SUMITOMO SEIYAKU KK.  
 Percent Similarity: 30.84% Conservative: 30  
 Best Local Similarity: 22.19% Mismatches: 95  
 Query Match: 6.74% Indels: 146  
 RESULT 1014  
 ID AA244728 standard; cDNA; 3674 BP.  
 DE Murine C16N-1 cDNA.  
 PN WO200001405-A1.  
 PD 13-JAN-2000.  
 PA (SUMU) SUMITOMO PHARM CO LTD.  
 Percent Similarity: 30.84% Conservative: 30  
 Best Local Similarity: 22.19% Mismatches: 95  
 Query Match: 6.74% Indels: 146  
 RESULT 1015  
 ID AAD07024 standard; DNA; 5054 BP.  
 DE Pseudomonas putida PHA synthase DNA.  
 PN WO200123596-A2.  
 PD 05-APR-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Percent Similarity: 39.16% Conservative: 35  
 Best Local Similarity: 25.86% Mismatches: 72  
 Query Match: 6.74% Indels: 89  
 RESULT 1016  
 ID ABA17139 standard; DNA; 32179 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 9470.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.89% Conservative: 31  
 Best Local Similarity: 22.59% Mismatches: 79  
 Query Match: 6.74% Indels: 123  
 RESULT 1017  
 Percent Similarity: 36.25% Conservative: 34  
 Best Local Similarity: 25.62% Mismatches: 119  
 Query Match: 6.74% Indels: 85



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RESULT 1018  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PN WO2002771179-A2.  
PD 03-OCT-2002.  
PA (REGC ) UNIV CALIFORNIA.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 33  
Mismatch: 78  
Indels: 48  
Best Local Similarity: 41.04%  
Query Match: 25.47%  
Conservative: 33  
Mismatch: 78  
Indels: 48  
Query Match: 6.74%  
RESULT 1019  
ID AAH64966 standard; DNA; 349980 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 1.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 39.29%  
Mismatch: 28  
Indels: 28  
Best Local Similarity: 25.00%  
Query Match: 6.74%  
Conservative: 28  
Mismatch: 28  
Indels: 28  
Query Match: 6.74%  
RESULT 1020  
ID ACD93801 standard; cDNA; 536 BP.  
DE Human colon cancer cell expressed cDNA #2213.  
PN US2002155438-A1.  
PD 24-OCT-2002.  
PA (SIMP/) SIMPSON A J G.  
PA (NETO/) NETO D D.  
PA (BREN/) BRENTANI R R.  
Percent Similarity: 34.64%  
Mismatch: 11  
Indels: 46  
Best Local Similarity: 28.49%  
Query Match: 6.70%  
Conservative: 11  
Mismatch: 46  
Indels: 46  
Query Match: 6.70%  
RESULT 1021  
ID ADM94403 standard; cDNA; 1069 BP.  
DE Wheat MRP4 ABC transporter cDNA #2.  
PN US6677502-B1.  
PD 13-JAN-2004.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Percent Similarity: 37.59%  
Mismatch: 39  
Indels: 82  
Best Local Similarity: 23.76%  
Query Match: 6.70%  
Conservative: 39  
Mismatch: 82  
Indels: 94  
Query Match: 6.70%  
RESULT 1022  
ID ADJ79603 standard; DNA; 1521 BP.  
DE Glycophosphate resistant corn BPSPS DNA with corn codon usage ID10.  
PN WO2004009761-A2.  
PD 29-JAN-2004.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Percent Similarity: 36.79%  
Mismatch: 34  
Indels: 87  
Best Local Similarity: 25.42%  
Query Match: 6.70%  
Conservative: 34  
Mismatch: 103  
Indels: 87  
Query Match: 6.70%  
RESULT 1023  
ID ADH76897 standard; cDNA; 1670 BP.  
DE Human SOX18 cDNA.  
PN US2002142415-A1.  
PD 03-OCT-2002.  
PA (KOOP/) KOOPMAN P A.  
PA (MUSC/) MUSCAT G E O.  
Percent Similarity: 34.28%  
Mismatch: 30  
Indels: 81  
Best Local Similarity: 23.67%  
Query Match: 6.70%  
Conservative: 30  
Mismatch: 105  
Indels: 81  
Query Match: 6.70%  
RESULT 1024  
ID ABD08413 standard; DNA; 1929 BP.  
DE Pseudomonas aeruginosa polynucleotide #7017.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.79%  
Mismatch: 20  
Indels: 45  
Best Local Similarity: 28.21%  
Query Match: 6.70%  
Conservative: 20  
Mismatch: 104  
Indels: 45  
Query Match: 6.70%  
RESULT 1025  
ID ABD08507 standard; DNA; 1947 BP.  
DE Pseudomonas aeruginosa polynucleotide #7111.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.79%  
Mismatch: 20  
Indels: 45  
Best Local Similarity: 28.21%  
Query Match: 6.70%  
Conservative: 20  
Mismatch: 104  
Indels: 45  
Query Match: 6.70%  
RESULT 1026  
ID ADA69772 standard; DNA; 2016 BP.  
DE Rice gene, SEQ ID 3095.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 32.14%  
Mismatch: 23  
Indels: 92  
Best Local Similarity: 23.93%  
Query Match: 6.70%  
Conservative: 23  
Mismatch: 92  
Indels: 92  
Query Match: 6.70%  
RESULT 1027  
ID ADB84163 standard; DNA; 2160 BP.  
DE Gene expression estimation method-related DNA sequence #23.  
PN WO2003044227-A1.  
PD 30-MAY-2003.  
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.  
Percent Similarity: 32.14%  
Mismatch: 23  
Indels: 92  
Best Local Similarity: 23.93%  
Query Match: 6.70%  
Conservative: 23  
Mismatch: 92  
Indels: 92  
Query Match: 6.70%  
RESULT 1028  
ID AAV62155 standard; DNA; 2341 BP.  
DE HSV-2 strain SB5 Contig ID 11 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Percent Similarity: 34.46%  
Mismatch: 22  
Indels: 86  
Best Local Similarity: 27.03%  
Query Match: 6.70%  
Conservative: 22  
Mismatch: 109  
Indels: 86  
Query Match: 6.70%  
RESULT 1029  
ID ABK14883 standard; DNA; 2499 BP.  
DE DNA encoding Tag DNA polymerase cold-sensitive mutant Cs#3.  
PN US6333159-B1.  
PD 25-DEC-2001.  
PA (UNIW ) UNIV WASHINGTON.  
Percent Similarity: 41.79%  
Mismatch: 44  
Indels: 57  
Best Local Similarity: 26.07%  
Query Match: 6.70%  
Conservative: 44  
Mismatch: 107  
Indels: 57  
Query Match: 6.70%  
RESULT 1030  
ID ABA97303 standard; DNA; 2499 BP.  
DE Cold sensitive mutant DNA polymerase DNA #3.  
PN US6316202-B1.  
PD 13-NOV-2001.  
PA (UNIW ) UNIV WASHINGTON.  
Percent Similarity: 41.79%  
Mismatch: 44  
Indels: 57  
Best Local Similarity: 26.07%  
Query Match: 6.70%  
Conservative: 44  
Mismatch: 107  
Indels: 57  
Query Match: 6.70%  
RESULT 1031  
ID AAV62145 standard; DNA; 2694 BP.  
DE HSV-2 strain SB5 Contig ID 90 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Percent Similarity: 34.46%  
Mismatch: 22  
Indels: 86  
Best Local Similarity: 27.03%  
Query Match: 6.70%  
Conservative: 22  
Mismatch: 109  
Indels: 86  
Query Match: 6.70%  
RESULT 1032  
ID ACC78004 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Mismatch: 33  
Indels: 74  
Best Local Similarity: 25.34%  
Query Match: 6.70%  
Conservative: 33  
Mismatch: 113  
Indels: 74  
Query Match: 6.70%  
RESULT 1033  
ID AAK90702 standard; DNA; 3281 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 4278.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.



Percent Similarity: 34.23% Conservative: 16  
 Best Local Similarity: 28.08% Mismatches: 101  
 Query Match: 6.70% Indels: 70  
 RESULT 1034  
 ID AAK90701 standard; DNA; 3704 BP.  
 DE Human digestive system antigen genomic sequence SEQ ID NO: 4277.  
 PN WO200155314-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.23% Conservative: 16  
 Best Local Similarity: 28.08% Mismatches: 101  
 Query Match: 6.70% Indels: 70  
 RESULT 1035  
 ID AAL44237 standard; DNA; 8651 BP.  
 DE Agromyces mediolanus Y1 operon (C50 carotenoid producing operon).  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI) CARGILL INC.  
 Percent Similarity: 34.55% Conservative: 21  
 Best Local Similarity: 26.02% Mismatches: 87  
 Query Match: 6.70% Indels: 74  
 RESULT 1036  
 ID AAZ23904 standard; DNA; 49999 BP.  
 DE Human LOBO homologue genomic DNA fragment 6.  
 PN WO9950284-A2.  
 PD 07-OCT-1999.  
 PA (ROSE/) ROSENTHAL A.  
 Percent Similarity: 36.11% Conservative: 22  
 Best Local Similarity: 25.93% Mismatches: 80  
 Query Match: 6.70% Indels: 58  
 RESULT 1037  
 Percent Similarity: 31.61% Conservative: 27  
 Best Local Similarity: 23.85% Mismatches: 85  
 Query Match: 6.70% Indels: 154  
 RESULT 1038  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1039  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1040  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1041  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1042  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1043  
 Percent Similarity: 38.04% Conservative: 29  
 Best Local Similarity: 26.67% Mismatches: 106  
 Query Match: 6.70% Indels: 52  
 RESULT 1044  
 ID AD122705 standard; DNA; 1052 BP.  
 DE S. pristinamycin papM gene SEQ ID NO:1.  
 PN WO2004003012-A2.  
 PD 08-JAN-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 Percent Similarity: 31.87% Conservative: 25  
 Best Local Similarity: 22.71% Mismatches: 121  
 Query Match: 6.66% Indels: 65  
 RESULT 1045  
 ID AD122711 standard; DNA; 1052 BP.  
 DE S. pristinamycin papM gene G828A mutant.  
 PN WO2004003012-A2.  
 PD 08-JAN-2004.  
 PA (AVET) AVENTIS PHARMA SA.

Percent Similarity: 31.87% Conservative: 25  
 Best Local Similarity: 22.71% Mismatches: 121  
 Query Match: 6.66% Indels: 65  
 RESULT 1046  
 ID ABD14793 standard; DNA; 1266 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13397.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.39% Conservative: 32  
 Best Local Similarity: 22.33% Mismatches: 100  
 Query Match: 6.66% Indels: 115  
 RESULT 1047  
 ID ABD14888 standard; DNA; 1359 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13492.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.39% Conservative: 32  
 Best Local Similarity: 22.33% Mismatches: 100  
 Query Match: 6.66% Indels: 115  
 RESULT 1048  
 ID ABD05006 standard; DNA; 1605 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3610.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77% Conservative: 24  
 Best Local Similarity: 25.97% Mismatches: 105  
 Query Match: 6.66% Indels: 101  
 RESULT 1049  
 ID ACC77989 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.84% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.66% Indels: 74  
 RESULT 1050  
 ID ABD05159 standard; DNA; 3270 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3763.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77% Conservative: 24  
 Best Local Similarity: 25.97% Mismatches: 105  
 Query Match: 6.66% Indels: 101  
 RESULT 1051  
 ID AAF90037 standard; DNA; 6462 BP.  
 DE Nucleotide sequence of a type I polyketide synthase.  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63% Conservative: 40  
 Best Local Similarity: 23.43% Mismatches: 89  
 Query Match: 6.66% Indels: 104  
 RESULT 1052  
 ID AAS32623 standard; DNA; 10646 BP.  
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 577.  
 PN WO200155319-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.23% Conservative: 19  
 Best Local Similarity: 30.14% Mismatches: 69  
 Query Match: 6.66% Indels: 59  
 RESULT 1053  
 ID AAA81519 standard; DNA; 16677 BP.  
 DE N. meningitidis partial DNA sequence gnm\_66 SEQ ID NO:66.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Percent Similarity: 37.80% Conservative: 33







Percent Similarity: 40.54% Conservative: 17  
 Query Match: 29.05% Mismatches: 54  
 RESULT 1072 Indels: 34

ID ABD10237 standard; DNA; 969 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8841.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.52% Conservative: 15  
 Best Local Similarity: 26.90% Mismatches: 83  
 Query Match: 6.59% Indels: 46  
 RESULT 1073

ID ABD10349 standard; DNA; 1008 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8953.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.52% Conservative: 15  
 Best Local Similarity: 26.90% Mismatches: 83  
 Query Match: 6.59% Indels: 46  
 RESULT 1074

ID AAS54191 standard; DNA; 1014 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #322.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.

PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1075

ID ACA42441 standard; DNA; 1014 BP.  
 DE Prokaryotic essential gene #24098.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1076

ID ABD01581 standard; DNA; 1035 BP.  
 DE Pseudomonas aeruginosa polynucleotide #185.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1077

ID ABD01558 standard; DNA; 1074 BP.  
 DE Pseudomonas aeruginosa polynucleotide #162.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1078

ID ACA23686 standard; DNA; 1263 BP.  
 DE Prokaryotic essential gene #5343.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.19% Conservative: 37  
 Best Local Similarity: 22.52% Mismatches: 82  
 Query Match: 6.59% Indels: 54  
 RESULT 1079

ID ABD13880 standard; DNA; 1293 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12484.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.03% Conservative: 23

Best Local Similarity: 23.82% Mismatches: 88  
 Query Match: 6.59% Indels: 132  
 RESULT 1080

ID ABD14385 standard; DNA; 1422 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12989.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.03% Conservative: 23  
 Best Local Similarity: 23.82% Mismatches: 88  
 Query Match: 6.59% Indels: 132  
 RESULT 1081

ID ABD01554 standard; DNA; 1455 BP.  
 DE Pseudomonas aeruginosa polynucleotide #158.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1082

ID ABX70924 standard; cDNA; 1696 BP.  
 DE Novel human cDNA sequence #149.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.

PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 34.55% Conservative: 23  
 Best Local Similarity: 26.18% Mismatches: 81  
 Query Match: 6.59% Indels: 100  
 RESULT 1083

ID AAN70309 standard; cDNA; 1814 BP.  
 DE Sequence of bovine mullerian inhibiting substance (MIS) cDNA.  
 PN EP221761-A.  
 PD 13-MAY-1987.

PA (BIOJ) BIOGEN NV.  
 Percent Similarity: 32.03% Conservative: 22  
 Best Local Similarity: 24.84% Mismatches: 99  
 Query Match: 6.59% Indels: 109  
 RESULT 1084

ID AAS87226 standard; cDNA; 2327 BP.  
 DE DNA encoding novel human diagnostic protein #23030.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1085

ID AAX87254 standard; cDNA; 2413 BP.  
 DE cDNA clone encoding human PRO201, amplified in tumour cells.  
 PN WO9935170-A2.  
 PD 15-JUL-1999.

PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1086

ID AAZ32137 standard; cDNA; 2413 BP.  
 DE Human PRO201 (Nsp1) protein encoding cDNA clone DNA30676.  
 PN WO9954467-A1.  
 PD 28-OCT-1999.

PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1087

ID AAZ89573 standard; cDNA; 2413 BP.  
 DE Human PRO201 cDNA.  
 PN US6051403-A.  
 PD 18-APR-2000.

PA (GETH) GENENTECH INC.



Percent Similarity: 32.92%	Conservative: 18
Best Local Similarity: 25.51%	Mismatches: 101
Query Match: 6.59%	Indels: 63
RESULT 1088	
ID AA289585 standard; cDNA; 2413 BP.	
DE Human PRO201 cDNA.	
FN US6051690-A.	
PD 18-APR-2000.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 32.92%	Conservative: 18
Best Local Similarity: 25.51%	Mismatches: 101
Query Match: 6.59%	Indels: 63
RESULT 1089	
ID AAA46900 standard; cDNA; 2413 BP.	
DE cDNA encoding novel polypeptide PRO201.	
FN WO200037640-A2.	
PD 29-JUN-2000.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 32.92%	Conservative: 18
Best Local Similarity: 25.51%	Mismatches: 101
Query Match: 6.59%	Indels: 63
RESULT 1090	
ID ADJ58630 standard; cDNA; 2413 BP.	
DE Human DNA30676 cDNA encoding PRO201 (NspI) protein.	
FN US2003191283-A1.	
PD 09-OCT-2003.	
PA (GETH ) GENENTECH INC.	
Percent Similarity: 32.92%	Conservative: 18
Best Local Similarity: 25.51%	Mismatches: 101
Query Match: 6.59%	Indels: 63
RESULT 1091	
ID AAV63400 standard; DNA; 2507 BP.	
DE DNA sequence encoding a DNA polymerase enzyme.	
FN US5837450-A.	
PD 17-NOV-1998.	
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.	
Percent Similarity: 40.43%	Conservative: 40
Best Local Similarity: 25.92%	Mismatches: 115
Query Match: 6.59%	Indels: 52
RESULT 1092	
ID ABD10528 standard; DNA; 2511 BP.	
DE Pseudomonas aeruginosa polynucleotide #9132.	
FN US6551795-B1.	
PD 22-APR-2003.	
PA (GENO-) GENOME THERAPEUTICS CORP.	
Percent Similarity: 34.52%	Conservative: 15
Best Local Similarity: 26.90%	Mismatches: 83
Query Match: 6.59%	Indels: 46
RESULT 1093	
ID ADD69661 standard; cDNA; 2846 BP.	
DE Human REMAP cDNA - SEQ ID 90.	
FN WO2003048305-A2.	
PD 12-JUN-2003.	
PA (INCY-) INCYTE GENOMICS INC.	
Percent Similarity: 37.83%	Conservative: 30
Best Local Similarity: 24.78%	Mismatches: 69
Query Match: 6.59%	Indels: 74
RESULT 1094	
ID AAA38444 standard; DNA; 2893 BP.	
DE Human desmin gene 5' flanking region, including the promoter region.	
FN EP999278-A1.	
PD 10-MAY-2000.	
PA (UYPA-) UNIV PARIS VII.	
Percent Similarity: 33.33%	Conservative: 41
Best Local Similarity: 21.02%	Mismatches: 106
Query Match: 6.59%	Indels: 116
RESULT 1095	
ID ACC77986 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity: 36.64%	Conservative: 34
Best Local Similarity: 25.00%	Mismatches: 113
Query Match: 6.59%	Indels: 74
RESULT 1096	
ID ACC77953 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity: 36.64%	Conservative: 34
Best Local Similarity: 25.00%	Mismatches: 113
Query Match: 6.59%	Indels: 74
RESULT 1097	
ID ACC77950 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity: 36.64%	Conservative: 34
Best Local Similarity: 25.00%	Mismatches: 113
Query Match: 6.59%	Indels: 74
RESULT 1098	
ID ACC77982 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity: 36.64%	Conservative: 34
Best Local Similarity: 25.34%	Mismatches: 113
Query Match: 6.59%	Indels: 74
RESULT 1099	
ID ADQ23554 standard; DNA; 3289 BP.	
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6374.	
FN WO2004048938-A2.	
PD 10-JUN-2004.	
PA (PROT-) PROTEIN DESIGN LABS INC.	
Percent Similarity: 32.78%	Conservative: 25
Best Local Similarity: 24.50%	Mismatches: 85
Query Match: 6.59%	Indels: 118
RESULT 1100	
ID ABR84417 standard; cDNA; 3633 BP.	
DE Human cDNA differentially expressed in granulocytic cells #988.	
FN WO200228999-A2.	
PD 11-APR-2002.	
PA (GENE-) GENE LOGIC INC.	
Percent Similarity: 38.80%	Conservative: 39
Best Local Similarity: 23.20%	Mismatches: 97
Query Match: 6.59%	Indels: 57
RESULT 1101	
ID ABL30051 standard; DNA; 4567 BP.	
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.	
FN WO200171042-A2.	
PD 27-SEP-2001.	
PA (PEKE ) PE CORP NY.	
Percent Similarity: 39.64%	Conservative: 27
Best Local Similarity: 27.48%	Mismatches: 77
Query Match: 6.59%	Indels: 57
RESULT 1102	
ID ADN41761 standard; DNA; 22459 BP.	
DE Novel human secreted protein polynucleotide seqid 883.	
FN US200404191-A1.	
PD 04-MAR-2004.	
PA (FISC/) FISCHER C L.	
PA (ROSE/) ROSEN C A.	
PA (SOPP/) SOPPET D R.	
PA (RUBE/) RUBEN S M.	
PA (KYAW/) KYAW H.	
PA (LIYY/) LI Y.	
PA (ZENG/) ZENG Z.	
PA (LAF/) LAFLEUR D W.	
PA (MOOR/) MOORE P A.	
PA (SHIY/) SHI Y.	
PA (OLSE/) OLSEN H.	
PA (EBNE/) EBNER R.	







Query Match:	6.55%	Indels:	69
RESULT 1124			
ID ADR66070 standard; DNA; 47988 BP.			
DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.			
PN WO2003082309-A1.			
PD 09-OCT-2003.			
PA (AMHP) WYETH.			
Percent Similarity: 38.10%	Conservative: 18		
Best Local Similarity: 28.57%	Mismatches: 83		
Query Match: 6.55%	Indels: 34		
RESULT 1125			
ID ABD02013 standard; DNA; 849 BP.			
DE Pseudomonas aeruginosa polynucleotide #617.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 35.29%	Conservative: 13		
Best Local Similarity: 26.80%	Mismatches: 46		
Query Match: 6.52%	Indels: 53		
RESULT 1126			
ID AAD1173 standard; DNA; 1053 BP.			
DE Pseudomonas stutzeri open reading frame-P (ORF-P) DNA.			
PN WO200153309-A1.			
PD 26-JUL-2001.			
PA (IDAH-) IDAHO RES FOUND INC.			
PA (PASZ-) PASZCZYNSKI A.			
PA (SEBA-) SEBAT J L.			
Percent Similarity: 38.24%	Conservative: 21		
Best Local Similarity: 29.41%	Mismatches: 88		
Query Match: 6.52%	Indels: 60		
RESULT 1127			
ID ADH76980 standard; DNA; 1402 BP.			
DE Human SOX18 related DNA.			
PN US2002142415-A1.			
PD 03-OCT-2002.			
PA (KOOP/) KOOPMAN P A.			
PA (MUSC/) MUSCAT G E O.			
Percent Similarity: 35.76%	Conservative: 37		
Best Local Similarity: 22.92%	Mismatches: 109		
Query Match: 6.52%	Indels: 78		
RESULT 1128			
ID ABD04496 standard; DNA; 1575 BP.			
DE Pseudomonas aeruginosa polynucleotide #3100.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 40.00%	Conservative: 23		
Best Local Similarity: 29.55%	Mismatches: 90		
Query Match: 6.52%	Indels: 42		
RESULT 1129			
ID ABD17609 standard; DNA; 1866 BP.			
DE Pseudomonas aeruginosa polynucleotide #16213.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 37.37%	Conservative: 35		
Best Local Similarity: 25.26%	Mismatches: 80		
Query Match: 6.52%	Indels: 102		
RESULT 1130			
ID ABD04585 standard; DNA; 1956 BP.			
DE Pseudomonas aeruginosa polynucleotide #3189.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 40.00%	Conservative: 23		
Best Local Similarity: 29.55%	Mismatches: 90		
Query Match: 6.52%	Indels: 42		
RESULT 1131			
ID ADB63152 standard; cDNA; 2082 BP.			
DE Human cDNA encoding clone SPLEN20043460.			
PN EPI308459-A2.			
PD 07-MAY-2003.			
PA (HELI-) HELIX RES INST.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Percent Similarity: 37.80%	Conservative: 17		
Best Local Similarity: 29.67%	Mismatches: 73		
Query Match: 6.52%	Indels: 57		
RESULT 1132			
ID ABD02082 standard; DNA; 2379 BP.			
DE Pseudomonas aeruginosa polynucleotide #686.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 34.24%	Conservative: 32		
Best Local Similarity: 23.39%	Mismatches: 87		
Query Match: 6.52%	Indels: 107		
RESULT 1133			
ID ABD02092 standard; DNA; 2499 BP.			
DE Pseudomonas aeruginosa polynucleotide #696.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity: 34.24%	Conservative: 32		
Best Local Similarity: 23.39%	Mismatches: 87		
Query Match: 6.52%	Indels: 107		
RESULT 1134			
ID ADI21750 standard; cDNA; 3212 BP.			
DE Novel human protein cDNA #9.			
PN WO2003025148-A2.			
PD 27-MAR-2003.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 34.92%	Conservative: 21		
Best Local Similarity: 26.59%	Mismatches: 83		
Query Match: 6.52%	Indels: 82		
RESULT 1135			
ID AAI57998 standard; cDNA; 4071 BP.			
DE Human polynucleotide SEQ ID NO 201.			
PN WO200153312-A1.			
PD 26-JUL-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 38.63%	Conservative: 26		
Best Local Similarity: 27.47%	Mismatches: 70		
Query Match: 6.52%	Indels: 74		
RESULT 1136			
ID ADR07615 standard; DNA; 4989 BP.			
DE Novel coding sequence (useful for identifying genetic disorders) #681.			
PN WO2003054152-A2.			
PD 03-JUL-2003.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 49.30%	Conservative: 8		
Best Local Similarity: 38.03%	Mismatches: 24		
Query Match: 6.52%	Indels: 12		
RESULT 1137			
ID ABL1939 standard; cDNA; 7335 BP.			
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30299.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE) PE CORP NY.			
Percent Similarity: 34.27%	Conservative: 34		
Best Local Similarity: 22.38%	Mismatches: 83		
Query Match: 6.52%	Indels: 106		
RESULT 1138			
ID AAH98395 standard; cDNA; 8836 BP.			
DE Human EST-derived coding sequence SEQ ID NO: 252.			
PN WO200154477-A2.			
PD 02-AUG-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity: 32.74%	Conservative: 27		
Best Local Similarity: 24.78%	Mismatches: 90		
Query Match: 6.52%	Indels: 138		
RESULT 1139			
ID AAS36759 standard; DNA; 9745 BP.			
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2959.			
PN WO200155321-A2.			
PD 02-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			



Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1140  
 ID ADB47453 standard; DNA; 9745 BP.  
 DE Human cardiovascular system related genomic DNA #1019.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1141  
 ID ABL1938 standard; cDNA; 10026 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30296.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 34.27% Conservative: 34  
 Best Local Similarity: 23.38% Mismatches: 83  
 Query Match: 6.52% Indels: 106  
 RESULT 1142  
 ID AAS36758 standard; DNA; 12149 BP.  
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2258.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1143  
 ID ADB47452 standard; DNA; 12149 BP.  
 DE Human cardiovascular system related genomic DNA #1018.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1144  
 ID AB274518 standard; DNA; 13361 BP.  
 DE Secreted protein gene 330 genomic fragment HTLCX82, SEQ ID NO:1665.  
 PN WO200277013-A2.  
 PD 03-OCT-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1145  
 ID ADC20950 standard; DNA; 13361 BP.  
 DE Human secreted protein-related DNA sequence #368.  
 PN WO200292787-A2.  
 PD 21-NOV-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1146  
 ID ADC26981 standard; DNA; 20922 BP.  
 DE Sorangium cellulosum tmbA gene cluster tmbB DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Percent Similarity: 34.55% Conservative: 25  
 Best Local Similarity: 25.45% Mismatches: 116  
 Query Match: 6.52% Indels: 65  
 RESULT 1147  
 ID AAD1177 standard; DNA; 25801 BP.  
 DE Pseudomonas stutzeri cosmid pT31 DNA.  
 PN WO200153309-A1.  
 PD 26-JUL-2001.  
 PA (IDAH-) IDAHO RES FOUND INC.  
 (PASZ/) PASZCZYNSKI A.

PA (SEBA/) SEBAT J L.  
 Percent Similarity: 38.34% Conservative: 21  
 Best Local Similarity: 29.41% Mismatches: 88  
 Query Match: 6.52% Indels: 60  
 RESULT 1148  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1149  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1150  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1151  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1152  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1153  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1154  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1155  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1156  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1157  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1158  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1159  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1160  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1161  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1162  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1163  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1164  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1165



ID ADL13694 standard; DNA; 247509 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #216.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 34.82%  
 Best Local Similarity: 25.89%  
 Query Match: 6.52%  
 RESULT 1166  
 ID ABD08014 standard; DNA; 930 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5618.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53%  
 Best Local Similarity: 27.19%  
 Query Match: 6.48%  
 RESULT 1167  
 ID ACA36198 standard; DNA; 1027 BP.  
 DE Prokaryotic essential gene #17855.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.32%  
 Best Local Similarity: 25.35%  
 Query Match: 6.48%  
 RESULT 1168  
 ID AA291271 standard; DNA; 1074 BP.  
 DE Nucleotide sequence fccr seq ID NO:36.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 24.13%  
 Query Match: 6.48%  
 RESULT 1169  
 ID ABD15610 standard; DNA; 1158 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14214.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.65%  
 Best Local Similarity: 26.09%  
 Query Match: 6.48%  
 RESULT 1170  
 ID ABD08045 standard; DNA; 1308 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6649.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53%  
 Best Local Similarity: 27.19%  
 Query Match: 6.48%  
 RESULT 1171  
 ID AA291259 standard; DNA; 1377 BP.  
 DE CoA ligase fccf nucleotide sequence SEQ ID NO:12.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76%  
 Best Local Similarity: 24.13%  
 Query Match: 6.48%  
 RESULT 1172  
 ID AAT74890 standard; DNA; 1535 BP.  
 DE Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.  
 PN WO9716548-A1.  
 PD 09-MAY-1997.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 PA (WEIN/) WEINTRAUB N.  
 Percent Similarity: 38.71%  
 Best Local Similarity: 31.61%  
 Query Match: 6.48%  
 RESULT 1173

ID ADL13694 standard; DNA; 247509 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #216.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Conservative: 20  
 Mismatches: 74  
 Indels: 72  
 Query Match: 6.52%  
 RESULT 1166  
 ID ABD08014 standard; DNA; 930 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5618.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Conservative: 19  
 Mismatches: 106  
 Indels: 41  
 Query Match: 6.48%  
 RESULT 1167  
 ID ACA36198 standard; DNA; 1027 BP.  
 DE Prokaryotic essential gene #17855.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Conservative: 34  
 Mismatches: 105  
 Indels: 73  
 Query Match: 6.48%  
 RESULT 1168  
 ID AA291271 standard; DNA; 1074 BP.  
 DE Nucleotide sequence fccr seq ID NO:36.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Conservative: 39  
 Mismatches: 101  
 Indels: 79  
 Query Match: 6.48%  
 RESULT 1169  
 ID ABD15610 standard; DNA; 1158 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14214.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Conservative: 22  
 Mismatches: 91  
 Indels: 58  
 Query Match: 6.48%  
 RESULT 1170  
 ID ABD08045 standard; DNA; 1308 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6649.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Conservative: 19  
 Mismatches: 106  
 Indels: 41  
 Query Match: 6.48%  
 RESULT 1171  
 ID AA291259 standard; DNA; 1377 BP.  
 DE CoA ligase fccf nucleotide sequence SEQ ID NO:12.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Conservative: 39  
 Mismatches: 101  
 Indels: 79  
 Query Match: 6.48%  
 RESULT 1172  
 ID AAT74890 standard; DNA; 1535 BP.  
 DE Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.  
 PN WO9716548-A1.  
 PD 09-MAY-1997.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 PA (WEIN/) WEINTRAUB N.  
 Conservative: 11  
 Mismatches: 59  
 Indels: 36  
 Query Match: 6.48%  
 RESULT 1173

ID AAV42931 standard; DNA; 1535 BP.  
 DE DNA encoding human neuroD2 protein, which is a bHLH protein.  
 PN US5795723-A.  
 PD 18-AUG-1998.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71%  
 Best Local Similarity: 31.61%  
 Query Match: 6.48%  
 RESULT 1174  
 ID ABS56389 standard; DNA; 1535 BP.  
 DE Human bHLH family neuroD2 genomic DNA, clone 14B1.  
 PN US6444463-B1.  
 PD 03-SEP-2002.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71%  
 Best Local Similarity: 31.61%  
 Query Match: 6.48%  
 RESULT 1175  
 ID ADP72550 standard; DNA; 1580 BP.  
 DE Renal toxin progression gene marker #1139.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 34.11%  
 Best Local Similarity: 22.09%  
 Query Match: 6.48%  
 RESULT 1176  
 ID AB211712 standard; cDNA; 1625 BP.  
 DE Human polynucleotide SEQ ID NO 594.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 41.10%  
 Best Local Similarity: 24.58%  
 Query Match: 6.48%  
 RESULT 1177  
 ID ADM44230 standard; cDNA; 1625 BP.  
 DE Novel human arginine-rich protein cDNA #594.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRNA/) DRMANAC R T.  
 Percent Similarity: 41.10%  
 Best Local Similarity: 24.58%  
 Query Match: 6.48%  
 RESULT 1178  
 ID ABD11546 standard; DNA; 1650 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10150.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91%  
 Best Local Similarity: 23.88%  
 Query Match: 6.48%  
 RESULT 1179  
 ID ABD11322 standard; DNA; 1725 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9926.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91%  
 Best Local Similarity: 23.88%  
 Query Match: 6.48%  
 RESULT 1180  
 ID ABD14631 standard; DNA; 2145 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13235.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.99%  
 Best Local Similarity: 24.83%  
 Query Match: 6.48%  
 RESULT 1181  
 ID ABD14631 standard; DNA; 2145 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13235.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.99%  
 Best Local Similarity: 24.83%  
 Query Match: 6.48%  
 RESULT 1182



RESULT 1181  
ID ADA52692 standard; cDNA; 2198 BP.  
DE Human coding sequence, SEQ ID 260.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.44%  
Best Local Similarity: 27.59%  
Query Match: 6.48%  
Conservative: 20  
Mismatch: 49  
Indels: 78  
RESULT 1182  
ID ABL24533 standard; DNA; 2244 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25072.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 41.61%  
Best Local Similarity: 26.85%  
Query Match: 6.48%  
Conservative: 22  
Mismatch: 58  
Indels: 29  
RESULT 1183  
ID ABA97188 standard; DNA; 2326 BP.  
DE Goat lactoferrin-associated DNA #2.  
PN KR98043944-A.  
PD 05-SEP-1998.  
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.  
Percent Similarity: 34.95%  
Best Local Similarity: 25.61%  
Query Match: 6.48%  
Conservative: 27  
Mismatch: 97  
Indels: 91  
RESULT 1184  
ID AC77593 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 39.38%  
Best Local Similarity: 26.71%  
Query Match: 6.48%  
Conservative: 37  
Mismatch: 97  
Indels: 81  
RESULT 1185  
ID AC77767 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 38.14%  
Best Local Similarity: 25.09%  
Query Match: 6.48%  
Conservative: 38  
Mismatch: 102  
Indels: 79  
RESULT 1186  
ID AAH02112 standard; DNA; 3297 BP.  
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2105.  
PN WO200123604-A2.  
PD 05-APR-2001.  
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
Percent Similarity: 36.73%  
Best Local Similarity: 26.94%  
Query Match: 6.48%  
Conservative: 24  
Mismatch: 100  
Indels: 56  
RESULT 1187  
ID AAH52090 standard; DNA; 3297 BP.  
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 144.  
PN WO200135317-A1.  
PD 17-MAY-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 36.73%  
Best Local Similarity: 26.94%  
Query Match: 6.48%  
Conservative: 24  
Mismatch: 100  
Indels: 56  
RESULT 1188  
ID ACH97234 standard; DNA; 3390 BP.  
DE Klebsiella pneumoniae polynucleotide segid 3029.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 26.88%  
Best Local Similarity: 20.58%  
Query Match: 6.48%  
Conservative: 26  
Mismatch: 101  
Indels: 201

RESULT 1189  
ID ABD07965 standard; DNA; 3741 BP.  
DE Pseudomonas aeruginosa polynucleotide #5569.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.53%  
Best Local Similarity: 27.19%  
Query Match: 6.48%  
Conservative: 19  
Mismatch: 106  
Indels: 41  
RESULT 1190  
ID AAI59784 standard; cDNA; 3913 BP.  
DE Human polynucleotide SEQ ID NO 3773.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.57%  
Best Local Similarity: 27.35%  
Query Match: 6.48%  
Conservative: 25  
Mismatch: 64  
Indels: 74  
RESULT 1191  
ID ABD14252 standard; DNA; 4431 BP.  
DE Pseudomonas aeruginosa polynucleotide #12856.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 30.34%  
Best Local Similarity: 24.34%  
Query Match: 6.48%  
Conservative: 16  
Mismatch: 79  
Indels: 109  
RESULT 1192  
ID ABL24532 standard; DNA; 4649 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25069.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 41.61%  
Best Local Similarity: 26.85%  
Query Match: 6.48%  
Conservative: 22  
Mismatch: 58  
Indels: 29  
RESULT 1193  
ID AAS59642 standard; DNA; 5870 BP.  
DE Propionibacterium acnes immunogenic protein encoding DNA #137.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 26.38%  
Query Match: 6.48%  
Conservative: 25  
Mismatch: 87  
Indels: 75  
RESULT 1194  
ID ACF64571 standard; DNA; 5870 BP.  
DE Propionibacterium acnes DNA contig sequence #137.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 26.38%  
Query Match: 6.48%  
Conservative: 25  
Mismatch: 87  
Indels: 75  
RESULT 1195  
ID ADH13157 standard; DNA; 6131 BP.  
DE Human malignant neoplasia-related gene SeqID6.  
PN EPI365034-A2.  
PD 26-NOV-2003.  
PA (FARB) BAYER AG.  
Percent Similarity: 38.71%  
Best Local Similarity: 31.61%  
Query Match: 6.48%  
Conservative: 11  
Mismatch: 59  
Indels: 36  
RESULT 1196  
ID ACA26658 standard; DNA; 7802 BP.  
DE Prokaryotic essential gene #8315.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.33%  
Best Local Similarity: 24.21%  
Query Match: 6.48%  
Conservative: 23  
Mismatch: 90  
Indels: 78  
RESULT 1197



ID AAV58938 standard; DNA; 10095 BP.  
 DE Mycobacterium tuberculosis embCAB operon.  
 PN WO9841533-A1.  
 PD 24-SEP-1998.  
 PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1198  
 ID ADN36912 standard; DNA; 20640 BP.  
 DE X. albilineans XALB1 gene cluster DNA encoding protein AlBI.  
 PN WO2004035760-A2.  
 PD 29-APR-2004.  
 PA (UVEL ) UNIV FLORIDA.  
 Percent Similarity: 38.13% Conservative: 32  
 Best Local Similarity: 25.68% Mismatches: 116  
 Query Match: 6.48% Indels: 44  
 RESULT 1199  
 ID AA291253 standard; DNA; 24494 BP.  
 DE Bacterium 2412.1 fumonis-catabolising gene cluster.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1200  
 ID ADN36893 standard; DNA; 55839 BP.  
 DE X. albilineans XALB1 gene cluster DNA.  
 PN WO2004035760-A2.  
 PD 29-APR-2004.  
 PA (UVEL ) UNIV FLORIDA.  
 Percent Similarity: 38.13% Conservative: 32  
 Best Local Similarity: 25.68% Mismatches: 116  
 Query Match: 6.48% Indels: 44  
 RESULT 1201  
 ID ADC26995 standard; DNA; 67251 BP.  
 DE Sorangium cellulosum tmbA gene cluster.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI) JULIEN B.  
 Percent Similarity: 40.59% Conservative: 28  
 Best Local Similarity: 26.73% Mismatches: 71  
 Query Match: 6.48% Indels: 50  
 RESULT 1202  
 Percent Similarity: 37.03% Conservative: 43  
 Best Local Similarity: 23.42% Mismatches: 107  
 Query Match: 6.48% Indels: 93  
 RESULT 1203  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1204  
 Percent Similarity: 37.03% Conservative: 43  
 Best Local Similarity: 23.42% Mismatches: 107  
 Query Match: 6.48% Indels: 93  
 RESULT 1205  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1206  
 Percent Similarity: 49.53% Conservative: 23  
 Best Local Similarity: 28.04% Mismatches: 36  
 Query Match: 6.48% Indels: 18  
 RESULT 1207  
 ID ABZ38468 standard; DNA; 507 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 1525.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 43.45% Conservative: 26

Best Local Similarity: 27.98% Mismatches: 64  
 Query Match: 6.44% Indels: 31  
 RESULT 1208  
 ID ACA39058 standard; DNA; 855 BP.  
 DE Prokaryotic essential gene #20715.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 44.26% Conservative: 20  
 Best Local Similarity: 27.87% Mismatches: 53  
 Query Match: 6.44% Indels: 15  
 RESULT 1209  
 ID ADL03828 standard; DNA; 888 BP.  
 DE DNA encoding a M. catarrhalis protein #1514.  
 PN US6673910-B1.  
 PD 06-JAN-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 44.26% Conservative: 20  
 Best Local Similarity: 27.87% Mismatches: 53  
 Query Match: 6.44% Indels: 15  
 RESULT 1210  
 ID AAH65144 standard; DNA; 921 BP.  
 DE C glucamucum coding sequence fragment SEQ ID NO: 179.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 35.74% Conservative: 31  
 Best Local Similarity: 23.29% Mismatches: 93  
 Query Match: 6.44% Indels: 68  
 RESULT 1211  
 ID ABD12950 standard; DNA; 1086 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11554.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.15% Conservative: 16  
 Best Local Similarity: 31.60% Mismatches: 90  
 Query Match: 6.44% Indels: 40  
 RESULT 1212  
 ID ABD05166 standard; DNA; 1251 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3770.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.77% Conservative: 20  
 Best Local Similarity: 28.07% Mismatches: 68  
 Query Match: 6.44% Indels: 35  
 RESULT 1213  
 ID ABD07415 standard; DNA; 1425 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6019.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.99% Conservative: 34  
 Best Local Similarity: 24.22% Mismatches: 97  
 Query Match: 6.44% Indels: 89  
 RESULT 1214  
 ID ADJ48292 standard; DNA; 1428 BP.  
 DE Maize oil-associated gene #110.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C.  
 PA (RAVA/) RAVANELLO M.  
 PA (SAVA/) SAVAGE T.  
 PA (LEDE/) LEDEUX J R.  
 PA (ROGE/) ROGERS J A.  
 Percent Similarity: 36.82% Conservative: 27  
 Best Local Similarity: 27.08% Mismatches: 78  
 Query Match: 6.44% Indels: 97  
 RESULT 1215  
 ID AAF59130 standard; DNA; 1546 BP.  
 DE Streptomyces sp. SK glucose isomerase nucleotide sequence SEQ ID NO:1.  
 PN JP2000333684-A.



PD 05-DEC-2000.  
 PA (NOVO) NOVO NORDISK AS.  
 Percent Similarity: 36.73%  
 Best Local Similarity: 26.55%  
 Query Match: 6.44%  
 Indels: 98  
 Conservative: 28  
 Mismatches: 77  
 RESULT 1216  
 ID AAS71366 standard; cDNA; 1588 BP.  
 DE DNA encoding novel human diagnostic protein #7170.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 43.40%  
 Best Local Similarity: 35.85%  
 Query Match: 6.44%  
 Indels: 31  
 Conservative: 8  
 Mismatches: 29  
 RESULT 1217  
 ID ABT1844 standard; DNA; 1666 BP.  
 DE Aspergillus fumigatus essential gene #842.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.72%  
 Best Local Similarity: 22.48%  
 Query Match: 6.44%  
 Indels: 81  
 Conservative: 29  
 Mismatches: 90  
 RESULT 1218  
 ID ACH96895 standard; DNA; 1707 BP.  
 DE Klebsiella pneumoniae polynucleotide seqid 2690.  
 PN US610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.84%  
 Best Local Similarity: 28.57%  
 Query Match: 6.44%  
 Indels: 68  
 Conservative: 24  
 Mismatches: 95  
 RESULT 1219  
 ID ABD07686 standard; DNA; 1989 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6290.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.99%  
 Best Local Similarity: 24.22%  
 Query Match: 6.44%  
 Indels: 89  
 Conservative: 34  
 Mismatches: 97  
 RESULT 1220  
 ID ADQ23026 standard; DNA; 1990 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5846.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 33.90%  
 Best Local Similarity: 25.42%  
 Query Match: 6.44%  
 Indels: 75  
 Conservative: 20  
 Mismatches: 82  
 RESULT 1221  
 ID ADM47721 standard; DNA; 2005 BP.  
 DE Polynucleotide sequence #139 useful in producing transgenic plants.  
 PN US200323670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D.  
 PA (CHOM/) CHOMET P S.  
 PA (LACC/) LACCETTI L B.  
 Percent Similarity: 35.39%  
 Best Local Similarity: 25.93%  
 Query Match: 6.44%  
 Indels: 76  
 Conservative: 23  
 Mismatches: 81  
 RESULT 1222  
 ID ADB62264 standard; cDNA; 2165 BP.  
 DE Human cDNA encoding clone CTONG20189000.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 38.83%  
 Best Local Similarity: 28.64%  
 Query Match: 6.44%  
 Indels: 43  
 Conservative: 21  
 Mismatches: 84  
 RESULT 1223  
 ID ABD02122 standard; DNA; 2367 BP.  
 DE Pseudomonas aeruginosa polynucleotide #726.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89%  
 Best Local Similarity: 25.93%  
 Query Match: 6.44%  
 Indels: 67  
 Conservative: 28  
 Mismatches: 65  
 RESULT 1224  
 ID ABA00886 standard; DNA; 2502 BP.  
 DE Novel TspJ51 DNA polymerase coding sequence.  
 PN WO2003004632-A2.  
 PD 16-JAN-2003.  
 PA (AMSH) AMERSHAM BIOSCIENCES CORP.  
 Percent Similarity: 34.44%  
 Best Local Similarity: 26.30%  
 Query Match: 6.44%  
 Indels: 83  
 Conservative: 22  
 Mismatches: 94  
 RESULT 1225  
 ID AAS62249 standard; cDNA; 2740 BP.  
 DE cDNA sequence #36 encoding novel human secreted protein.  
 PN WO200177291-A2.  
 PD 18-OCT-2001.  
 PA (GEMY) GENETICS INST INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Conservative: 24  
 Mismatches: 92  
 RESULT 1226  
 ID AAT32326 standard; DNA; 3049 BP.  
 DE Thermus flavus DNA polymerase I coding sequence.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.86%  
 Best Local Similarity: 25.94%  
 Query Match: 6.44%  
 Indels: 75  
 Conservative: 32  
 Mismatches: 112  
 RESULT 1227  
 ID AAD29059 standard; cDNA; 3075 BP.  
 DE Human guanine nucleotide exchange factor (GEF) 32529 cDNA.  
 PN WO200206325-A2.  
 PD 24-JAN-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 38.83%  
 Best Local Similarity: 28.84%  
 Query Match: 6.44%  
 Indels: 43  
 Conservative: 21  
 Mismatches: 84  
 RESULT 1228  
 ID ADI81640 standard; DNA; 3213 BP.  
 DE Malaria mosquito DNA encoding protein ebip7471.  
 PN US2004009537-A1.  
 PD 15-JAN-2004.  
 PA (ROOS/) ROOS J.  
 PA (STAU/) STAUDEMAN K.  
 PA (VELI/) VELICELEBI G.  
 Percent Similarity: 41.97%  
 Best Local Similarity: 29.56%  
 Query Match: 6.44%  
 Indels: 69  
 Conservative: 34  
 Mismatches: 90  
 RESULT 1229  
 ID ACC77949 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30%  
 Best Local Similarity: 25.00%  
 Query Match: 6.44%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 114  
 RESULT 1230  
 ID ACC77952 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30%  
 Best Local Similarity: 25.00%  
 Query Match: 6.44%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 114  
 RESULT 1231



DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PD WO9533818-A2.  
 PD 14-DEC-1995.  
 PA (CIRA ) CIBA GEIGY AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1240  
 ID AAT89955 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster genomic DNA.  
 PD US5652898-A.  
 PD 02-SEP-1997.  
 PA (CIBA ) CIBA GEIGY CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1241  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PD US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1242  
 ID AAV39840 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PD WO9824919-A1.  
 PD 11-JUN-1998.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1243  
 ID AAX99371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PD US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1244  
 ID AA75298 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene region.  
 PD US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1245  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PD WO20022684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1246  
 ID AC28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PD US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA) MURAD F.  
 PA (SHAR) SHARINA I G.  
 PA (KRUM) KRUMENACKER J S.  
 PA (MART) MARTIN E.  
 Percent Similarity: 41.73%  
 Best Local Similarity: 28.06%  
 Query Match: 6.44%  
 RESULT 1247  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PD US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1248  
 ID AAX99371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PD US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1249  
 ID AA75298 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene region.  
 PD US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1250  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PD WO20022684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1251  
 ID AC28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PD US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA) MURAD F.  
 PA (SHAR) SHARINA I G.  
 PA (KRUM) KRUMENACKER J S.  
 PA (MART) MARTIN E.  
 Percent Similarity: 41.73%  
 Best Local Similarity: 28.06%  
 Query Match: 6.44%  
 RESULT 1252  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PD US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1253  
 ID AAX99371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PD US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1254  
 ID AA75298 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene region.  
 PD US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1255  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PD WO20022684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1256  
 ID AC28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PD US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA) MURAD F.  
 PA (SHAR) SHARINA I G.  
 PA (KRUM) KRUMENACKER J S.  
 PA (MART) MARTIN E.  
 Percent Similarity: 41.73%  
 Best Local Similarity: 28.06%  
 Query Match: 6.44%  
 RESULT 1257  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PD US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1258  
 ID AAX99371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PD US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1259  
 ID AA75298 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene region.  
 PD US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1260  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PD WO20022684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1261  
 ID AC28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PD US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA) MURAD F.  
 PA (SHAR) SHARINA I G.  
 PA (KRUM) KRUMENACKER J S.  
 PA (MART) MARTIN E.  
 Percent Similarity: 41.73%  
 Best Local Similarity: 28.06%  
 Query Match: 6.44%  
 RESULT 1262  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PD US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1263  
 ID AAX99371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PD US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1264  
 ID AA75298 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene region.  
 PD US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22%  
 Best Local Similarity: 23.74%  
 Query Match: 6.44%  
 RESULT 1265  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PD WO20022684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 RESULT 1266  
 ID



RESULT 1247  
 ID ADL33384 standard; DNA; 7706 BP.  
 DE Human transporter and ion channel (TRICH) gene #29.  
 PN WO2003083085-A2.  
 PD 09-OCT-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1248  
 ID ABX70982 standard; cDNA; 8037 BP.  
 DE Novel human cDNA sequence #207.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.  
 PA (HYSE-) HYSEQ INC.  
 PA (GOOD/) GOODRICH R W.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1249  
 ID AAF57452 standard; cDNA; 8040 BP.  
 DE Human ABCA2 transporter protein encoding cDNA.  
 PN WO200121798-A2.  
 PD 29-MAR-2001.  
 PA (FOXC-) FOX CHASE CANCER CENT.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1250  
 ID ABV74350 standard; DNA; 8056 BP.  
 DE Human ABC transporter ABCA2 encoding polynucleotide SEQ ID NO 3.  
 PN WO200264781-A2.  
 PD 22-AUG-2002.  
 PA (ACTI-) ACTIVE PASS PHARM INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1251  
 ID AAH75187 standard; cDNA; 8195 BP.  
 DE Nucleotide sequence of a human 17114 transporter polypeptide.  
 PN WO200164875-A2.  
 PD 07-SEP-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1252  
 ID ABI53009 standard; DNA; 8269 BP.  
 DE Human ATP binding cassette transporter protein, ABCA2, coding sequence.  
 PN WO200208424-A1.  
 PD 31-JAN-2002.  
 PA (BANY) BANYU PHARM CO LTD.  
 Percent Similarity: 37.44%  
 Best Local Similarity: 26.07%  
 Query Match: 6.44%  
 Indels: 40  
 Mismatches: 92  
 Conservatives: 24  
 RESULT 1253  
 ID AAK68713 standard; DNA; 11477 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23525.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 Indels: 92  
 Mismatches: 101  
 Conservatives: 30  
 RESULT 1254  
 ID AAK71247 standard; DNA; 11477 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26059.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 Indels: 92  
 Mismatches: 101  
 Conservatives: 30

Query Match: 6.44%  
 Indels: 92  
 RESULT 1255  
 ID AAK68712 standard; DNA; 11482 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 Indels: 92  
 Mismatches: 101  
 Conservatives: 30  
 RESULT 1256  
 ID AAK71246 standard; DNA; 11482 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 33.33%  
 Best Local Similarity: 22.92%  
 Query Match: 6.44%  
 Indels: 92  
 Mismatches: 101  
 Conservatives: 30  
 RESULT 1257  
 ID AAS59566 standard; DNA; 34088 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #61.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 25.10%  
 Query Match: 6.44%  
 Indels: 75  
 Mismatches: 80  
 Conservatives: 42  
 RESULT 1258  
 ID ACF64495 standard; DNA; 34088 BP.  
 DE Propionibacterium acnes DNA contig sequence #61.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 25.10%  
 Query Match: 6.44%  
 Indels: 75  
 Mismatches: 80  
 Conservatives: 42  
 RESULT 1259  
 ID ADH48030 standard; DNA; 37507 BP.  
 DE Clone FS3-135 DNA sequence SEQ ID NO:2.  
 PN EPI386966-A1.  
 PD 04-FEB-2004.  
 PA (LIBR-) LIBRAGEN.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 31.25%  
 Query Match: 6.44%  
 Indels: 35  
 Mismatches: 61  
 Conservatives: 14  
 RESULT 1260  
 ID AAD54230 standard; DNA; 50543 BP.  
 DE Streptomyces amphibiosporus lactimidomycin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 39.06%  
 Best Local Similarity: 26.18%  
 Query Match: 6.44%  
 Indels: 55  
 Mismatches: 90  
 Conservatives: 30  
 RESULT 1261  
 ID AAC55842 standard; DNA; 53500 BP.  
 DE Complete nucleotide sequence of the mitomycin biosynthetic genes.  
 PN WO200053737-A2.  
 PD 14-SEP-2000.  
 PA (MINU) UNIV MINNESOTA.  
 PA (SHER/) SHERMAN D H.  
 PA (MAOY/) MAO Y.  
 PA (VARO/) VAROGLU M.  
 PA (HEMM/) HE M.  
 PA (SHEL/) SHELTON P C.  
 Percent Similarity: 34.74%  
 Best Local Similarity: 25.96%  
 Query Match: 6.44%  
 Indels: 65  
 Mismatches: 121  
 Conservatives: 25  
 RESULT 1262  
 ID ADE10261 standard; DNA; 53500 BP.  
 DE S. lavendulae mitomycin biosynthetic genes complete sequence.  
 PN US2003134398-A1.



PD 17-JUL-2003.	PA (SHER/) SHERMAN D H.		
PA (MAOY/) MAO Y.	PA (KREB/) KREPS J.		
PA (VARO/) VAROGLU M.	PA (PROV/) PROVART N.		
PA (HEMM/) HE M.	PA (RICK/) RICE D.		
PA (SHEL/) SHELTON P.	PA (ZHUT/) ZHU T.		
Percent Similarity: 34.74%	Percent Similarity: 34.15%		
Best Local Similarity: 25.96%	Best Local Similarity: 24.39%		
Query Match: 6.44%	Query Match: 6.40%		
Conservative: 25	Conservative: 28		
Mismatches: 121	Mismatches: 83		
Indels: 65	Indels: 106		
RESULT 1263	RESULT 1271		
ID AAF28545 standard; DNA; 62909 BP.	ID AAC74893 standard; cDNA; 1119 BP.		
DE Genomic fragment #32.	DE Human ORF448 polynucleotide sequence SEQ ID NO:895.		
PN WO200078968-A2.	PN WO200058473-A2.		
PD 28-DEC-2000.	PD 05-OCT-2000.		
PA (INCY-) INCYTE GENOMICS INC.	PA (CURA-) CURAGEN CORP.		
Percent Similarity: 44.26%	Percent Similarity: 37.75%		
Best Local Similarity: 27.87%	Best Local Similarity: 26.51%		
Query Match: 6.44%	Query Match: 6.40%		
Conservative: 20	Conservative: 28		
Mismatches: 53	Mismatches: 86		
Indels: 15	Indels: 69		
RESULT 1264	RESULT 1272		
ID ACC45150 standard; DNA; 96649 BP.	ID ABD08503 standard; DNA; 1221 BP.		
DE Human NAC nucleotide sequence SEQ ID NO:10.	DE Pseudomonas aeruginosa polynucleotide #7107.		
PN WO2003024988-A1.	PN US6551795-B1.		
PD 27-MAR-2003.	PD 22-APR-2003.		
PA (ISIS-) ISIS PHARM INC.	PA (GENO-) GENOME THERAPEUTICS CORP.		
Percent Similarity: 33.33%	Percent Similarity: 36.12%		
Best Local Similarity: 22.92%	Best Local Similarity: 24.08%		
Query Match: 6.44%	Query Match: 6.40%		
Conservative: 30	Conservative: 36		
Mismatches: 101	Mismatches: 101		
Indels: 92	Indels: 90		
RESULT 1265	RESULT 1273		
ID ABD07574 standard; DNA; 822 BP.	ID ADI21915 standard; cDNA; 1368 BP.		
DE Pseudomonas aeruginosa polynucleotide #6178.	DE Novel human protein cDNA #174.		
PN US6551795-B1.	PN WO2003025148-A2.		
PD 22-APR-2003.	PD 27-MAR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.	PA (HYSE-) HYSEQ INC.		
Percent Similarity: 36.53%	Percent Similarity: 35.80%		
Best Local Similarity: 26.48%	Best Local Similarity: 26.46%		
Query Match: 6.40%	Query Match: 6.40%		
Conservative: 42	Conservative: 24		
Mismatches: 106	Mismatches: 104		
Indels: 129	Indels: 61		
RESULT 1266	RESULT 1274		
ID ABD07574 standard; DNA; 822 BP.	ID ABD10627 standard; DNA; 1488 BP.		
DE Pseudomonas aeruginosa polynucleotide #6178.	DE Pseudomonas aeruginosa polynucleotide #9231.		
PN US6551795-B1.	PN US6551795-B1.		
PD 22-APR-2003.	PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.	PA (GENO-) GENOME THERAPEUTICS CORP.		
Percent Similarity: 36.53%	Percent Similarity: 34.20%		
Best Local Similarity: 26.48%	Best Local Similarity: 26.94%		
Query Match: 6.40%	Query Match: 6.40%		
Conservative: 29	Conservative: 14		
Mismatches: 105	Mismatches: 60		
Indels: 78	Indels: 67		
RESULT 1268	RESULT 1275		
ID AAN70355 standard; cDNA to mRNA; 909 BP.	ID ABT19078 standard; DNA; 1581 BP.		
DE Sequence encoding AA sequence (III) of a polypeptide having human	DE Aspergillus fumigatus essential gene #1436.		
DE haematopoietic cell growth potentiating factor (HCGPF) activity.	PN WO200286030-A2.		
PN EP232707-A.	PD 31-OCT-2002.		
PD 19-AUG-1987.	PA (ELIT-) ELITRA PHARM INC.		
PA (AJIN) AJINOMOTO KK.	PA (ELIT-) ELITRA PHARM INC.		
Percent Similarity: 38.58%	Percent Similarity: 33.47%		
Best Local Similarity: 27.17%	Best Local Similarity: 21.37%		
Query Match: 6.40%	Query Match: 6.40%		
Conservative: 29	Conservative: 30		
Mismatches: 94	Mismatches: 83		
Indels: 63	Indels: 82		
RESULT 1269	RESULT 1276		
ID ADC26975 standard; DNA; 942 BP.	ID AAQ2784 standard; cDNA; 1906 BP.		
DE Sorangium cellulosum tmbA gene cluster ORF 3 DNA.	DE Mullerian inhibiting substance cDNA.		
PN US2003054547-A1.	PN US5427780-A.		
PD 20-MAR-2003.	PD 27-JUN-1995.		
PA (JULI) JULIEN B.	PA (BIOI) BIOGEN INC.		
Percent Similarity: 40.50%	Percent Similarity: 32.41%		
Best Local Similarity: 27.50%	Best Local Similarity: 24.69%		
Query Match: 6.40%	Query Match: 6.40%		
Conservative: 26	Conservative: 25		
Mismatches: 73	Mismatches: 112		
Indels: 48	Indels: 107		
RESULT 1270	RESULT 1277		
ID ADU39859 standard; cDNA; 1030 BP.	ID ABD10214 standard; DNA; 2019 BP.		
DE Plant cDNA #859.	DE Pseudomonas aeruginosa polynucleotide #8818.		
PN US2004016025-A1.	PN US6551795-B1.		
PD 22-JAN-2004.	PD 22-APR-2003.		
PA (BUDW/) BUDWORTH P.	PA (GENO-) GENOME THERAPEUTICS CORP.		
PA (MOUG/) MOUGHAMER T.	PA (GENO-) GENOME THERAPEUTICS CORP.		
PA (BRIG/) BRIGGS S P.	Percent Similarity: 34.20%		
PA (COOP/) COOPER B.	Best Local Similarity: 26.94%		
PA (GLAZ/) GLAZEBROOK J.	Query Match: 6.40%		
	Conservative: 14		
	Mismatches: 60		
	Indels: 67		



RESULT 1278  
 ID ABD08834 standard; DNA; 2094 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7438.  
 PN US651795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.86%  
 Best Local Similarity: 24.15%  
 Query Match: 6.40%  
 RESULT 1279  
 ID ADG91050 standard; DNA; 2120 BP.  
 DE Hepatic specific nucleic acid encoding sequence #239.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Query Match: 6.40%  
 RESULT 1280  
 ID AA120576 standard; DNA; 2144 BP.  
 DE Probe #10509 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1281  
 ID ABA65620 standard; DNA; 2144 BP.  
 DE Human foetal liver single exon nucleic acid probe #13925.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1282  
 ID AA145786 standard; DNA; 2144 BP.  
 DE Probe #14472 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1283  
 ID ABA47725 standard; DNA; 2144 BP.  
 DE Human breast cell single exon nucleic acid probe #6420.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1284  
 ID ABA32707 standard; DNA; 2144 BP.  
 DE Probe #11173 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1285  
 ID AA39770 standard; DNA; 2144 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 14327.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1286  
 ID ABA42329 standard; DNA; 2463 BP.

ID AAK14023 standard; DNA; 2144 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 14014.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1287  
 ID ABS39357 standard; DNA; 2144 BP.  
 DE Human liver single exon probe, SEQ ID No 14347.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1288  
 ID AA106275 standard; DNA; 2144 BP.  
 DE Probe #6266 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1289  
 ID ABS13864 standard; DNA; 2144 BP.  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 13855.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1290  
 ID AA161256 standard; cDNA; 2174 BP.  
 DE Human polynucleotide SEQ ID NO 5245.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Query Match: 6.40%  
 RESULT 1291  
 ID ADG91053 standard; DNA; 2280 BP.  
 DE Hepatic specific nucleic acid encoding sequence #242.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Query Match: 6.40%  
 RESULT 1292  
 ID ADG91055 standard; DNA; 2321 BP.  
 DE Hepatic specific nucleic acid encoding sequence #244.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Query Match: 6.40%  
 RESULT 1293  
 ID ADG91049 standard; DNA; 2457 BP.  
 DE Hepatic specific nucleic acid encoding sequence #238.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Query Match: 6.40%  
 RESULT 1294  
 ID ACA42329 standard; DNA; 2463 BP.



DE prokaryotic essential gene #23986.  
 PN WO200277193-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.65%  
 Best Local Similarity: 26.35%  
 Mismatches: 117  
 Indels: 94  
 Query Match:  
 RESULT 1295  
 ID ADG91048 standard; DNA; 2489 BP.  
 DE Hepatic specific nucleic acid encoding sequence #237.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Mismatches: 85  
 Indels: 74  
 Query Match:  
 RESULT 1296  
 ID ADG91047 standard; DNA; 2520 BP.  
 DE Hepatic specific nucleic acid encoding sequence #236.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Mismatches: 85  
 Indels: 74  
 Query Match:  
 RESULT 1297  
 ID ADG91054 standard; DNA; 2641 BP.  
 DE Hepatic specific nucleic acid encoding sequence #243.  
 PN WO2003066877-A2.  
 PD 14-AUG-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Percent Similarity: 42.75%  
 Best Local Similarity: 29.71%  
 Mismatches: 85  
 Indels: 74  
 Query Match:  
 RESULT 1298  
 ID ABD17161 standard; DNA; 2814 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15765.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.65%  
 Best Local Similarity: 26.35%  
 Mismatches: 117  
 Indels: 94  
 Query Match:  
 RESULT 1299  
 ID ABD08894 standard; DNA; 3012 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7498.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.86%  
 Best Local Similarity: 24.15%  
 Mismatches: 92  
 Indels: 57  
 Query Match:  
 RESULT 1300  
 ID ACC77568 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Mismatches: 99  
 Indels: 79  
 Query Match:  
 RESULT 1301  
 ID ACC77580 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Mismatches: 99  
 Indels: 79  
 Query Match:  
 RESULT 1302  
 ID ACC77561 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.

PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 42.09%  
 Best Local Similarity: 26.62%  
 Mismatches: 109  
 Indels: 53  
 Query Match:  
 RESULT 1303  
 ID ACC77598 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.62%  
 Best Local Similarity: 24.83%  
 Mismatches: 101  
 Indels: 79  
 Query Match:  
 RESULT 1304  
 ID ACC77839 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Mismatches: 99  
 Indels: 79  
 Query Match:  
 RESULT 1305  
 ID ACC77780 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.62%  
 Best Local Similarity: 25.17%  
 Mismatches: 101  
 Indels: 79  
 Query Match:  
 RESULT 1306  
 ID ACC77777 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.62%  
 Best Local Similarity: 25.17%  
 Mismatches: 101  
 Indels: 79  
 Query Match:  
 RESULT 1307  
 ID ABD17264 standard; DNA; 3357 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15868.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.65%  
 Best Local Similarity: 26.35%  
 Mismatches: 117  
 Indels: 94  
 Query Match:  
 RESULT 1308  
 ID ADL45191 standard; DNA; 3574 BP.  
 DE Human ovarian cancer DNA marker #19081.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Percent Similarity: 36.09%  
 Best Local Similarity: 23.91%  
 Mismatches: 73  
 Indels: 74  
 Query Match:  
 RESULT 1309  
 ID AAX87412 standard; cDNA; 3607 BP.  
 DE Hepatocellular carcinoma marker gene L4 cDNA.  
 PN WO9939200-A1.  
 PD 05-AUG-1999.  
 PA (UVJE-) UNIV JEFFERSON THOMAS.  
 Percent Similarity: 30.69%  
 Best Local Similarity: 26.35%  
 Mismatches: 87  
 Indels: 105  
 Query Match:  
 RESULT 1310  
 ID AAI59470 standard; cDNA; 3613 BP.  
 DE Human polynucleotide SEQ ID NO 1673.  
 PN WO200153312-A1.



PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC. Conservative: 12  
 Best Local Similarity: 30.69%  
 Mismatches: 87  
 Query Match: 6.40% Indels: 105  
 RESULT 1311  
 ID AD883409 standard; DNA; 4134 BP.  
 DE Rat Gene W73049, SEQ ID NO 11004.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG. Conservative: 23  
 Best Local Similarity: 35.52%  
 Mismatches: 94  
 Query Match: 6.40% Indels: 56  
 RESULT 1312  
 ID ADH76479 standard; DNA; 11364 BP.  
 DE Chimeric pPCR-GalV-1 plasmid DNA sequence.  
 PN FR2832424-A1.  
 PD 23-MAY-2003.  
 PA (GENE-) GENETHON III. Conservative: 33  
 Best Local Similarity: 35.31%  
 Mismatches: 91  
 Query Match: 6.40% Indels: 105  
 RESULT 1313  
 ID ABA20357 standard; DNA; 11585 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 12688.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC. Conservative: 12  
 Best Local Similarity: 30.69%  
 Mismatches: 87  
 Query Match: 6.40% Indels: 105  
 RESULT 1314  
 ID AAH48620 standard; DNA; 16951 BP.  
 DE Human fascin DNA fragment SEQ ID 72.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESKE-KUNZ A. Conservative: 25  
 Best Local Similarity: 23.49%  
 Mismatches: 98  
 Query Match: 6.40% Indels: 118  
 RESULT 1315  
 ID AAH48622 standard; DNA; 16951 BP.  
 DE Human fascin DNA fragment #2.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESKE-KUNZ A. Conservative: 25  
 Best Local Similarity: 23.49%  
 Mismatches: 98  
 Query Match: 6.40% Indels: 118  
 RESULT 1316  
 ID AAF30757 standard; DNA; 47981 BP.  
 DE Micromonospora megalomicea megalomycin biosynthetic gene cluster.  
 PN WO200151631-A2.  
 PD 19-JUL-2001.  
 PA (RESK/) RESKE-KUNZ A. Conservative: 36  
 Best Local Similarity: 34.58%  
 Mismatches: 131  
 Query Match: 6.40% Indels: 79  
 RESULT 1317  
 ID AAF14299 standard; cDNA; 637 BP.  
 DE Aspergillus oryzae EST SEQ ID NO:6822.  
 PN WO200056762-A2.  
 PD 28-SEP-2000.  
 PA (NOVO) NOVO NORDISK INC. Conservative: 23  
 Best Local Similarity: 34.93%  
 Mismatches: 88  
 Query Match: 6.40% Indels: 48  
 RESULT 1318  
 ID AAF14299 standard; cDNA; 637 BP.  
 DE Aspergillus oryzae EST SEQ ID NO:6822.  
 PN WO200056762-A2.  
 PD 28-SEP-2000.  
 PA (NOVO) NOVO NORDISK INC. Conservative: 23  
 Best Local Similarity: 34.93%  
 Mismatches: 88  
 Query Match: 6.40% Indels: 48

PA (NOVO) NOVO NORDISK AS. Conservative: 24  
 Best Local Similarity: 36.49%  
 Mismatches: 59  
 Query Match: 6.37% Indels: 75  
 RESULT 1319  
 ID ABZ37810 standard; DNA; 810 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 209.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA. Conservative: 26  
 Best Local Similarity: 39.04%  
 Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1320  
 ID ABZ40942 standard; DNA; 810 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 6473.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA. Conservative: 26  
 Best Local Similarity: 39.04%  
 Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1321  
 ID ABD14325 standard; DNA; 909 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12929.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 19  
 Best Local Similarity: 32.30%  
 Mismatches: 97  
 Query Match: 6.37% Indels: 100  
 RESULT 1322  
 ID ABZ80091 standard; cDNA; 930 BP.  
 DE Synecococcus methyltransferase encoding cDNA SEQ ID NO:44.  
 PN WO2003016482-A2.  
 PD 27-FEB-2003.  
 PA (MONS) MONSANTO TECHNOLOGY LLC. Conservative: 17  
 Best Local Similarity: 35.20%  
 Mismatches: 61  
 Query Match: 6.37% Indels: 66  
 RESULT 1323  
 ID ABZ37722 standard; DNA; 981 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 33.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA. Conservative: 26  
 Best Local Similarity: 39.04%  
 Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1324  
 ID ABZ41892 standard; DNA; 1023 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 8373.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA. Conservative: 26  
 Best Local Similarity: 39.04%  
 Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1325  
 ID ACA25487 standard; DNA; 1221 BP.  
 DE Prokaryotic essential gene #7144.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Conservative: 30  
 Best Local Similarity: 35.58%  
 Mismatches: 78  
 Query Match: 6.37% Indels: 94  
 RESULT 1326  
 ID ABD10094 standard; DNA; 1269 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8698.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 30  
 Best Local Similarity: 35.58%  
 Mismatches: 78  
 Query Match: 6.37% Indels: 94



Percent Similarity: 37.59% Conservative: 37  
 Best Local Similarity: 23.68% Mismatches: 97  
 Query Match: 6.37% Indels: 69  
 RESULT 1327  
 ID ABA211155 standard; DNA; 1695 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 13486.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1328  
 ID AAS30164 standard; DNA; 1695 BP.  
 DE Human lung antigen genomic DNA #234.  
 PN WO200155303-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1329  
 ID ADB33501 standard; DNA; 1695 BP.  
 DE Human novel lung related polypeptide DNA SEQ ID NO 428.  
 PN US2003054368-A1.  
 PD 20-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1330  
 ID ABD10477 standard; DNA; 1944 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9081.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.59% Conservative: 37  
 Best Local Similarity: 23.68% Mismatches: 97  
 Query Match: 6.37% Indels: 69  
 RESULT 1331  
 ID ADB63664 standard; cDNA; 2315 BP.  
 DE Human cDNA encoding clone THYM20130470.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 35.16% Conservative: 23  
 Best Local Similarity: 26.17% Mismatches: 102  
 Query Match: 6.37% Indels: 64  
 RESULT 1332  
 ID AAH18701 standard; cDNA; 2551 BP.  
 DE Human cDNA sequence SEQ ID NO:18968.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 42.86% Conservative: 32  
 Best Local Similarity: 25.93% Mismatches: 76  
 Query Match: 6.37% Indels: 32  
 RESULT 1333  
 ID ACA89902 standard; cDNA; 2637 BP.  
 DE Gene differentially regulated in cardiovascular disease #23.  
 PN WO2003031650-A2.  
 PD 17-APR-2003.  
 PA (FARB-) BAYER AG.  
 Percent Similarity: 33.98% Conservative: 28  
 Best Local Similarity: 23.17% Mismatches: 95  
 Query Match: 6.37% Indels: 77  
 RESULT 1334  
 ID ACC77944 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.

Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.37% Indels: 74  
 RESULT 1335  
 ID ACC77941 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.37% Indels: 74  
 RESULT 1336  
 ID ACC77948 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.37% Indels: 74  
 RESULT 1337  
 ID ACC77956 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.37% Indels: 74  
 RESULT 1338  
 ID ACC77947 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.37% Indels: 74  
 RESULT 1339  
 ID ACF79531 standard; cDNA; 4035 BP.  
 DE Human E-cadherin repressed clone 1a (hECRepla) cDNA.  
 PN WO2003070759-A2.  
 PD 28-AUG-2003.  
 PA (VLAA-) VLAAms INTERUNIVERSITAIR INST BIOTECHNOG.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1340  
 ID AAD02722 standard; cDNA; 6792 BP.  
 DE Human ATP binding cassette2 (ABC2) transporter protein cDNA.  
 PN WO200114414-A2.  
 PD 01-MAR-2001.  
 PA (ACTI-) ACTIVEPASS PHARM INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.37% Indels: 40  
 RESULT 1341  
 ID AAL61173 standard; DNA; 9975 BP.  
 DE Actinosynema pretiosum polyketide synthase (PKS) gene #4.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW-) UNIV WASHINGTON.  
 Percent Similarity: 30.61% Conservative: 19  
 Best Local Similarity: 24.15% Mismatches: 97  
 Query Match: 6.37% Indels: 108  
 RESULT 1342  
 ID AAF80047 standard; DNA; 13591 BP.  
 DE Nucleotide sequence of odorant binding polypeptide OBPIIb gene.  
 PN WO200112806-A2.  
 PD 22-FEB-2001.  
 PA (UYAU-) UNIV AUVERGNE.  
 PA (PITI-) PITIOT G.



DE	Lung cancer related gene sequence SEQ ID NO:5143.	
PN	WO200194629-A2.	
PD	13-DEC-2001.	
PA	(AVAL-) AVALON PHARM.	
Percent Similarity:	37.06%	Conservative: 9
Best Local Similarity:	31.76%	Mismatches: 54
Query Match:	6.33%	Indels: 53
RESULT 1352		
ID	ABL68898 standard; DNA; 145831 BP.	
DE	Kidney cancer related gene sequence SEQ ID NO:6925.	
PN	WO200194629-A2.	
PD	13-DEC-2001.	
PA	(AVAL-) AVALON PHARM.	
Percent Similarity:	37.06%	Conservative: 9
Best Local Similarity:	31.76%	Mismatches: 54
Query Match:	6.33%	Indels: 53
RESULT 1353		
ID	ABL62309 standard; DNA; 145831 BP.	
DE	Colon adenocarcinoma related gene sequence SEQ ID NO:646.	
PN	WO200194629-A2.	
PD	13-DEC-2001.	
PA	(AVAL-) AVALON PHARM.	
Percent Similarity:	37.06%	Conservative: 9
Best Local Similarity:	31.76%	Mismatches: 54
Query Match:	6.33%	Indels: 53
RESULT 1354		
ID	ABT10149 standard; cDNA; 145831 BP.	
DE	Human breast cancer associated coding sequence SEQ ID NO: 283.	
PN	WO200259271-A2.	
PD	01-AUG-2002.	
PA	(GENE-) GENE LOGIC INC.	
Percent Similarity:	37.06%	Conservative: 9
Best Local Similarity:	31.76%	Mismatches: 54
Query Match:	6.33%	Indels: 53
RESULT 1355		
ID	ABD08598 standard; DNA; 666 BP.	
DE	Pseudomonas aeruginosa polynucleotide #7202.	
PN	US6551795-B1.	
PD	22-APR-2003.	
PA	(GENO-) GENOME THERAPEUTICS CORP.	
Percent Similarity:	36.75%	Conservative: 30
Best Local Similarity:	23.93%	Mismatches: 91
Query Match:	6.33%	Indels: 57
RESULT 1356		
ID	ADF02355 standard; DNA; 798 BP.	
DE	Bacterial polynucleotide #2640.	
PN	US6605709-B1.	
PD	12-AUG-2003.	
PA	(GENO-) GENOME THERAPEUTICS CORP.	
Percent Similarity:	44.96%	Conservative: 20
Best Local Similarity:	29.46%	Mismatches: 53
Query Match:	6.33%	Indels: 18
RESULT 1357		
ID	ADH76894 standard; DNA; 1023 BP.	
DE	Partial human SOX18 coding DNA.	
PN	US2002142415-A1.	
PD	03-OCT-2002.	
PA	(KOOP/) KOOPMAN P A.	
PA	(MUSC/) MUSCAR G E O.	
Percent Similarity:	32.92%	Conservative: 22
Best Local Similarity:	23.87%	Mismatches: 84
Query Match:	6.33%	Indels: 79
RESULT 1358		
ID	ABK42735 standard; DNA; 1081 BP.	
DE	Genomic sequence #634 encoding novel human connective tissue p	
PN	WO200155343-A1.	
PD	02-AUG-2001.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
Percent Similarity:	39.74%	Conservative: 38
Best Local Similarity:	27.36%	Mismatches: 100
Query Match:	6.33%	Indels: 87
RESULT 1359		
ID	AAS36751 standard; DNA; 1081 BP.	



DE Human cardiovascular system antigen genomic DNA SEQ ID No 2251.  
PN WO200155321-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 39.74%  
Best Local Similarity: 27.36%  
Query Match: 6.33%  
Conservative: 38  
Mismatches: 100  
Indels: 87  
RESULT 1360  
ID ADB60891 standard; DNA; 1081 BP.  
DE Connective tissue related genomic DNA #634.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 39.74%  
Best Local Similarity: 27.36%  
Query Match: 6.33%  
Conservative: 38  
Mismatches: 100  
Indels: 87  
RESULT 1361  
ID ADE47445 standard; DNA; 1081 BP.  
DE Human cardiovascular system related genomic DNA #1011.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 39.74%  
Best Local Similarity: 27.36%  
Query Match: 6.33%  
Conservative: 38  
Mismatches: 100  
Indels: 87  
RESULT 1362  
ID ADH76899 standard; DNA; 1155 BP.  
DE Human SOX18 coding DNA.  
PN US2002142415-A1.  
PD 03-OCT-2002.  
PA (MUSC/) MUSCAT G E O.  
Percent Similarity: 32.92%  
Best Local Similarity: 23.87%  
Query Match: 6.33%  
Conservative: 22  
Mismatches: 84  
Indels: 79  
RESULT 1363  
ID AAS54093 standard; DNA; 1305 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #224.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.98%  
Best Local Similarity: 27.80%  
Query Match: 6.33%  
Conservative: 27  
Mismatches: 90  
Indels: 31  
RESULT 1364  
ID ACA4238 standard; DNA; 1305 BP.  
DE Prokaryotic essential gene #23895.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.98%  
Best Local Similarity: 27.80%  
Query Match: 6.33%  
Conservative: 27  
Mismatches: 90  
Indels: 31  
RESULT 1365  
ID ADN95131 standard; cDNA; 1339 BP.  
DE Human Sox18 cDNA sequence SeqID53.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Percent Similarity: 32.92%  
Best Local Similarity: 23.87%  
Query Match: 6.33%  
Conservative: 22  
Mismatches: 84  
Indels: 79  
RESULT 1366  
ID ADH76892 standard; cDNA; 1421 BP.  
DE Partial human SOX18 cDNA.  
PN US2002142415-A1.  
PD 03-OCT-2002.  
PA (KOOP/) KOOPMAN P A.  
Percent Similarity: 32.92%  
Best Local Similarity: 23.87%  
Query Match: 6.33%  
Conservative: 22  
Mismatches: 84  
Indels: 79  
RESULT 1367  
ID ACA98969 standard; cDNA; 1729 BP.  
DE cDNA encoding human nucleic acid-associated protein (NAAP) #50.  
PN WO2003023003-A2.  
PD 20-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 37.37%  
Best Local Similarity: 28.11%  
Query Match: 6.33%  
Conservative: 26  
Mismatches: 97  
Indels: 80  
RESULT 1368  
ID ABS73866 standard; cDNA; 1755 BP.  
DE Human cDNA encoding NAAP6, incyte 2294975CB1.  
PN WO200274913-A2.  
PD 26-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 32.92%  
Best Local Similarity: 23.87%  
Query Match: 6.33%  
Conservative: 22  
Mismatches: 84  
Indels: 79  
RESULT 1369  
ID ABK35373 standard; cDNA; 1872 BP.  
DE Human cDNA encoding secreted protein #511.  
PN WO200177288-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Percent Similarity: 36.69%  
Best Local Similarity: 26.61%  
Query Match: 6.33%  
Conservative: 25  
Mismatches: 90  
Indels: 67  
RESULT 1370  
ID ADH76895 standard; DNA; 1919 BP.  
DE Partial human SOX18 genomic DNA.  
PN US2002142415-A1.  
PD 03-OCT-2002.  
PA (KOOP/) KOOPMAN P A.  
Percent Similarity: 32.92%  
Best Local Similarity: 23.87%  
Query Match: 6.33%  
Conservative: 22  
Mismatches: 84  
Indels: 79  
RESULT 1371  
ID ADB62907 standard; cDNA; 2135 BP.  
DE Human cDNA encoding clone PLACE60064180.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 35.80%  
Best Local Similarity: 25.29%  
Query Match: 6.33%  
Conservative: 27  
Mismatches: 97  
Indels: 68  
RESULT 1372  
ID ADQ24453 standard; DNA; 2221 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7273.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 36.18%  
Best Local Similarity: 26.42%  
Query Match: 6.33%  
Conservative: 24  
Mismatches: 94  
Indels: 63  
RESULT 1373  
ID ACA5288 standard; DNA; 2265 BP.  
DE Prokaryotic essential gene #26945.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 39.02%  
Best Local Similarity: 28.05%  
Query Match: 6.33%  
Conservative: 18  
Mismatches: 46  
Indels: 55  
RESULT 1374  
ID ACA51088 standard; DNA; 2373 BP.  
DE Prokaryotic essential gene #32745.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 36.80%  
Best Local Similarity: 28.57%  
Query Match: 6.33%  
Conservative: 19  
Mismatches: 91



Query Match: 6.33% Indels: 57  
 RESULT 1375  
 ID ADB63375 standard; cDNA; 2442 BP.  
 DE Human cDNA encoding clone TESTI20104090.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 36.69%  
 Best Local Similarity: 26.61%  
 Query Match: 6.33%  
 RESULT 1376  
 ID AQ080749 standard; DNA; 2505 BP.  
 DE T. aquaticus DNA-polymerase.  
 PN WO9429482-A1.  
 PD 22-DEC-1994.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 41.16%  
 Best Local Similarity: 25.99%  
 Query Match: 6.33%  
 RESULT 1377  
 ID ABO61045 standard; cDNA; 2620 BP.  
 DE TEA domain family member 2 encoding sequence.  
 PN WO200231111-A2.  
 PD 18-APR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 36.69%  
 Best Local Similarity: 26.61%  
 Query Match: 6.33%  
 RESULT 1378  
 ID AC47695 standard; DNA; 2694 BP.  
 DE Thermus sp. X-1 DNA polymerase (TX1 DNA polymerase)-encoding gene.  
 PN KR2002067092-A.  
 PD 22-AUG-2002.  
 PA (KWON/) KWON S T.  
 PA (SUPE-) SUPER BIO CO LTD.  
 Percent Similarity: 39.81%  
 Best Local Similarity: 26.54%  
 Query Match: 6.33%  
 RESULT 1379  
 ID ACCT7670 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.36%  
 Best Local Similarity: 26.03%  
 Query Match: 6.33%  
 RESULT 1380  
 ID ACCT7631 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.33%  
 RESULT 1381  
 ID ACCT7835 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.33%  
 RESULT 1382  
 ID ACCT7667 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.62%  
 Query Match: 6.33%  
 Indels: 41

Best Local Similarity: 24.48%  
 Query Match: 6.33%  
 Mismatches: 101  
 Indels: 79  
 RESULT 1383  
 ID ACCT7844 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.33%  
 RESULT 1384  
 ID AAQ10324 standard; cDNA; 3697 BP.  
 DE Human Natriuretic Peptide Receptor B.  
 PN WO9100292-A.  
 PD 10-JAN-1991.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 34.72%  
 Best Local Similarity: 27.08%  
 Query Match: 6.33%  
 RESULT 1385  
 ID AAK52426 standard; cDNA; 5553 BP.  
 DE Human polynucleotide SEQ ID NO 971.  
 PN WO200457150-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 31.97%  
 Best Local Similarity: 21.93%  
 Query Match: 6.33%  
 RESULT 1386  
 ID ABT43729 standard; cDNA; 5987 BP.  
 DE Molecule for disease detection and treatment (MDT)-37 cDNA sequence.  
 PN WO2003052049-A2.  
 PD 26-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 31.97%  
 Best Local Similarity: 21.93%  
 Query Match: 6.33%  
 RESULT 1387  
 ID AAJ59145 standard; DNA; 7178 BP.  
 DE DNA encoding a peptide synthetase unit-PKS module.  
 PN EP1026248-A2.  
 PD 09-AUG-2000.  
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.  
 Percent Similarity: 36.97%  
 Best Local Similarity: 23.53%  
 Query Match: 6.33%  
 RESULT 1388  
 ID ADQ20518 standard; DNA; 7296 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3338.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 31.97%  
 Best Local Similarity: 21.93%  
 Query Match: 6.33%  
 RESULT 1389  
 ID ADJ75976 standard; DNA; 7943 BP.  
 DE Marker gene SEQ ID NO:1228.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Percent Similarity: 30.21%  
 Best Local Similarity: 22.98%  
 Query Match: 6.33%  
 RESULT 1390  
 ID AAX60096 standard; DNA; 17091 BP.  
 DE Acetobacter xylinum JCM7664 cellulose synthase gene.  
 PN JP11127867-A.  
 PD 18-MAY-1999.  
 PA (TOEP) TOKYO ELECTRIC POWER CO INC.  
 Percent Similarity: 39.13%  
 Best Local Similarity: 27.27%  
 Mismatches: 30  
 Indels: 92



Query Match: 6.33% Indels: 62  
 RESULT 1391  
 ID AAS59514 standard; DNA; 21567 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #9.  
 PN WO2000181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 39.46%  
 Best Local Similarity: 27.80%  
 Mismatches: 83  
 Indels: 54  
 Query Match:  
 RESULT 1392  
 ID ACF64443 standard; DNA; 21567 BP.  
 DE Propionibacterium acnes DNA contig sequence #9.  
 PN WO20003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 39.46%  
 Best Local Similarity: 27.80%  
 Mismatches: 83  
 Indels: 54  
 Query Match:  
 RESULT 1393  
 ID ACF04818 standard; DNA; 51855 BP.  
 DE Melithiazol biosynthetic gene cluster.  
 PN WO20003080828-A2.  
 PD 02-OCT-2003.  
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.  
 Percent Similarity: 37.29%  
 Best Local Similarity: 27.12%  
 Mismatches: 92  
 Indels: 56  
 Query Match:  
 RESULT 1394  
 ID AAM58471 standard; DNA; 58857 BP.  
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.  
 PN WO200040704-A1.  
 PD 13-JUL-2000.  
 PA (REGC) UNIV CALIFORNIA.  
 Percent Similarity: 34.26%  
 Best Local Similarity: 26.29%  
 Mismatches: 88  
 Indels: 77  
 Query Match:  
 RESULT 1395  
 ID ABX04971 standard; DNA; 103599 BP.  
 DE S. cinamonensis monensin type I polyketide synthase gene cluster.  
 PN WO2000168867-A1.  
 PD 20-SEP-2001.  
 PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 24.50%  
 Mismatches: 79  
 Indels: 49  
 Query Match:  
 RESULT 1396  
 ID ABQ88139 standard; cDNA; 103747 BP.  
 DE Human osteoblast differentiation related cDNA SEQ ID NO 46.  
 PN WO200250301-A2.  
 PD 27-JUN-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.81%  
 Best Local Similarity: 23.38%  
 Mismatches: 101  
 Indels: 84  
 Query Match:  
 RESULT 1397  
 ID AAV30458 standard; DNA; 534720 BP.  
 DE Rhizobium species plasmid pNGR234.  
 PN WO20004033845-A2.  
 PD 22-APR-2004.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Mismatches: 79  
 Indels: 72  
 Query Match:  
 RESULT 1398  
 ID AAV30459 standard; DNA; 536165 BP.  
 DE Rhizobium species symbiotic plasmid pNGR234.  
 PN WO9802560-A2.  
 PD 22-JAN-1998.  
 PA (MOLE-) INST MOLECULAIRE PLANTES SUPERIE.  
 Percent Similarity: 37.22%  
 Best Local Similarity: 23.38%  
 Mismatches: 116  
 Indels: 51  
 Query Match:  
 RESULT 1399  
 ID AAV30459 standard; DNA; 536165 BP.  
 DE Rhizobium species symbiotic plasmid pNGR234.  
 PN WO9802560-A2.  
 PD 22-JAN-1998.  
 PA (MOLE-) INST MOLECULAIRE PLANTES SUPERIE.  
 Percent Similarity: 37.22%  
 Best Local Similarity: 23.38%  
 Mismatches: 116  
 Indels: 51  
 Query Match:  
 RESULT 1400  
 ID AAN81032 standard; cDNA; 909 BP.  
 DE cDNA encoding a polypeptide having human haematopoietic cell growth  
 DE DE potentiating factor (HCGPF) activity.  
 PN EP274560-A.  
 PD 20-JUL-1988.  
 PA (AJIN) AJINOMOTO KK.  
 Percent Similarity: 38.34%  
 Best Local Similarity: 26.09%  
 Mismatches: 94  
 Indels: 63  
 Query Match:  
 RESULT 1401  
 ID AAN81032 standard; cDNA; 909 BP.  
 DE cDNA encoding a polypeptide having human haematopoietic cell growth  
 DE DE potentiating factor (HCGPF) activity.  
 PN EP274560-A.  
 PD 20-JUL-1988.  
 PA (AJIN) AJINOMOTO KK.  
 Percent Similarity: 38.34%  
 Best Local Similarity: 26.09%  
 Mismatches: 94  
 Indels: 63  
 Query Match:  
 RESULT 1402  
 ID ABK35605 standard; DNA; 1056 BP.  
 DE Gene encoding novel human secreted or membrane-associated protein #24.  
 PN WO200204600-A2.  
 PD 17-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Percent Similarity: 34.27%  
 Best Local Similarity: 26.61%  
 Mismatches: 85  
 Indels: 78  
 Query Match:  
 RESULT 1403  
 ID ABJ02649 standard; cDNA; 1128 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2429.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 38.16%  
 Best Local Similarity: 27.30%  
 Mismatches: 102  
 Indels: 86  
 Query Match:  
 RESULT 1404  
 ID ADP98700 standard; DNA; 1137 BP.  
 DE C. albicans specific gene, orf6.1285, DNA sequence.  
 PN WO20004056965-A2.  
 PD 08-JUL-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.58%  
 Best Local Similarity: 21.82%  
 Mismatches: 68  
 Indels: 35  
 Query Match:  
 RESULT 1405  
 ID AAF83684 standard; DNA; 1161 BP.  
 DE Short form of motilin receptor, GPR-38B isoform encoding DNA.  
 PN WO200138355-A2.  
 PD 31-MAY-2001.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Mismatches: 79  
 Indels: 72  
 Query Match:  
 RESULT 1406  
 ID ADN11762 standard; cDNA; 1161 BP.  
 DE Human motilin receptor GPR-38B coding sequence.  
 PN WO20004033845-A2.  
 PD 22-APR-2004.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Mismatches: 79  
 Indels: 72  
 Query Match:  
 RESULT 1407  
 ID ACA44039 standard; DNA; 1176 BP.  
 DE Prokaryotic essential gene #25696.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.38%  
 Best Local Similarity: 24.23%  
 Mismatches: 29  
 Indels: 78

Percent Similarity: 37.22%  
 Best Local Similarity: 23.31%  
 Mismatches: 51  
 Indels: 51  
 Query Match:  
 RESULT 1400  
 ID AAN81032 standard; cDNA; 909 BP.  
 DE cDNA encoding a polypeptide having human haematopoietic cell growth  
 DE DE potentiating factor (HCGPF) activity.  
 PN EP274560-A.  
 PD 20-JUL-1988.  
 PA (AJIN) AJINOMOTO KK.  
 Percent Similarity: 38.34%  
 Best Local Similarity: 26.09%  
 Mismatches: 94  
 Indels: 63  
 Query Match:  
 RESULT 1401  
 ID AAN81032 standard; cDNA; 909 BP.  
 DE cDNA encoding a polypeptide having human haematopoietic cell growth  
 DE DE potentiating factor (HCGPF) activity.  
 PN EP274560-A.  
 PD 20-JUL-1988.  
 PA (AJIN) AJINOMOTO KK.  
 Percent Similarity: 38.34%  
 Best Local Similarity: 26.09%  
 Mismatches: 94  
 Indels: 63  
 Query Match:  
 RESULT 1402  
 ID ABK35605 standard; DNA; 1056 BP.  
 DE Gene encoding novel human secreted or membrane-associated protein #24.  
 PN WO200204600-A2.  
 PD 17-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Percent Similarity: 34.27%  
 Best Local Similarity: 26.61%  
 Mismatches: 85  
 Indels: 78  
 Query Match:  
 RESULT 1403  
 ID ABJ02649 standard; cDNA; 1128 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2429.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 38.16%  
 Best Local Similarity: 27.30%  
 Mismatches: 102  
 Indels: 86  
 Query Match:  
 RESULT 1404  
 ID ADP98700 standard; DNA; 1137 BP.  
 DE C. albicans specific gene, orf6.1285, DNA sequence.  
 PN WO20004056965-A2.  
 PD 08-JUL-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.58%  
 Best Local Similarity: 21.82%  
 Mismatches: 68  
 Indels: 35  
 Query Match:  
 RESULT 1405  
 ID AAF83684 standard; DNA; 1161 BP.  
 DE Short form of motilin receptor, GPR-38B isoform encoding DNA.  
 PN WO200138355-A2.  
 PD 31-MAY-2001.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Mismatches: 79  
 Indels: 72  
 Query Match:  
 RESULT 1406  
 ID ADN11762 standard; cDNA; 1161 BP.  
 DE Human motilin receptor GPR-38B coding sequence.  
 PN WO20004033845-A2.  
 PD 22-APR-2004.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Mismatches: 79  
 Indels: 72  
 Query Match:  
 RESULT 1407  
 ID ACA44039 standard; DNA; 1176 BP.  
 DE Prokaryotic essential gene #25696.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.38%  
 Best Local Similarity: 24.23%  
 Mismatches: 29  
 Indels: 78



Query Match: 6.29% Indels: 91  
 RESULT 1408  
 ID ADA83986 standard; DNA; 1186 BP.  
 DE Human CDK2R2 gene.  
 PN WO2002103028-A2.  
 PD 27-DEC-2002.  
 PA (BIOM-) BIOMEDICAL CENT.  
 Percent Similarity: 38.5%  
 Best Local Similarity: 27.14%  
 Query Match: 6.29%  
 RESULT 1409  
 ID ABD07713 standard; DNA; 1260 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6317.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 30.26%  
 Best Local Similarity: 22.51%  
 Query Match: 6.29%  
 RESULT 1410  
 ID AA245404 standard; cDNA; 1390 BP.  
 DE cDNA encoding the motilin receptor splice variant MTL-R1B.  
 PN WO9964436-A1.  
 PD 16-DEC-1999.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Query Match: 6.29%  
 RESULT 1411  
 ID ABD10868 standard; DNA; 1524 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9472.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.86%  
 Best Local Similarity: 27.24%  
 Query Match: 6.29%  
 RESULT 1412  
 ID ABL26243 standard; DNA; 1863 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30202.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 37.74%  
 Best Local Similarity: 28.40%  
 Query Match: 6.29%  
 RESULT 1413  
 ID AAA46116 standard; cDNA; 2040 BP.  
 DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.  
 PN WO200022131-A2.  
 PD 20-APR-2000.  
 PA (AREN-) ARENA PHARM INC.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Query Match: 6.29%  
 RESULT 1414  
 ID ADG86512 standard; DNA; 2040 BP.  
 DE Human orphan GPCR-associated DNA #1.  
 PN US2003229216-A1.  
 PD 11-DEC-2003.  
 PA (CHEN/) CHEN R.  
 PA (LIAM/) LIAM C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Query Match: 6.29%  
 RESULT 1415  
 ID ADG86490 standard; cDNA; 2040 BP.  
 DE Human hGPR38 V297K mutant cDNA.  
 PN US2003229216-A1.  
 PD 11-DEC-2003.

PA (CHEN/) CHEN R.  
 PA (LIAM/) LIAM C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Query Match: 6.29%  
 RESULT 1416  
 ID ADP20283 standard; DNA; 2040 BP.  
 DE Human GPCR GPR38 V297K mutant DNA.  
 PN US2004110218-A1.  
 PD 10-JUN-2004.  
 PA (CHEN/) CHEN R.  
 PA (LIAM/) LIAM C W.  
 PA (LOWI/) LOWITZ K.  
 PA (CHAL/) CHALMERS D T.  
 PA (BEHA/) BEHAN D P.  
 Percent Similarity: 34.35%  
 Best Local Similarity: 25.22%  
 Query Match: 6.29%  
 RESULT 1417  
 ID AAF61014 standard; DNA; 2397 BP.  
 DE P. putida KT2440-associated DNA ORF04125.  
 PN DE19935088-A1.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GRFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Percent Similarity: 34.70%  
 Best Local Similarity: 23.88%  
 Query Match: 6.29%  
 RESULT 1418  
 ID ABD12695 standard; DNA; 2406 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11299.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 27.32%  
 Query Match: 6.29%  
 RESULT 1419  
 ID ADO00918 standard; cDNA; 2904 BP.  
 DE Fruit fly AD-related cDNA CG14918.  
 PN US2004067535-A1.  
 PD 08-APR-2004.  
 PA (LIFE-) LIFE SCI DEV CORP.  
 Percent Similarity: 37.74%  
 Best Local Similarity: 28.40%  
 Query Match: 6.29%  
 RESULT 1420  
 ID AAL61203 standard; DNA; 3018 BP.  
 DE Actinosynnema pretiosum cytochrome P450 gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 26.22%  
 Query Match: 6.29%  
 RESULT 1421  
 ID ACC77755 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.93%  
 Best Local Similarity: 24.48%  
 Query Match: 6.29%  
 RESULT 1422  
 ID AA245402 standard; DNA; 3066 BP.  
 DE Genomic sequence of the motilin receptor gene including 5' UTR.



PN WO9964436-A1.  
PA 16-DEC-1999.  
PA (MERI ) MERCK & CO INC.  
Percent Similarity: 34.35%  
Best Local Similarity: 25.22%  
Query Match: 6.29%  
Conservative: 21  
Mismatches: 79  
Indels: 72  
RESULT 1423  
ID ACC77957 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.30%  
Best Local Similarity: 25.00%  
Query Match: 6.29%  
Conservative: 33  
Mismatches: 114  
Indels: 74  
RESULT 1424  
ID ACC77946 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.30%  
Best Local Similarity: 25.00%  
Query Match: 6.29%  
Conservative: 33  
Mismatches: 114  
Indels: 74  
RESULT 1425  
ID AAX87773 standard; cDNA; 3358 BP.  
DE Human mucin gene MUC 5AC cDNA.  
PN WO9941270-A1.  
PD 19-AUG-1999.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 37.17%  
Best Local Similarity: 28.32%  
Query Match: 6.29%  
Conservative: 20  
Mismatches: 79  
Indels: 64  
RESULT 1426  
ID ADJ60926 standard; DNA; 4157 BP.  
DE Concatemer of PDE4A oligonucleotides.  
PN WO2004011613-A2.  
PD 05-FEB-2004.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Percent Similarity: 41.40%  
Best Local Similarity: 25.81%  
Query Match: 6.29%  
Conservative: 29  
Mismatches: 72  
Indels: 37  
RESULT 1427  
ID ADO46415 standard; DNA; 4167 BP.  
DE Human oligonucleotide #1781.  
PN US2004049022-A1.  
PD 11-MAR-2004.  
PA (NYCE/) NYCE J W.  
PA (SAND/) SANDRASAGRA A.  
PA (TANG/) TANG L.  
PA (AGUI/) AGUILAR D.  
PA (MILL/) MILLER S.  
PA (SHAH/) SHAHABUDDIN S.  
PA (LUHH/) LU H.  
PA (CONG/) CONG H.  
Percent Similarity: 41.40%  
Best Local Similarity: 25.81%  
Query Match: 6.29%  
Conservative: 29  
Mismatches: 72  
Indels: 37  
RESULT 1428  
ID AAH48621 standard; DNA; 13055 BP.  
DE Human fascin DNA fragment #1.  
PN WO200151631-A2.  
PD 19-JUL-2001.  
PA (RESK/) RESKE-KUNZ A.  
PA (ROSS/) ROSS X.  
PA (ROSS/) ROSS R.  
PA (BROS/) BROS M.  
Percent Similarity: 32.54%  
Best Local Similarity: 23.39%  
Query Match: 6.29%  
Conservative: 27  
Mismatches: 92  
Indels: 107  
RESULT 1429  
ID ABL12192 standard; cDNA; 15372 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31058.

PN WO200171042-A2.  
PA 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.24%  
Best Local Similarity: 23.69%  
Query Match: 6.29%  
Conservative: 36  
Mismatches: 84  
Indels: 100  
RESULT 1430  
ID AAF87198 standard; DNA; 22735 BP.  
DE Human ion3 coding sequence #2.  
PN WO200144283-A2.  
PD 21-JUN-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Percent Similarity: 43.48%  
Best Local Similarity: 29.81%  
Query Match: 6.29%  
Conservative: 22  
Mismatches: 49  
Indels: 42  
RESULT 1431  
ID AAQ10190 standard; DNA; 23666 BP.  
DE Cephalosporin antibiotic biosynthetic genes.  
PN JP02291274-A.  
PD 03-DEC-1990.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Percent Similarity: 35.80%  
Best Local Similarity: 24.28%  
Query Match: 6.29%  
Conservative: 28  
Mismatches: 90  
Indels: 66  
RESULT 1432  
ID AAX24332 standard; DNA; 34446 BP.  
DE Bovine adenovirus type 3 genome.  
PN WO9859063-A2.  
PD 30-DEC-1998.  
PA (UYSA-) UNIV SASKATCHEWAN.  
Percent Similarity: 33.46%  
Best Local Similarity: 25.00%  
Query Match: 6.29%  
Conservative: 23  
Mismatches: 78  
Indels: 103  
RESULT 1433  
ID ABA92463 standard; DNA; 34446 BP.  
DE Bovine adenovirus type 3 complete genomic DNA sequence SEQ ID NO:35.  
PN US6319716-B1.  
PD 20-NOV-2001.  
PA (UYSA-) UNIV SASKATCHEWAN.  
Percent Similarity: 33.46%  
Best Local Similarity: 25.00%  
Query Match: 6.29%  
Conservative: 23  
Mismatches: 78  
Indels: 103  
RESULT 1434  
ID ABA97532 standard; DNA; 34446 BP.  
DE Bovine adenovirus 3 genome.  
PN WO200192547-A2.  
PD 06-DEC-2001.  
PA (UYSA-) UNIV SASKATCHEWAN.  
Percent Similarity: 33.46%  
Best Local Similarity: 25.00%  
Query Match: 6.29%  
Conservative: 23  
Mismatches: 78  
Indels: 103  
RESULT 1435  
ID ADO47033 standard; DNA; 48480 BP.  
DE Human oligonucleotide #2399.  
PN US2004049022-A1.  
PD 11-MAR-2004.  
PA (NYCE/) NYCE J W.  
PA (SAND/) SANDRASAGRA A.  
PA (TANG/) TANG L.  
PA (AGUI/) AGUILAR D.  
PA (MILL/) MILLER S.  
PA (SHAH/) SHAHABUDDIN S.  
PA (LUHH/) LU H.  
PA (CONG/) CONG H.  
Percent Similarity: 41.40%  
Best Local Similarity: 25.81%  
Query Match: 6.29%  
Conservative: 29  
Mismatches: 72  
Indels: 37  
RESULT 1436  
ID ADJ61643 standard; DNA; 48765 BP.  
DE Concatemer of all oligonucleotides of invention.  
PN WO2004011613-A2.  
PD 05-FEB-2004.  
PA (EPIG-) EPIGENESIS PHARM INC.



Percent Similarity: 41.40% Conservative: 29  
 Best Local Similarity: 25.81% Mismatches: 37  
 Query Match: 6.29% Indels: 37  
 RESULT 1437  
 ID ABQ77491 standard; DNA; 67459 BP.  
 DE S. aurantiaca DNA containing sti gene cluster.  
 PN DE10128661-A1.  
 PD 19-DEC-2002.  
 PA (GBPB) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Percent Similarity: 34.66% Conservative: 32  
 Best Local Similarity: 23.10% Mismatches: 100  
 Query Match: 6.29% Indels: 82  
 RESULT 1438  
 ID ADG70447 standard; DNA; 410846 BP.  
 DE Human ANGE-CLLD8-CLLD7 hybrid gene.  
 PN WO2003000727-A2.  
 PD 03-JAN-2003.  
 PA (ISIS-) ISIS INNOVATIONS LTD.  
 Percent Similarity: 34.35% Conservative: 21  
 Best Local Similarity: 25.22% Mismatches: 79  
 Query Match: 6.29% Indels: 72  
 RESULT 1439  
 ID AB279565 standard; DNA; 410846 BP.  
 DE CLLD8 and NY-REN-34 encoding DNA.  
 PN WO200300296-A2.  
 PD 03-JAN-2003.  
 PA (ISIS-) ISIS INNOVATIONS LTD.  
 Percent Similarity: 34.35% Conservative: 21  
 Best Local Similarity: 25.22% Mismatches: 79  
 Query Match: 6.29% Indels: 72  
 RESULT 1440  
 ID ABQ63083 standard; DNA; 314 BP.  
 DE Mycobacterium tuberculosis BAC vector clone Rv45T7.  
 PN WO9954487-A2.  
 PD 28-OCT-1999.  
 PA (INSP) INST PASTEUR.  
 Percent Similarity: 53.06% Conservative: 6  
 Best Local Similarity: 40.82% Mismatches: 19  
 Query Match: 6.25% Indels: 4  
 RESULT 1441  
 ID ADC75612 standard; DNA; 611 BP.  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 536.  
 PN WO2003020905-A2.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.  
 Percent Similarity: 34.71% Conservative: 15  
 Best Local Similarity: 25.88% Mismatches: 59  
 Query Match: 6.25% Indels: 52  
 RESULT 1442  
 ID ADN37281 standard; cDNA; 633 BP.  
 DE Wheat thaumatin-like protein encoding cDNA SEQ ID NO:25.  
 PN WO2004035790-A1.  
 PD 29-APR-2004.  
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINERS LTD.  
 Percent Similarity: 44.07% Conservative: 12  
 Best Local Similarity: 33.90% Mismatches: 43  
 Query Match: 6.25% Indels: 23  
 RESULT 1443  
 ID AAT12172 standard; cDNA; 971 BP.  
 DE Partial pUG4-5-CDK-BP cDNA clone #121 encoding CDK4 binding protein.  
 PN WO9533819-A2.  
 PD 14-DEC-1995.  
 PA (MITO-) MITOTIX INC.  
 Percent Similarity: 35.19% Conservative: 19  
 Best Local Similarity: 26.39% Mismatches: 85  
 Query Match: 6.25% Indels: 55  
 RESULT 1444  
 ID AAA50562 standard; DNA; 1017 BP.  
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.

Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1445  
 ID AAA50560 standard; DNA; 1020 BP.  
 DE DNA encoding BHV-1 truncated mature gD antigen.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1446  
 ID ACA40569 standard; DNA; 1032 BP.  
 DE Prokaryotic essential gene #22226.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.61% Conservative: 13  
 Best Local Similarity: 30.38% Mismatches: 62  
 Query Match: 6.25% Indels: 36  
 RESULT 1447  
 ID ABD17716 standard; DNA; 1065 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16320.  
 PN US5551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.00% Conservative: 20  
 Best Local Similarity: 28.00% Mismatches: 73  
 Query Match: 6.25% Indels: 51  
 RESULT 1448  
 ID AAA50555 standard; DNA; 1079 BP.  
 DE DNA encoding BHV-1 truncated gD antigen.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1449  
 ID AAA50564 standard; DNA; 1144 BP.  
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1450  
 ID ACD20408 standard; DNA; 1144 BP.  
 DE DNA encoding human NOV23 protein.  
 PN WO200298917-A2.  
 PD 12-DEC-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 37.30% Conservative: 22  
 Best Local Similarity: 28.57% Mismatches: 75  
 Query Match: 6.25% Indels: 84  
 RESULT 1451  
 ID AAA50559 standard; DNA; 1179 BP.  
 DE DNA encoding bovine GnrH tetramer-truncated BHV-1 gD fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1452  
 ID ABK64534 standard; DNA; 1238 BP.  
 DE Human benign prostatic hyperplasia gene #429.  
 PN WO200212440-A2.  
 PD 14-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 PA (NIBS) JAPAN TOBACCO INC.



Percent Similarity: 37.61% Conservative: 32  
 Best Local Similarity: 23.93% Mismatches: 96  
 Query Match: 6.25% Indels: 50  
 RESULT 1453  
 ID ACH00815 standard; DNA; 1238 BP.  
 DE Human spermidine synthase coding sequence.  
 PN WO2003075945-A2.  
 PD 18-SEP-2003.  
 PA (DVE-) DVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
 Percent Similarity: 37.61% Conservative: 32  
 Best Local Similarity: 23.93% Mismatches: 96  
 Query Match: 6.25% Indels: 50  
 RESULT 1454  
 ID AD019193 standard; cDNA; 1238 BP.  
 DE Human PRO polynucleotide #64.  
 PN WO2004043361-A2.  
 PD 27-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 37.61% Conservative: 32  
 Best Local Similarity: 23.93% Mismatches: 96  
 Query Match: 6.25% Indels: 50  
 RESULT 1455  
 ID AAA50556 standard; DNA; 1241 BP.  
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1456  
 ID AAA50549 standard; DNA; 1265 BP.  
 DE DNA encoding bovine herpesvirus type 1 gD antigen.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1457  
 ID AAA50563 standard; DNA; 1272 BP.  
 DE DNA encoding GnrH tetramer-BHV-1 truncated gD-GnrH tetramer fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1458  
 ID AAA50551 standard; DNA; 1279 BP.  
 DE DNA encoding BHV-1 truncated gD antigen-6His fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1459  
 ID AAV73326 standard; DNA; 1290 BP.  
 DE Human CD18 pseudogene clone 6 DNA.  
 PN DE19716346-C1.  
 PD 19-NOV-1998.  
 PA (WAGE/) WAGENER C.  
 Percent Similarity: 32.55% Conservative: 22  
 Best Local Similarity: 23.92% Mismatches: 80  
 Query Match: 6.25% Indels: 93  
 RESULT 1460  
 ID ABD17357 standard; DNA; 1332 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15961.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.00% Conservative: 20

Best Local Similarity: 28.00% Mismatches: 73  
 Query Match: 6.25% Indels: 51  
 RESULT 1461  
 ID ABD17940 standard; DNA; 1341 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16544.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.35% Conservative: 23  
 Best Local Similarity: 28.11% Mismatches: 88  
 Query Match: 6.25% Indels: 69  
 RESULT 1462  
 ID AAA50553 standard; DNA; 1360 BP.  
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1463  
 ID AAA50552 standard; DNA; 1360 BP.  
 DE DNA encoding bovine GnrH tetramer-truncated BHV-1 gD fusion.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (PFIZ) PFIZER PROD INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1464  
 ID AAQ42687 standard; DNA; 1405 BP.  
 DE Sequence encoding a recombinant subunit antigen comprising a truncated  
 DE bovine herpesvirus type 1 (BHV-1) giv glycoprotein.  
 PN WO9311792-A1.  
 PD 24-JUN-1993.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1465  
 ID AAQ48251 standard; DNA; 1405 BP.  
 DE Bovine herpesvirus type 1 giv gene.  
 PN CA2057387-A.  
 PD 12-JUN-1993.  
 PA (VETE-) VETERINARY INFECTIOUS DISEASE.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1466  
 ID AAQ94354 standard; DNA; 1405 BP.  
 DE BHV1 giv glycoprotein genomic DNA.  
 PN US5462734-A.  
 PD 31-OCT-1995.  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1467  
 ID AAV62389 standard; DNA; 1405 BP.  
 DE Bovine herpes virus type-1 glycoprotein IV (BHV-1-gD) encoding DNA.  
 PN EP873752-A2.  
 PD 28-OCT-1998.  
 PA (PFIZ) PFIZER INC.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1468  
 ID AAA50550 standard; DNA; 1405 BP.  
 DE DNA encoding bovine herpesvirus type 1 gD antigen.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.  
 PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.  
 Percent Similarity: 37.97% Conservative: 27  
 Best Local Similarity: 26.58% Mismatches: 93  
 Query Match: 6.25% Indels: 55  
 RESULT 1469  
 ID AAA50550 standard; DNA; 1405 BP.  
 DE DNA encoding bovine herpesvirus type 1 gD antigen.  
 PN EP1035133-A2.  
 PD 13-SEP-2000.



PA (PFIZ ) PRIZER PROD INC.  
Percent Similarity: 27  
Best Local Similarity: 27.97%  
Query Match: 93  
Mismatch: 55  
Indels: 55  
RESULT 1469  
ID AAA50554 standard; DNA; 1441 BP.  
DE DNA encoding GNRH tetramer-BHV-1 truncated gp-GNRH tetramer fusion.  
PN EPI035133-A2.  
PD 13-SEP-2000.  
PA (PFIZ ) PRIZER PROD INC.  
Percent Similarity: 27  
Best Local Similarity: 27.97%  
Query Match: 93  
Mismatch: 55  
Indels: 55  
RESULT 1470  
ID ADQ23266 standard; DNA; 1737 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6086.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 25  
Best Local Similarity: 23.22%  
Query Match: 73  
Mismatch: 107  
Indels: 107  
RESULT 1471  
ID AAQ98947 standard; DNA; 1785 BP.  
DE bg11 insert encoding a B-G subregion fragment of fowl MHC.  
PN US5451670-A.  
PD 19-SEP-1995.  
PA (CITY ) CITY OF HOPE.  
Percent Similarity: 27  
Best Local Similarity: 40.31%  
Query Match: 77  
Mismatch: 77  
Indels: 38  
RESULT 1472  
ID AAD03976 standard; cDNA; 1785 BP.  
DE Chicken bg11 cDNA clone.  
PN US6218106-B1.  
PD 17-APR-2001.  
PA (CITY ) CITY OF HOPE.  
Percent Similarity: 27  
Best Local Similarity: 26.18%  
Query Match: 38  
Mismatch: 38  
Indels: 38  
RESULT 1473  
ID ACA51944 standard; DNA; 1935 BP.  
DE Prokaryotic essential gene #33601.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 39.77%  
Best Local Similarity: 25.00%  
Query Match: 81  
Mismatch: 81  
Indels: 81  
RESULT 1474  
ID AAH17684 standard; cDNA; 1948 BP.  
DE Human cDNA sequence SEQ ID NO:17259.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 26  
Best Local Similarity: 35.32%  
Query Match: 101  
Mismatch: 63  
Indels: 63  
RESULT 1475  
ID ACA42420 standard; DNA; 1995 BP.  
DE Prokaryotic essential gene #24077.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 39.53%  
Best Local Similarity: 24.51%  
Query Match: 47  
Mismatch: 47  
Indels: 47  
RESULT 1476  
ID ABD03241 standard; DNA; 2055 BP.  
DE Pseudomonas aeruginosa polynucleotide #1845.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Percent Similarity: 31.18%  
Best Local Similarity: 22.65%  
Query Match: 91  
Mismatch: 144  
Indels: 144  
RESULT 1477  
ID ABD02794 standard; DNA; 2067 BP.  
DE Pseudomonas aeruginosa polynucleotide #1398.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 39.53%  
Best Local Similarity: 24.51%  
Query Match: 47  
Mismatch: 106  
Indels: 47  
RESULT 1478  
ID ABD02605 standard; DNA; 2100 BP.  
DE Pseudomonas aeruginosa polynucleotide #1209.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 39.53%  
Best Local Similarity: 24.51%  
Query Match: 47  
Mismatch: 106  
Indels: 47  
RESULT 1479  
ID AAF60839 standard; DNA; 2122 BP.  
DE Pseudomonas sp export system associated DNA ORF02378a.  
PN DE19935105-A1.  
PD 01-FEB-2001.  
PA (TIGR-) TIGR INST GENOMIC RES.  
PA (QUIA-) QUIAGEN GMBH.  
PA (GRFB ) GFS BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA (DFEZ-) DFEZ DEUT KREBSFORSCHUNGSZENTRUM.  
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
Percent Similarity: 35  
Best Local Similarity: 25.09%  
Query Match: 101  
Mismatch: 65  
Indels: 65  
RESULT 1480  
ID ADN95102 standard; DNA; 2225 BP.  
DE Human LEC gene sequence SeqID24.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Percent Similarity: 35.32%  
Best Local Similarity: 25.00%  
Query Match: 63  
Mismatch: 63  
Indels: 63  
RESULT 1481  
ID ADK17423 standard; cDNA; 2367 BP.  
DE Murine disrupted-in-schizophrenia 1 (Disc 1) splice variant cDNA.  
PN WO2003099995-A2.  
PD 04-DEC-2003.  
PA (MERI ) MERCK & CO INC.  
Percent Similarity: 36.06%  
Best Local Similarity: 24.54%  
Query Match: 93  
Mismatch: 79  
Indels: 93  
RESULT 1482  
ID ADM01554 standard; cDNA; 2406 BP.  
DE Human cDNA of the invention SEQ ID NO:239.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 35.32%  
Best Local Similarity: 25.00%  
Query Match: 63  
Mismatch: 26  
Indels: 63  
RESULT 1483  
ID ADM02518 standard; cDNA; 2489 BP.  
DE Human cDNA of the invention SEQ ID NO:1203.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 34.76%  
Best Local Similarity: 19.74%  
Query Match: 32  
Mismatch: 120  
Indels: 32  
RESULT 1484  
ID ADK17421 standard; cDNA; 2556 BP.



DE cDNA encoding murine disrupted-in-schizophrenia 1 (Disc 1) protein.  
 PN WO200309995-A2.  
 PD 04-DEC-2003.  
 PA (MERI ) MERCK & CO INC.  
 Percent Similarity: 36.06%  
 Best Local Similarity: 24.54%  
 Query Match: 6.25%  
 RESULT 1485  
 ID ABK92062 standard; DNA; 2995 BP.  
 DE DNA encoding novel UNC5 receptor-like protein.  
 PN WO200229058-A2.  
 PD 11-APR-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 35.32%  
 Best Local Similarity: 25.00%  
 Query Match: 6.25%  
 RESULT 1486  
 ID ACC77578 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.25%  
 RESULT 1487  
 ID ACC77757 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.25%  
 RESULT 1488  
 ID ACC77625 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1489  
 ID ACC77702 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.97%  
 Best Local Similarity: 24.83%  
 Query Match: 6.25%  
 RESULT 1490  
 ID ACC77768 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.93%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1491  
 ID ACC77851 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1492  
 ID ACC77629 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1493  
 ID ACC77759 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.93%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1494  
 ID ACC77576 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.25%  
 RESULT 1495  
 ID ACC77703 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.25%  
 RESULT 1496  
 ID ACC77861 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1497  
 ID ACC77766 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.93%  
 Best Local Similarity: 24.48%  
 Query Match: 6.25%  
 RESULT 1498  
 ID AAA51260 standard; cDNA; 3121 BP.  
 DE Human DNA encoding PRO539, a Costal-2 homologue.  
 PN WO200036102-A2.  
 PD 22-JUN-2000.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.16%  
 Best Local Similarity: 25.25%  
 Query Match: 6.25%  
 RESULT 1499  
 ID ABS68384 standard; cDNA; 3121 BP.  
 DE Human cDNA encoding secreted protein PRO539.  
 PN US2002098506-A1.  
 PD 25-JUL-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.16%  
 Best Local Similarity: 25.25%  
 Query Match: 6.25%  
 RESULT 1500  
 ID ABS67452 standard; cDNA; 3121 BP.  
 DE cDNA encoding novel human secreted protein #2.  
 PN US2002098505-A1.



PD 25-JUL-2002  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.16%  
Best Local Similarity: 25.25%  
Query Match: 6.25%  
Conservative: 18  
Mismatches: 65  
Indels: 68



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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 15:13:22 ; Search time 114 Seconds  
(without alignment)  
6166.405 Million cell updates/sec

Perfect score: 989  
Sequence: 1 gcgggccgcgagtcgaga.....caaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents NA:\*

1: /cgm2\_6/ptodata/1/ina/5A COMB.seq:\*

2: /cgm2\_6/ptodata/1/ina/5B COMB.seq:\*

3: /cgm2\_6/ptodata/1/ina/6A COMB.seq:\*

4: /cgm2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgm2\_6/ptodata/1/ina/PCTUS COMB.seq:\*

6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	19.1	846	4	US-09-252-991A-3196
2	161.8	16.4	953	4	US-09-452-239-45
3	159.2	16.1	1049	4	US-09-452-239-43
4	158.6	16.0	997	4	US-09-452-239-13
5	157.2	15.9	1078	4	US-09-452-239-41
6	155.6	15.7	1018	4	US-09-452-239-35
7	154	15.6	891	4	US-09-452-239-1
8	153	15.5	77536	4	US-09-410-551B-1
9	153	15.5	77536	4	US-09-940-316B-1
10	148	15.0	1118	4	US-09-452-239-37
11	148	15.0	1146	4	US-09-452-239-3
12	144.4	14.6	1057	4	US-09-452-239-5
13	140.6	14.2	1058	4	US-09-452-239-11
14	126	12.7	923	4	US-09-452-239-7
15	122.8	12.4	1810	1	US-07-708-866A-1
16	122.8	12.4	1810	1	US-07-708-866A-2
17	96.8	9.8	1012	4	US-09-615-192A-94
18	96.8	9.8	1012	4	US-09-169-789-94
19	96.8	9.8	1026	2	US-08-713-000-6
20	96.8	9.8	1026	2	US-08-975-316-6
21	96.8	9.8	1026	3	US-09-211-710-6
22	96.8	9.8	1026	4	US-09-615-192A-6
23	96.8	9.8	1026	4	US-09-169-789-6
24	93.4	9.4	675	4	US-09-489-039A-6750
25	88	8.9	931	4	US-09-452-239-17
26	87.8	8.9	534	4	US-09-452-239-47
27	85.6	8.7	962	4	US-09-452-239-23
28	85.6	8.7	1023	4	US-09-452-239-25

29	82.8	8.4	1258	1	US-08-335-518-1	Sequence 1, Appli
30	82.8	8.4	1258	3	US-08-988-054-1	Sequence 1, Appli
31	79.2	8.0	980	4	US-09-452-239-21	Sequence 21, Appl
32	76.2	7.7	760	2	US-08-975-316-25	Sequence 25, Appl
33	76.2	7.7	760	4	US-09-615-192A-25	Sequence 25, Appl
34	76.2	7.7	760	4	US-09-169-789-25	Sequence 25, Appl
35	74.4	7.5	929	4	US-09-452-239-19	Sequence 19, Appl
36	73.2	7.4	870	4	US-09-453-323-2	Sequence 2, Appli
37	70	7.1	811	4	US-09-453-323-3	Sequence 3, Appli
38	66.8	6.8	1074	2	US-08-975-316-54	Sequence 54, Appl
39	66.8	6.8	1074	4	US-09-615-192A-54	Sequence 54, Appl
40	66.8	6.8	1074	4	US-09-169-789-54	Sequence 54, Appl
41	66.8	6.8	1075	2	US-08-975-316-55	Sequence 55, Appl
42	66.8	6.8	1075	4	US-09-615-192A-55	Sequence 55, Appl
43	66.8	6.8	1075	4	US-09-169-789-55	Sequence 55, Appl
44	64.2	6.7	912	4	US-09-452-239-27	Sequence 27, Appl
45	64.2	6.6	967	4	US-09-453-323-5	Sequence 5, Appli
46	64.4	6.5	143	4	US-09-513-999C-15362	Sequence 15362, A
47	64.2	6.5	600	4	US-09-452-239-39	Sequence 39, Appl
48	63.6	6.4	510	4	US-09-452-239-9	Sequence 2, Appli
49	62.8	6.3	4403765	3	US-09-103-840A-2	Sequence 1, Appli
50	62.8	6.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
51	62.4	6.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
52	62.4	6.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
53	61.6	6.2	845	4	US-09-453-323-4	Sequence 4, Appli
54	60.8	6.1	1578	1	US-08-681-129-1	Sequence 1, Appli
55	60	6.1	982	4	US-09-452-239-31	Sequence 31, Appl
56	59.6	6.0	399	4	US-09-615-192A-194	Sequence 194, App
57	58.4	5.9	1288	1	US-08-440-856A-9	Sequence 9, Appli
58	57	5.8	11219	1	US-07-642-734C-1	Sequence 1, Appli
59	57	5.8	11219	3	US-08-439-009A-1	Sequence 1, Appli
60	57	5.8	38494	4	US-08-311-731A-24	Sequence 24, Appl
61	57	5.8	38675	4	US-08-311-731A-135	Sequence 135, App
62	56.8	5.7	1182	3	US-09-385-028-19	Sequence 19, Appl
63	56.8	5.7	1182	4	US-09-726-614-19	Sequence 19, Appl
64	56.8	5.7	1182	4	US-09-385-040-19	Sequence 19, Appl
65	56.8	5.7	11604	3	US-09-385-028-13	Sequence 13, Appl
66	56.8	5.7	11604	4	US-09-726-614-13	Sequence 13, Appl
67	56.8	5.7	11604	4	US-09-385-040-13	Sequence 13, Appl
68	56.8	5.7	15079	3	US-09-385-028-1	Sequence 1, Appli
69	56.8	5.7	15079	4	US-09-726-614-1	Sequence 1, Appli
70	56.8	5.7	15120	4	US-09-385-040-1	Sequence 1, Appli
71	56.8	5.7	22976	4	US-08-289-939A-19	Sequence 19, Appl
72	56.2	5.7	2793	1	US-08-209-747-1	Sequence 1, Appli
73	56.2	5.7	2793	1	US-08-458-298-1	Sequence 1, Appli
74	56	5.7	1098	4	US-09-252-991A-14407	Sequence 14407, A
75	56	5.7	1566	4	US-09-252-991A-14264	Sequence 14264, A
76	56	5.7	1908	4	US-09-252-991A-14353	Sequence 14353, A
77	56	5.7	2109	4	US-09-370-838-153	Sequence 153, App
78	56	5.7	2109	2	US-08-854-133-153	Sequence 153, App
79	56	5.7	4257	2	US-08-690-473-1	Sequence 1, Appli
80	56	5.7	4257	3	US-09-259-821A-1	Sequence 1, Appli
81	56	5.7	4257	3	US-08-843-659-1	Sequence 1, Appli
82	56	5.7	4257	4	US-09-825-288A-1	Sequence 1, Appli
83	56	5.7	12001	1	US-08-458-588A-11	Sequence 11, Appl
84	55.8	5.6	1926	4	US-09-249-585A-2	Sequence 2, Appli
85	55.8	5.6	1926	4	US-09-410-399-3	Sequence 3, Appli
86	55.8	5.6	2580	3	US-09-050-863-2	Sequence 2, Appli
87	55.8	5.6	2580	3	US-09-359-081-2	Sequence 2, Appli
88	55.8	5.6	5452	2	US-09-130-114-1	Sequence 1, Appli
89	55.8	5.6	5452	4	US-09-647-344A-14	Sequence 14, Appl
90	55.8	5.6	9551	2	US-08-056-200-93	Sequence 93, Appl
91	55.8	5.6	9551	2	US-08-800-644-93	Sequence 93, Appl
92	55.8	5.6	9600	3	US-08-910-647-1	Sequence 1, Appli
93	55.8	5.6	9600	4	US-09-620-925-1	Sequence 1, Appli
94	55.8	5.6	10596	1	US-07-884-811-15	Sequence 15, Appl
95	55.8	5.6	10596	1	US-07-885-971-15	Sequence 15, Appl
96	55.8	5.6	10596	1	US-08-087-783A-15	Sequence 15, Appl
97	55.8	5.6	10596	2	US-08-194-088B-15	Sequence 15, Appl
98	55.8	5.6	10596	2	US-08-194-087-15	Sequence 15, Appl
99	55.8	5.6	10596	5	PCT-US93-04548-15	Sequence 15, Appl
100	55.8	5.6	16080	4	US-09-724-566A-48	Sequence 48, Appl
101	55.4	5.6	774	4	US-09-252-991A-9665	Sequence 9665, Ap



102	55.4	5.6	3033	4	US-09-724-797-81	Sequence 81, Appl	c 175	49.8	5.0	3411	4	US-09-252-991A-14823	Sequence 14823, A
103	55	5.6	2559	4	US-09-657-013-40	Sequence 40, Appl	c 176	49.6	5.0	678	4	US-09-252-991A-2221	Sequence 2221, Ap
104	54.8	5.5	594	4	US-09-615-192A-105	Sequence 105, Appl	c 177	49.6	5.0	753	4	US-09-252-991A-2382	Sequence 2382, Ap
105	54.8	5.5	594	4	US-09-169-789-105	Sequence 105, Appl	c 178	49.6	5.0	2814	4	US-09-252-991A-2537	Sequence 2537, Ap
106	54.8	5.5	607	2	US-08-975-316-23	Sequence 23, Appl	c 179	49.4	5.0	1419	4	US-09-252-991A-152	Sequence 152, App
107	54.8	5.5	607	4	US-09-615-192A-23	Sequence 23, Appl	c 180	49.4	5.0	1692	4	US-09-252-991A-157	Sequence 157, App
108	54.8	5.5	607	4	US-09-169-789-23	Sequence 23, Appl	c 181	49.4	5.0	1698	4	US-09-252-991A-186	Sequence 186, App
109	54.6	5.5	1308	4	US-08-937-067-18	Sequence 18, Appl	c 182	49.4	5.0	2214	3	US-08-864-038A-1	Sequence 1, Appl
110	54.6	5.5	2830	2	US-09-010-928B-1	Sequence 1, Appl	c 183	49.4	5.0	2745	1	US-08-363-255-13	Sequence 13, Appl
c 111	54	5.5	4530	4	US-09-793-451-881	Sequence 81, Appl	c 184	49.4	5.0	2745	1	US-08-363-255-13	Sequence 2, Appl
112	53.8	5.4	2082	4	US-09-818-780-67	Sequence 67, Appl	c 185	49.4	5.0	3331	3	US-08-864-038A-2	Sequence 2, Appl
113	53.8	5.4	44377	2	US-08-804-227C-7	Sequence 7, Appl	c 186	49.4	5.0	3331	3	US-08-864-038A-4	Sequence 4, Appl
114	53.8	5.4	44377	2	US-08-804-198-1	Sequence 1, Appl	c 187	49.4	5.0	3489	2	US-08-728-323A-1	Sequence 1, Appl
115	53.8	5.4	114793	4	US-10-148-806-3	Sequence 3, Appl	c 188	49.4	5.0	3489	3	US-09-298-568-1	Sequence 1, Appl
c 116	53.4	5.4	2248	3	US-09-345-214-20	Sequence 20, Appl	c 189	49.4	5.0	3489	3	US-09-410-399-1	Sequence 1, Appl
c 117	53.4	5.4	2248	3	US-09-743-980-20	Sequence 20, Appl	c 190	49.4	5.0	3489	2	US-09-894-273-1	Sequence 1, Appl
118	53.4	5.4	2338	1	US-08-425-069-1	Sequence 1, Appl	c 191	49.4	5.0	32207	2	US-08-770-379-20	Sequence 20, Appl
119	53.4	5.4	2338	1	US-08-317-844B-1	Sequence 1, Appl	c 192	49.4	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
c 120	53	5.3	632	4	US-09-221-017B-655	Sequence 655, Appl	c 193	49.4	5.0	32207	3	US-09-230-371A-20	Sequence 20, Appl
c 121	52.8	5.3	1236	1	US-08-440-856A-1	Sequence 1, Appl	c 194	49.2	5.0	789	4	US-09-252-991A-15913	Sequence 15913, A
c 122	52.6	5.3	2561	4	US-09-616-289-48	Sequence 48, Appl	c 195	49.2	5.0	795	4	US-09-252-991A-11852	Sequence 11852, A
123	52.4	5.3	3978	3	US-08-728-214-1	Sequence 41, Appl	c 196	49.2	5.0	888	4	US-09-252-991A-16512	Sequence 16512, A
124	52.4	5.3	5640	4	US-09-620-312D-41	Sequence 41, Appl	c 197	49.2	5.0	1221	4	US-09-252-991A-11531	Sequence 11531, A
c 125	52	5.3	1248	4	US-09-252-991A-1437	Sequence 1437, Ap	c 198	49.2	5.0	1263	4	US-09-252-991A-13658	Sequence 13658, A
126	52	5.3	1302	4	US-09-252-991A-1437	Sequence 1437, Ap	c 199	49.2	5.0	1263	4	US-09-252-991A-15778	Sequence 15778, A
127	52	5.3	1956	4	US-09-252-991A-1494	Sequence 1494, Ap	c 200	49.2	5.0	1521	4	US-09-252-991A-15957	Sequence 15957, A
128	51.8	5.2	498	4	US-09-252-991A-10389	Sequence 10389, A	c 201	49.2	5.0	1569	4	US-09-252-991A-15991	Sequence 15991, A
c 129	51.8	5.2	561	4	US-09-252-991A-10580	Sequence 10580, A	c 202	49.2	5.0	2400	4	US-09-531-589-3	Sequence 3, Appl
c 130	51.8	5.2	1053	4	US-09-252-991A-10684	Sequence 10684, A	c 203	49.2	5.0	3318	3	US-09-615-192A-193	Sequence 193, App
c 131	51.8	5.2	1233	4	US-09-252-991A-3104	Sequence 3104, Ap	c 204	49.2	5.0	399	4	US-09-724-797-33	Sequence 33, Appl
c 132	51.8	5.2	1386	4	US-09-252-991A-2867	Sequence 2867, Ap	c 205	49	5.0	843	4	US-08-415-655-14	Sequence 14, Appl
c 133	51.8	5.2	1926	4	US-09-249-585A-4	Sequence 4, Appl	c 206	49	5.0	1355	3	US-09-616-289-45	Sequence 45, Appl
c 134	51.8	5.2	1931	2	US-09-130-114-2	Sequence 2, Appl	c 207	49	5.0	1614	4	US-09-616-289-50	Sequence 50, Appl
c 135	51.8	5.2	2075	4	US-09-087-031E-2	Sequence 2, Appl	c 208	49	5.0	12425	4	US-09-410-551B-1	Sequence 1, Appl
136	51.8	5.2	2075	4	US-09-546-043-1	Sequence 1, Appl	c 209	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appl
137	51.8	5.2	2075	4	US-09-514-885-2	Sequence 2, Appl	c 210	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appl
c 138	51.6	5.2	1311	4	US-09-252-991A-14065	Sequence 14065, A	c 211	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appl
c 139	51.6	5.2	2850	4	US-09-252-991A-14205	Sequence 14205, A	c 212	48.8	4.9	852	4	US-09-252-991A-7607	Sequence 7607, Ap
140	51.4	5.2	7847	4	US-09-799-451-591	Sequence 591, App	c 213	48.8	4.9	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
141	51.2	5.2	2277	1	US-08-676-967-5	Sequence 5, Appl	c 214	48.8	4.9	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
142	51.2	5.2	2277	1	US-08-676-967-5	Sequence 5, Appl	c 215	48.8	4.9	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
143	51.2	5.2	2277	2	US-09-098-487-5	Sequence 5, Appl	c 216	48.8	4.9	2232	4	US-09-252-991A-11756	Sequence 11756, A
144	51	5.2	501	4	US-09-252-991A-11947	Sequence 11947, A	c 217	48.8	4.9	2274	4	US-09-252-991A-11609	Sequence 11609, A
145	51	5.2	1500	4	US-09-252-991A-11907	Sequence 11907, A	c 218	48.8	4.9	2613	4	US-09-252-991A-11836	Sequence 11836, A
146	51	5.2	2561	4	US-09-616-289-48	Sequence 48, Appl	c 219	48.8	4.9	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
147	51	5.2	8438	1	US-07-945-283-1	Sequence 1, Appl	c 220	48.6	4.9	528	4	US-09-452-239-33	Sequence 33, Appl
c 148	50.8	5.1	741	4	US-09-724-797-73	Sequence 73, Appl	c 221	48.6	4.9	1320	4	US-09-724-797-85	Sequence 85, Appl
149	50.8	5.1	1155	3	US-08-818-112-12	Sequence 12, Appl	c 222	48.6	4.9	1479	1	US-08-644-271-31	Sequence 31, Appl
150	50.8	5.1	1155	3	US-08-818-111-12	Sequence 12, Appl	c 223	48.6	4.9	1479	4	US-09-077-955-35	Sequence 35, Appl
151	50.8	5.1	1155	3	US-09-056-556-12	Sequence 12, Appl	c 224	48.6	4.9	1575	4	US-09-252-991A-11212	Sequence 11212, A
152	50.8	5.1	1155	4	US-09-072-596-12	Sequence 12, Appl	c 225	48.6	4.9	1620	4	US-09-252-991A-11146	Sequence 11146, A
153	50.8	5.1	1155	4	US-09-072-967-12	Sequence 12, Appl	c 226	48.6	4.9	2040	2	US-08-533-669A-5	Sequence 5, Appl
154	50.6	5.1	508	4	US-09-452-239-15	Sequence 15, Appl	c 227	48.6	4.9	2040	3	US-09-183-861-5	Sequence 5, Appl
155	50.4	5.1	23673	3	US-09-773-816-1	Sequence 1, Appl	c 228	48.6	4.9	2040	3	US-09-022-765-5	Sequence 5, Appl
156	50.2	5.1	864	4	US-09-252-991A-10932	Sequence 10932, A	c 229	48.6	4.9	2040	4	US-09-551-974A-5	Sequence 5, Appl
c 157	50.2	5.1	2211	4	US-09-252-991A-11256	Sequence 11256, A	c 230	48.6	4.9	2040	4	US-09-565-501A-5	Sequence 5, Appl
158	50.2	5.1	2289	4	US-09-252-991A-10995	Sequence 10995, A	c 231	48.6	4.9	2040	4	US-09-639-206A-5	Sequence 5, Appl
159	50.2	5.1	4826	4	US-09-772-304A-1	Sequence 1, Appl	c 232	48.6	4.9	2040	4	US-09-874-923-5	Sequence 5, Appl
c 160	50	5.1	888	4	US-09-311-021-155	Sequence 155, App	c 233	48.6	4.9	2040	4	US-08-798-841-5	Sequence 5, Appl
161	50	5.1	13842	3	US-09-105-537-30	Sequence 30, Appl	c 234	48.6	4.9	2472	3	US-09-252-991A-11043	Sequence 11043, A
162	50	5.1	36778	3	US-09-105-537-5	Sequence 5, Appl	c 235	48.6	4.9	2712	3	US-09-025-691-4	Sequence 4, Appl
163	50	5.1	38506	3	US-09-320-808-19	Sequence 19, Appl	c 236	48.4	4.9	562	2	US-08-975-316-53	Sequence 53, Appl
164	50	5.1	38506	4	US-09-141-908-1	Sequence 1, Appl	c 237	48.4	4.9	562	4	US-09-615-192A-53	Sequence 53, Appl
165	50	5.1	38506	4	US-09-657-440-19	Sequence 19, Appl	c 238	48.4	4.9	756	1	US-09-169-789-53	Sequence 53, Appl
c 166	50	5.1	229354	4	US-09-765-400-64	Sequence 64, Appl	c 239	48.4	4.9	822	4	US-08-642-255-50	Sequence 50, Appl
c 167	50	5.1	229354	4	US-09-705-400-64	Sequence 64, Appl	c 240	48.2	4.9	920	4	US-09-252-991A-11707	Sequence 11707, A
168	49.8	5.0	3003	4	US-09-252-991A-14790	Sequence 14790, A	c 241	48.2	4.9	1035	1	US-09-620-312D-132	Sequence 132, App
169	49.8	5.0	3113	4	US-09-894-998A-52	Sequence 52, Appl	c 242	48.2	4.9	1035	1	US-07-601-094-30	Sequence 30, Appl
170	49.8	5.0	3132	4	US-09-252-991A-14540	Sequence 14540, A	c 243	48.2	4.9	1035	3	US-08-012-731A-3	Sequence 3, Appl
171	49.8	5.0	3147	2	US-08-781-802-7	Sequence 7, Appl	c 244	48.2	4.9	1914	1	US-09-593-711A-3	Sequence 3, Appl
172	49.8	5.0	3147	3	US-08-694-078-7	Sequence 7, Appl	c 245	48.2	4.9	1914	1	US-07-601-094-1	Sequence 1, Appl
173	49.8	5.0	3147	3	US-08-058-260-7	Sequence 7, Appl	c 246	48.2	4.9	1914	1	US-08-012-735-1	Sequence 1, Appl
174	49.8	5.0	3345	4	US-09-894-998A-49	Sequence 49, Appl	c 247	48.2	4.9	2009	4	US-09-646-403-1	Sequence 1, Appl



248	48.2	4.9	2023	4	US-09-491-522-6	Sequence 6, Appli	321	47.4	4.8	50937	3	US-09-428-517-1	Sequence 1, Appli
249	48.2	4.9	2034	4	US-09-646-403-2	Sequence 2, Appli	c 322	47.4	4.8	50937	3	US-09-428-517-1	Sequence 1, Appli
250	48.2	4.9	2450	4	US-09-491-522-2	Sequence 2, Appli	c 323	47.2	4.8	714	4	US-09-252-991A-16021	Sequence 16021, A
c 251	48.2	4.9	3350	4	US-09-894-998A-48	Sequence 48, Appli	324	47.2	4.8	888	3	US-08-765-907A-2	Sequence 2, Appli
c 252	48.2	4.9	6692	4	US-09-491-522-1	Sequence 1, Appli	325	47.2	4.8	999	4	US-09-252-991A-970	Sequence 970, App
c 253	48	4.9	465	4	US-09-252-991A-2233	Sequence 2233, Ap	326	47.2	4.8	1110	4	US-09-252-991A-1014	Sequence 1014, Ap
c 254	48	4.9	822	4	US-09-252-991A-7080	Sequence 7080, Ap	327	47.2	4.8	1194	4	US-09-724-797-25	Sequence 25, Appl
c 255	48	4.9	852	4	US-09-252-991A-2447	Sequence 2447, Ap	c 328	47.2	4.8	1275	4	US-09-252-991A-1080	Sequence 1080, Ap
256	48	4.9	1071	4	US-09-252-991A-1635	Sequence 1635, Ap	329	47.2	4.8	1347	4	US-09-724-797-43	Sequence 43, Appl
257	48	4.9	1128	4	US-09-622-439-1	Sequence 1, Appli	330	47.2	4.8	1944	4	US-09-252-991A-16245	Sequence 16245, A
258	48	4.9	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	331	47.2	4.8	2133	4	US-09-252-991A-5907	Sequence 5907, Ap
c 259	48	4.9	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	332	47.2	4.8	2808	4	US-09-475-515-84	Sequence 84, Appl
c 260	48	4.9	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	333	47.2	4.8	2808	4	US-09-252-991A-16466	Sequence 16466, A
c 261	48	4.9	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	c 334	47.2	4.8	2862	4	US-09-252-991A-10659	Sequence 10659, A
c 262	48	4.9	1806	4	US-09-252-991A-1534	Sequence 1534, Ap	c 335	47.2	4.8	2888	3	US-08-765-907A-1	Sequence 1, Appli
c 263	48	4.9	1929	4	US-09-252-991A-7017	Sequence 7017, Ap	336	47.2	4.8	2910	4	US-09-252-991A-10414	Sequence 10414, A
c 264	48	4.9	1947	4	US-09-252-991A-7111	Sequence 7111, Ap	337	47.2	4.8	3111	4	US-09-252-991A-10504	Sequence 10504, A
c 265	48	4.9	2253	4	US-09-252-991A-7191	Sequence 7191, Ap	338	47.2	4.8	3135	4	US-09-252-991A-5922	Sequence 5922, Ap
c 266	48	4.9	2409	4	US-09-252-991A-7253	Sequence 7253, Ap	339	47.2	4.8	4319	4	US-09-475-515-6	Sequence 6, Appli
c 267	48	4.9	2490	4	US-09-252-991A-7447	Sequence 7447, Ap	340	47.2	4.8	11220	3	US-09-105-537-32	Sequence 32, Appl
268	48	4.9	3529	3	US-09-144-085-3	Sequence 3, Appli	c 341	47	4.8	441	4	US-09-252-991A-14658	Sequence 14658, A
c 269	47.8	4.8	309	4	US-09-252-991A-6725	Sequence 6725, Ap	342	47	4.8	758	4	US-09-902-331B-5	Sequence 5, Appli
c 270	47.8	4.8	801	4	US-09-252-991A-15941	Sequence 15941, A	c 343	47	4.8	1260	4	US-09-252-991A-14526	Sequence 14526, A
c 271	47.8	4.8	819	4	US-09-252-991A-14581	Sequence 14581, A	344	47	4.8	1260	4	US-09-252-991A-14838	Sequence 14838, A
c 272	47.8	4.8	966	4	US-09-252-991A-6895	Sequence 6895, Ap	c 345	47	4.8	1320	2	US-08-461-775-8	Sequence 8, Appli
c 273	47.8	4.8	1218	4	US-09-252-991A-16453	Sequence 16453, A	c 346	47	4.8	1320	3	US-09-031-606-8	Sequence 8, Appli
c 274	47.8	4.8	1485	4	US-09-252-991A-6815	Sequence 6815, Ap	347	47	4.8	1416	3	US-08-911-853-3	Sequence 3, Appli
c 275	47.8	4.8	1509	4	US-09-252-991A-6930	Sequence 6930, Ap	348	47	4.8	1416	3	US-09-479-409-3	Sequence 3, Appli
c 276	47.8	4.8	1771	2	US-09-533-669A-7	Sequence 7, Appli	349	47	4.8	1416	3	US-09-479-453-3	Sequence 3, Appli
c 277	47.8	4.8	1771	2	US-08-511-872-1	Sequence 1, Appli	c 350	47	4.8	1620	2	US-08-461-775-10	Sequence 10, Appl
c 278	47.8	4.8	1771	3	US-09-183-861-7	Sequence 7, Appli	c 351	47	4.8	1620	3	US-09-031-606-10	Sequence 10, Appl
c 279	47.8	4.8	1771	3	US-09-022-765-7	Sequence 7, Appli	352	47	4.8	1707	4	US-09-724-797-15	Sequence 15, Appl
c 280	47.8	4.8	1771	4	US-09-551-974A-7	Sequence 7, Appli	353	47	4.8	4377	3	US-08-911-853-28	Sequence 28, Appl
c 281	47.8	4.8	1771	4	US-09-565-501A-7	Sequence 7, Appli	354	47	4.8	4377	3	US-09-479-409-28	Sequence 28, Appl
c 282	47.8	4.8	1771	4	US-09-639-206A-7	Sequence 7, Appli	355	47	4.8	4377	3	US-09-479-453-28	Sequence 28, Appl
c 283	47.8	4.8	1771	4	US-09-874-923-7	Sequence 7, Appli	356	47	4.8	80161	3	US-09-036-987A-1	Sequence 1, Appli
c 284	47.8	4.8	1771	4	US-08-798-841-7	Sequence 7, Appli	357	47	4.8	80161	3	US-09-370-700-1	Sequence 1, Appli
c 285	47.8	4.8	1962	4	US-09-252-991A-16037	Sequence 16037, A	358	47	4.8	80161	3	US-09-603-207-1	Sequence 1, Appli
c 286	47.8	4.8	2526	4	US-09-252-991A-16563	Sequence 16563, A	359	46.8	4.7	296	4	US-09-615-192A-195	Sequence 195, App
c 287	47.8	4.8	3126	4	US-09-252-991A-9066	Sequence 9066, Ap	360	46.8	4.7	792	4	US-09-252-991A-4971	Sequence 4971, Ap
c 288	47.8	4.8	4524	2	US-08-845-998-7	Sequence 7, Appli	361	46.8	4.7	801	2	US-08-770-379-16	Sequence 16, Appl
c 289	47.8	4.8	4524	3	US-09-206-537-7	Sequence 7, Appli	362	46.8	4.7	801	3	US-08-757-669A-16	Sequence 16, Appl
c 290	47.8	4.8	4524	3	US-09-430-854-7	Sequence 7, Appli	363	46.8	4.7	801	3	US-09-298-568-3	Sequence 3, Appli
c 291	47.8	4.8	5121	4	US-09-252-991A-15189	Sequence 15189, A	364	46.8	4.7	801	3	US-09-230-371A-16	Sequence 16, Appl
c 292	47.8	4.8	6327	3	US-09-252-991A-14931	Sequence 14931, A	365	46.8	4.7	801	4	US-09-894-273-3	Sequence 3, Appli
c 293	47.8	4.8	71989	3	US-09-443-501A-2	Sequence 2, Appli	366	46.8	4.7	1071	4	US-09-252-991A-4955	Sequence 4955, Ap
c 294	47.6	4.8	930	4	US-09-252-991A-15663	Sequence 15663, A	367	46.8	4.7	1131	4	US-09-252-991A-4994	Sequence 4994, Ap
c 295	47.6	4.8	1248	4	US-09-252-991A-2635	Sequence 2635, Ap	368	46.8	4.7	1215	4	US-09-252-991A-4984	Sequence 4984, Ap
c 296	47.6	4.8	1278	4	US-09-252-991A-3896	Sequence 3896, Ap	c 369	46.8	4.7	3171	4	US-09-252-991A-7591	Sequence 7591, Ap
c 297	47.6	4.8	1971	4	US-09-252-991A-2197	Sequence 2197, Ap	370	46.8	4.7	3210	4	US-09-252-991A-7962	Sequence 7962, Ap
c 298	47.6	4.8	1977	4	US-09-252-991A-3924	Sequence 3924, Ap	371	46.6	4.7	270	4	US-09-252-991A-14378	Sequence 14378, A
c 299	47.6	4.8	2091	4	US-09-252-991A-4016	Sequence 4016, Ap	372	46.6	4.7	489	4	US-09-252-991A-452	Sequence 452, App
c 300	47.6	4.8	2211	4	US-09-252-991A-2477	Sequence 2477, Ap	c 373	46.6	4.7	777	4	US-09-252-991A-12568	Sequence 12568, A
c 301	47.6	4.8	2305	4	US-09-475-515-80	Sequence 80, Appl	374	46.6	4.7	786	4	US-09-252-991A-13239	Sequence 13239, A
c 302	47.6	4.8	2306	4	US-09-475-515-82	Sequence 82, Appl	c 375	46.6	4.7	981	4	US-09-252-991A-431	Sequence 431, App
c 303	47.6	4.8	2481	4	US-09-894-998A-35	Sequence 35, Appli	376	46.6	4.7	981	4	US-09-252-991A-10487	Sequence 10487, A
c 304	47.6	4.8	9960	3	US-08-822-586-46	Sequence 46, Appl	377	46.6	4.7	1062	4	US-09-252-991A-6751	Sequence 6751, Ap
c 305	47.4	4.8	948	4	US-09-252-991A-8762	Sequence 8762, Ap	378	46.6	4.7	1380	4	US-09-252-991A-3550	Sequence 3550, Ap
c 306	47.4	4.8	954	4	US-09-252-991A-9192	Sequence 9192, Ap	c 379	46.6	4.7	1530	4	US-09-252-991A-6874	Sequence 6874, Ap
c 307	47.4	4.8	954	4	US-09-252-991A-5807	Sequence 5807, Ap	380	46.6	4.7	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
c 308	47.4	4.8	1116	4	US-09-252-991A-10924	Sequence 10924, A	381	46.6	4.7	2325	4	US-09-252-991A-12916	Sequence 12916, A
c 309	47.4	4.8	1149	4	US-09-252-991A-8983	Sequence 8983, Ap	c 382	46.6	4.7	7419	4	US-09-252-991A-481	Sequence 481, App
c 310	47.4	4.8	1209	4	US-09-252-991A-11138	Sequence 11138, A	383	46.6	4.7	7449	4	US-09-252-991A-396	Sequence 396, App
c 311	47.4	4.8	1248	4	US-09-724-797-23	Sequence 23, Appl	c 384	46.4	4.7	981	4	US-09-252-991A-14299	Sequence 14299, A
c 312	47.4	4.8	1251	4	US-09-252-991A-5844	Sequence 5844, Ap	385	46.4	4.7	1072	3	US-09-088-549-2	Sequence 2, Appli
c 313	47.4	4.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap	386	46.4	4.7	1263	4	US-09-252-991A-14349	Sequence 14349, A
c 314	47.4	4.8	1869	4	US-09-252-991A-3231	Sequence 3231, Ap	387	46.4	4.7	2235	4	US-09-252-991A-14374	Sequence 14374, A
c 315	47.4	4.8	1881	4	US-09-252-991A-11264	Sequence 11264, A	c 388	46.2	4.7	432	1	US-08-642-255-48	Sequence 48, Appl
c 316	47.4	4.8	1986	4	US-09-252-991A-5767	Sequence 5767, Ap	389	46.2	4.7	1362	4	US-09-724-797-31	Sequence 31, Appl
c 317	47.4	4.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	390	46.2	4.7	1509	4	US-09-724-797-89	Sequence 89, Appl
c 318	47.4	4.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	391	46.2	4.7	3102	4	US-09-252-991A-4429	Sequence 4429, Ap
c 319	47.4	4.8	2634	1	US-08-196-218-31	Sequence 31, Appl	392	46.2	4.7	30001	1	US-08-125-466-1	Sequence 1, Appli
c 320	47.4	4.8	2634	1	US-08-681-953-31	Sequence 31, Appl	393	46.2	4.7	30001	2	US-08-474-933-1	Sequence 1, Appli



C 384	46.2	4.7	53500	4	US-09-266-965-76	Sequence 76, Appl	467	45.4	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Ap
C 395	46	4.7	606	4	US-09-252-991A-2567	Sequence 2567, Ap	468	45.4	4.6	1548	2	US-08-762-106-5	Sequence 5, Appl
C 396	46	4.7	609	4	US-09-252-991A-9531	Sequence 9531, Ap	469	45.4	4.6	1548	3	US-09-320-774-5	Sequence 5, Appl
C 397	46	4.7	906	4	US-09-252-991A-1329	Sequence 1329, Ap	470	45.4	4.6	1572	4	US-09-252-991A-3270	Sequence 3270, Ap
C 398	46	4.7	1023	4	US-09-252-991A-1283	Sequence 1283, Ap	471	45.4	4.6	1581	2	US-08-762-106-6	Sequence 6, Appl
C 399	46	4.7	1044	1	US-07-975-536-3	Sequence 3, Appl	472	45.4	4.6	1581	3	US-09-320-774-6	Sequence 6, Appl
C 400	46	4.7	1044	3	US-07-974-409C-425	Sequence 425, App	473	45.4	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Ap
C 401	46	4.7	1077	4	US-09-252-991A-7892	Sequence 7892, Ap	474	45.4	4.6	1843	1	US-07-918-023-1	Sequence 1, Appl
C 402	46	4.7	1080	4	US-09-252-991A-1187	Sequence 1187, Ap	475	45.4	4.6	1965	2	US-09-252-991A-3234	Sequence 9, Appl
C 403	46	4.7	1112	3	US-09-434-288-9	Sequence 9, Appl	476	45.4	4.6	2167	3	US-09-031-606-9	Sequence 9, Appl
C 404	46	4.7	1266	4	US-09-252-991A-10804	Sequence 10804, A	477	45.4	4.6	2167	3	US-09-252-991A-3336	Sequence 3336, Ap
C 405	46	4.7	1275	4	US-09-252-991A-2484	Sequence 2484, A	478	45.4	4.6	2196	4	US-09-252-991A-3413	Sequence 3413, Ap
C 406	46	4.7	1371	4	US-09-252-991A-9717	Sequence 9717, Ap	479	45.4	4.6	2325	4	US-09-252-991A-3413	Sequence 1, Appl
C 407	46	4.7	1383	4	US-09-252-991A-2350	Sequence 2350, Ap	480	45.4	4.6	2571	4	US-09-984-880-1	Sequence 1, Appl
C 408	46	4.7	1443	4	US-09-252-991A-10228	Sequence 10228, A	481	45.4	4.6	2571	4	US-10-277-032-1	Sequence 11, Appl
C 409	46	4.7	1418	4	US-09-252-991A-10345	Sequence 10345, A	482	45.4	4.6	2668	2	US-08-461-775-11	Sequence 11, Appl
C 410	46	4.7	1935	4	US-09-620-312D-236	Sequence 236, App	483	45.4	4.6	2668	3	US-09-031-606-11	Sequence 9, Appl
C 411	46	4.7	2400	1	US-08-967-513-1	Sequence 1, Appl	484	45.4	4.6	2688	4	US-09-031-606-11	Sequence 9, Appl
C 412	46	4.7	2400	2	US-08-687-645B-1	Sequence 1, Appl	485	45.2	4.6	357	3	US-08-556-978B-83	Sequence 8, Appl
C 413	46	4.7	17612	3	US-08-911-853-29	Sequence 29, Appl	486	45.2	4.6	447	4	US-09-252-991A-4677	Sequence 4677, Ap
C 414	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl	487	45.2	4.6	504	4	US-09-252-991A-4720	Sequence 4720, Ap
C 415	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl	488	45.2	4.6	522	4	US-09-252-991A-12264	Sequence 12264, A
C 416	45.8	4.6	657	4	US-09-252-991A-4833	Sequence 4833, Ap	489	45.2	4.6	702	4	US-09-252-991A-4703	Sequence 4703, Ap
C 417	45.8	4.6	774	3	US-08-956-307B-12	Sequence 12, Appl	490	45.2	4.6	807	4	US-09-252-991A-12392	Sequence 12392, A
C 418	45.8	4.6	774	3	US-08-956-307B-11	Sequence 11, Appl	491	45.2	4.6	888	4	US-09-252-991A-7041	Sequence 7041, Ap
C 419	45.8	4.6	1245	4	US-09-252-991A-13463	Sequence 13463, A	492	45.2	4.6	897	4	US-09-252-991A-8854	Sequence 8854, Ap
C 420	45.8	4.6	1401	4	US-09-252-991A-4911	Sequence 4911, Ap	493	45.2	4.6	1026	4	US-09-252-991A-12295	Sequence 12295, A
C 421	45.8	4.6	1569	4	US-09-252-991A-13880	Sequence 13880, A	494	45.2	4.6	1095	4	US-09-252-991A-6626	Sequence 6626, Ap
C 422	45.8	4.6	2259	4	US-09-252-991A-13556	Sequence 13556, A	495	45.2	4.6	1419	4	US-09-252-991A-10421	Sequence 10421, A
C 423	45.8	4.6	5661	3	US-08-938-105-2	Sequence 2, Appl	496	45.2	4.6	1602	4	US-09-252-991A-6639	Sequence 6639, Ap
C 424	45.8	4.6	43280	2	US-08-804-227C-1	Sequence 1, Appl	497	45.2	4.6	1695	4	US-09-252-991A-6989	Sequence 6989, Ap
C 425	45.6	4.6	900	4	US-09-252-991A-14108	Sequence 14108, A	498	45.2	4.6	2363	4	US-09-252-991A-10319	Sequence 10319, A
C 426	45.6	4.6	900	4	US-09-252-991A-1017	Sequence 1017, Ap	499	45.2	4.6	2376	4	US-09-252-991A-10741	Sequence 10741, A
C 427	45.6	4.6	924	4	US-09-252-991A-1483	Sequence 1483, Ap	500	45.2	4.6	2379	4	US-09-252-991A-9205	Sequence 9205, A
C 428	45.6	4.6	1035	4	US-09-252-991A-14017	Sequence 14017, A	501	45.2	4.6	2844	4	US-09-252-991A-4764	Sequence 4764, Ap
C 429	45.6	4.6	1200	4	US-09-787-292-4	Sequence 4, Appl	502	45.2	4.6	3084	4	US-09-252-991A-6639	Sequence 6639, Ap
C 430	45.6	4.6	1209	6	5352575-4	Patent No. 5352575	503	45.2	4.6	3273	4	US-09-252-991A-6578	Sequence 6578, Ap
C 431	45.6	4.6	1213	3	US-09-232-468A-7	Sequence 7, Appl	504	45.2	4.6	30001	2	US-08-125-468-1	Sequence 1, Appl
C 432	45.6	4.6	1213	4	US-09-784-984B-6	Sequence 6, Appl	505	45.2	4.6	30001	2	US-08-474-933-1	Sequence 1, Appl
C 433	45.6	4.6	1365	4	US-09-252-991A-14122	Sequence 14122, A	506	45	4.6	582	4	US-09-252-991A-6152	Sequence 6152, Ap
C 434	45.6	4.6	1458	4	US-09-252-991A-1112	Sequence 1112, Ap	507	45	4.6	820	3	US-09-150-900-48	Sequence 48, Appl
C 435	45.6	4.6	1461	4	US-09-252-991A-972	Sequence 972, App	508	45	4.6	1187	1	US-08-440-856A-2	Sequence 2, Appl
C 436	45.6	4.6	1505	1	US-07-915-246-1	Sequence 1, Appl	509	45	4.6	1377	4	US-09-585-173B-43	Sequence 43, Appl
C 437	45.6	4.6	1588	4	US-09-490-291-7	Sequence 7, Appl	510	45	4.6	1413	4	US-09-252-991A-6071	Sequence 6071, Ap
C 438	45.6	4.6	1663	4	US-09-398-522-108	Sequence 108, App	511	45	4.6	1491	4	US-09-252-991A-6232	Sequence 6232, Ap
C 439	45.6	4.6	1768	4	US-09-485-523-13	Sequence 13, Appl	512	45	4.6	1506	4	US-09-252-991A-6228	Sequence 6228, Ap
C 440	45.6	4.6	2124	4	US-09-266-965-44	Sequence 44, Appl	513	45	4.6	1690	4	US-09-620-312D-69	Sequence 69, Appl
C 441	45.6	4.6	2125	4	US-09-485-523-14	Sequence 14, Appl	514	45	4.6	3651	2	US-08-790-374-1	Sequence 1, Appl
C 442	45.6	4.6	2282	4	US-09-922-445-50	Sequence 50, Appl	515	45	4.6	7812	3	US-09-368-590-1	Sequence 1, Appl
C 443	45.6	4.6	3681	4	US-09-581-105-1	Sequence 1, Appl	516	45	4.6	2187	4	US-09-499-522-1	Sequence 1, Appl
C 444	45.6	4.6	4095	4	US-09-252-991A-10309	Sequence 10309, A	517	44.8	4.5	753	4	US-09-252-991A-6830	Sequence 6830, Ap
C 445	45.6	4.6	4233	4	US-09-551-974A-99	Sequence 99, Appl	518	44.8	4.5	783	4	US-09-252-991A-8452	Sequence 8452, A
C 446	45.6	4.6	4233	4	US-09-565-501A-99	Sequence 99, Appl	519	44.8	4.5	948	4	US-09-252-991A-14810	Sequence 14810, A
C 447	45.6	4.6	4233	4	US-09-639-206A-99	Sequence 99, Appl	520	44.8	4.5	1110	4	US-09-252-991A-8388	Sequence 8388, Ap
C 448	45.6	4.6	4233	4	US-09-874-923-99	Sequence 99, Appl	521	44.8	4.5	1131	4	US-09-252-991A-8486	Sequence 8486, Ap
C 449	45.6	4.6	4563	4	US-09-252-991A-930	Sequence 930, App	522	44.8	4.5	1162	2	US-09-252-991A-9616	Sequence 52, Appl
C 450	45.6	4.6	4917	4	US-09-551-974A-100	Sequence 100, App	523	44.8	4.5	1320	4	US-09-727-238-1	Sequence 1, Appl
C 451	45.6	4.6	4917	4	US-09-565-501A-100	Sequence 100, App	524	44.8	4.5	1365	3	US-09-319-832-1	Sequence 1, Appl
C 452	45.6	4.6	4917	4	US-09-639-206A-100	Sequence 100, App	525	44.8	4.5	1428	4	US-09-252-991A-14802	Sequence 14802, A
C 453	45.6	4.6	4917	4	US-09-874-923-100	Sequence 100, App	526	44.8	4.5	1668	4	US-09-252-991A-14950	Sequence 14950, A
C 454	45.6	4.6	4929	4	US-09-551-974A-98	Sequence 98, Appl	527	44.8	4.5	1899	4	US-09-252-991A-6781	Sequence 6781, Ap
C 455	45.6	4.6	4929	4	US-09-565-501A-98	Sequence 98, Appl	528	44.8	4.5	2028	4	US-09-252-991A-7091	Sequence 7091, Ap
C 456	45.6	4.6	4929	4	US-09-639-206A-98	Sequence 98, Appl	529	44.8	4.5	2064	4	US-09-252-991A-9616	Sequence 9616, Ap
C 457	45.6	4.6	4929	4	US-09-874-923-98	Sequence 98, Appl	530	44.8	4.5	2235	4	US-09-252-991A-7032	Sequence 7032, Ap
C 458	45.4	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap	531	44.8	4.5	3078	3	US-09-418-817-9	Sequence 9, Appl
C 459	45.4	4.6	538	1	US-10-095-946-13	Sequence 13, Appl	532	44.8	4.5	5162	4	US-09-252-991A-9569	Sequence 9569, Ap
C 460	45.4	4.6	538	3	US-09-183-959-13	Sequence 13, Appl	533	44.8	4.5	5064	4	US-09-774-528-224	Sequence 224, App
C 461	45.4	4.6	538	4	US-09-535-315-13	Sequence 13, Appl	534	44.8	4.5	6217	3	US-09-418-817-1	Sequence 1, Appl
C 462	45.4	4.6	845	4	US-09-347-650-1	Sequence 1, Appl	535	44.6	4.5	813	4	US-09-252-991A-5455	Sequence 5455, Ap
C 463	45.4	4.6	954	3	US-08-911-853-24	Sequence 24, Appl	536	44.6	4.5	837	4	US-09-252-991A-5983	Sequence 5983, Ap
C 464	45.4	4.6	954	3	US-09-479-409-24	Sequence 24, Appl	537	44.6	4.5	897	4	US-09-252-991A-8789	Sequence 8789, Ap
C 465	45.4	4.6	954	4	US-09-479-453-24	Sequence 24, Appl	538	44.6	4.5	1236	4	US-09-252-991A-8061	Sequence 8061, Ap
C 466	45.4	4.6	975	4	US-09-489-039A-791	Sequence 791, App	539	44.6	4.5	1272	4	US-09-252-991A-14082	Sequence 14082, A



540	44.6	4.5	1329	4	US-09-252-991A-14036	Sequence 14036, A	613	44.2	4.5	1740	4	US-09-252-991A-13753	Sequence 13753, A
c 541	44.6	4.5	1378	4	US-09-252-991A-14036	Sequence 14036, A	614	44.2	4.5	1835	4	US-09-417-704-2	Sequence 2, Appl
542	44.6	4.5	1587	4	US-09-252-991A-16504	Sequence 16504, A	c 615	44.2	4.5	1848	4	US-09-252-991A-15408	Sequence 15408, A
c 543	44.6	4.5	1620	4	US-09-252-991A-14186	Sequence 14186, A	c 616	44.2	4.5	2040	4	US-09-252-991A-12316	Sequence 12316, A
544	44.6	4.5	1623	4	US-09-252-991A-14186	Sequence 14186, A	c 617	44.2	4.5	2040	4	US-09-252-991A-12316	Sequence 12316, A
545	44.6	4.5	1656	4	US-10-140-002-239	Sequence 239, App	618	44.2	4.5	2483	1	US-08-464-340A-3	Sequence 3, Appl
546	44.6	4.5	1656	4	US-10-140-002-239	Sequence 239, App	618	44.2	4.5	2483	1	US-08-464-340A-3	Sequence 3, Appl
c 547	44.6	4.5	2070	4	US-09-482-273-15	Sequence 15, Appl	c 619	44.2	4.5	2751	4	PCT-US94-08449A-3	Sequence 14671, A
c 548	44.6	4.5	2070	4	US-09-482-273-15	Sequence 15, Appl	c 619	44.2	4.5	2751	4	PCT-US94-08449A-3	Sequence 14671, A
549	44.6	4.5	2154	4	US-09-252-991A-16098	Sequence 16098, A	c 620	44.2	4.5	2872	3	US-09-327-487A-2	Sequence 2, Appl
550	44.6	4.5	2163	4	US-09-252-991A-1458	Sequence 1458, A	c 621	44.2	4.5	3201	4	US-09-252-991A-14959	Sequence 14959, A
c 551	44.6	4.5	2556	4	US-09-252-991A-1458	Sequence 1458, A	c 622	44.2	4.5	3255	4	US-09-252-991A-10617	Sequence 10617, A
552	44.6	4.5	2556	4	US-09-252-991A-1458	Sequence 1458, A	c 623	44.2	4.5	3375	4	US-09-252-991A-10239	Sequence 10239, A
c 553	44.6	4.5	2664	4	US-09-482-273-83	Sequence 83, Appl	c 624	44.2	4.5	3402	4	US-09-252-991A-14791	Sequence 14791, A
554	44.6	4.5	3453	4	US-09-252-991A-8100	Sequence 8100, App	c 625	44.2	4.5	4689	3	US-09-105-537-34	Sequence 34, Appl
c 555	44.6	4.5	3453	4	US-09-252-991A-8100	Sequence 8100, App	c 625	44.2	4.5	4689	3	US-09-105-537-34	Sequence 34, Appl
556	44.6	4.5	3978	4	US-09-252-991A-1909	Sequence 1909, App	c 626	44.2	4.5	13842	3	US-09-105-537-30	Sequence 30, Appl
557	44.6	4.5	8931	3	US-09-266-965-19	Sequence 19, Appl	c 627	44.2	4.5	20235	1	US-07-642-734C-3	Sequence 3, Appl
c 558	44.6	4.5	8931	3	US-09-266-965-19	Sequence 19, Appl	c 627	44.2	4.5	20235	1	US-07-642-734C-3	Sequence 3, Appl
559	44.6	4.5	12249	4	US-09-266-965-74	Sequence 74, Appl	c 628	44.2	4.5	20235	1	US-07-642-734C-3	Sequence 3, Appl
560	44.6	4.5	18331	4	US-09-266-965-96	Sequence 96, Appl	c 629	44.2	4.5	38506	4	US-09-439-009A-3	Sequence 3, Appl
c 561	44.6	4.5	18331	4	US-09-266-965-96	Sequence 96, Appl	c 629	44.2	4.5	38506	4	US-09-439-009A-3	Sequence 3, Appl
562	44.6	4.5	720	4	US-09-252-991A-14268	Sequence 14268, A	c 630	44.2	4.5	38506	4	US-09-320-878-19	Sequence 19, Appl
c 563	44.6	4.5	720	4	US-09-252-991A-14268	Sequence 14268, A	c 630	44.2	4.5	38506	4	US-09-320-878-19	Sequence 19, Appl
564	44.6	4.5	756	4	US-09-252-991A-15229	Sequence 15229, A	c 631	44.2	4.5	38506	4	US-09-657-440-19	Sequence 19, Appl
c 565	44.6	4.5	756	4	US-09-252-991A-15229	Sequence 15229, A	c 631	44.2	4.5	38506	4	US-09-657-440-19	Sequence 19, Appl
566	44.6	4.5	8161	4	US-09-252-991A-10489	Sequence 10489, A	c 632	44.2	4.5	426	4	US-09-252-991A-16285	Sequence 16285, A
c 567	44.6	4.5	8161	4	US-09-252-991A-10489	Sequence 10489, A	c 632	44.2	4.5	426	4	US-09-252-991A-16285	Sequence 16285, A
568	44.6	4.5	1305	4	US-09-252-991A-11607	Sequence 11607, A	c 633	44.2	4.5	426	4	US-09-252-991A-2270	Sequence 2270, Ap
c 569	44.6	4.5	1305	4	US-09-252-991A-11607	Sequence 11607, A	c 633	44.2	4.5	426	4	US-09-252-991A-2270	Sequence 2270, Ap
570	44.6	4.5	1317	4	US-09-252-991A-1551	Sequence 1551, App	c 634	44.2	4.5	492	4	US-09-252-991A-4051	Sequence 4051, Ap
c 571	44.6	4.5	1317	4	US-09-252-991A-1551	Sequence 1551, App	c 634	44.2	4.5	492	4	US-09-252-991A-4051	Sequence 4051, Ap
572	44.6	4.5	1677	4	US-09-434-288-10	Sequence 10, Appl	c 635	44.2	4.5	897	3	US-09-434-288-6	Sequence 6, Appl
c 573	44.6	4.5	1677	4	US-09-434-288-10	Sequence 10, Appl	c 635	44.2	4.5	897	3	US-09-434-288-6	Sequence 6, Appl
574	44.6	4.5	2176	6	US-09-252-991A-1616	Sequence 1616, App	c 636	44.2	4.5	948	4	US-09-252-991A-2569	Sequence 2569, Ap
c 575	44.6	4.5	2176	6	US-09-252-991A-1616	Sequence 1616, App	c 636	44.2	4.5	948	4	US-09-252-991A-2569	Sequence 2569, Ap
576	44.6	4.5	2430	4	US-09-252-991A-15188	Sequence 15188, A	c 637	44.2	4.5	957	4	US-09-252-991A-5476	Sequence 5476, Ap
c 577	44.6	4.5	2430	4	US-09-252-991A-15188	Sequence 15188, A	c 637	44.2	4.5	957	4	US-09-252-991A-5476	Sequence 5476, Ap
578	44.6	4.5	2772	4	US-09-252-991A-10577	Sequence 10577, A	c 638	44.2	4.5	1026	4	US-09-252-991A-5453	Sequence 5453, Ap
c 579	44.6	4.5	2772	4	US-09-252-991A-10577	Sequence 10577, A	c 638	44.2	4.5	1026	4	US-09-252-991A-5453	Sequence 5453, Ap
580	44.6	4.5	2946	4	US-09-252-991A-194	Sequence 194, App	c 639	44.2	4.5	1110	4	US-09-252-991A-2349	Sequence 2349, A
c 581	44.6	4.5	2946	4	US-09-252-991A-194	Sequence 194, App	c 639	44.2	4.5	1110	4	US-09-252-991A-2349	Sequence 2349, A
582	44.6	4.5	3603	4	US-09-252-991A-227	Sequence 227, App	c 640	44.2	4.5	1110	4	US-09-252-991A-16067	Sequence 16067, A
c 583	44.6	4.5	3603	4	US-09-252-991A-227	Sequence 227, App	c 640	44.2	4.5	1110	4	US-09-252-991A-16067	Sequence 16067, A
584	44.6	4.5	4267	3	US-08-948-155-51	Sequence 51, Appl	c 641	44.2	4.5	1116	4	US-09-252-991A-1858	Sequence 1858, Ap
c 585	44.6	4.5	4267	3	US-08-948-155-51	Sequence 51, Appl	c 641	44.2	4.5	1116	4	US-09-252-991A-1858	Sequence 1858, Ap
586	44.6	4.5	4267	3	US-09-819-964-51	Sequence 51, Appl	c 642	44.2	4.5	1116	4	US-09-252-991A-8823	Sequence 8823, Ap
c 587	44.6	4.5	4267	3	US-09-819-964-51	Sequence 51, Appl	c 642	44.2	4.5	1116	4	US-09-252-991A-8823	Sequence 8823, Ap
588	44.6	4.5	483	4	US-09-252-991A-15272	Sequence 15272, A	c 643	44.2	4.5	1126	3	US-08-949-155-5	Sequence 5, Appl
c 589	44.6	4.5	483	4	US-09-252-991A-15272	Sequence 15272, A	c 643	44.2	4.5	1126	3	US-08-949-155-5	Sequence 5, Appl
590	44.6	4.5	594	4	US-09-252-991A-3950	Sequence 3950, App	c 644	44.2	4.5	1132	3	US-09-252-991A-1791	Sequence 1791, Ap
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592	44.6	4.5	798	4	US-09-252-991A-9181	Sequence 9181, App	c 645	44.2	4.5	1254	3	US-09-252-991A-1126	Sequence 1126, A
c 593	44.6	4.5	798	4	US-09-252-991A-9181	Sequence 9181, App	c 645	44.2	4.5	1254	3	US-09-252-991A-1126	Sequence 1126, A
594	44.6	4.5	810	4	US-09-252-991A-3647	Sequence 3647, App	c 650	44.2	4.5	1254	3	US-09-252-991A-1126	Sequence 1126, A
c 595	44.6	4.5	810	4	US-09-252-991A-3647	Sequence 3647, App	c 650	44.2	4.5	1254	3	US-09-252-991A-1126	Sequence 1126, A
596	44.6	4.5	837	4	US-09-252-991A-14326	Sequence 14326, A	c 651	44.2	4.5	1254	3	US-09-252-991A-9061	Sequence 9061, Ap
c 597	44.6	4.5	837	4	US-09-252-991A-14326	Sequence 14326, A	c 651	44.2	4.5	1254	3	US-09-252-991A-9061	Sequence 9061, Ap
598	44.6	4.5	879	4	US-09-252-991A-3602	Sequence 3602, App	c 652	44.2	4.5	1254	3	US-09-252-991A-16529	Sequence 16529, A
c 599	44.6	4.5	879	4	US-09-252-991A-3602	Sequence 3602, App	c 652	44.2	4.5	1254	3	US-09-252-991A-16529	Sequence 16529, A
600	44.6	4.5	903	4	US-09-252-991A-8894	Sequence 8894, App	c 653	44.2	4.5	1254	3	US-09-252-991A-10956	Sequence 10956, A
c 601	44.6	4.5	903	4	US-09-252-991A-8894	Sequence 8894, App	c 653	44.2	4.5	1254	3	US-09-252-991A-10956	Sequence 10956, A
602	44.6	4.5	975	4	US-09-252-991A-12244	Sequence 12244, A	c 654	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 603	44.6	4.5	975	4	US-09-252-991A-12244	Sequence 12244, A	c 654	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
604	44.6	4.5	1018	1	US-08-444-083-6	Sequence 6, Appl	c 655	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 605	44.6	4.5	1018	1	US-08-444-083-6	Sequence 6, Appl	c 655	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
606	44.6	4.5	1018	1	US-08-442-745-6	Sequence 6, Appl	c 656	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 607	44.6	4.5	1018	1	US-08-442-745-6	Sequence 6, Appl	c 656	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
608	44.6	4.5	1018	1	US-08-443-129-6	Sequence 6, Appl	c 657	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 609	44.6	4.5	1018	1	US-08-443-129-6	Sequence 6, Appl	c 657	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
610	44.6	4.5	1018	1	US-08-443-130-6	Sequence 6, Appl	c 658	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 611	44.6	4.5	1018	1	US-08-443-130-6	Sequence 6, Appl	c 658	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
612	44.6	4.5	1018	1	US-08-898-911-6	Sequence 6, Appl	c 659	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 613	44.6	4.5	1018	1	US-08-898-911-6	Sequence 6, Appl	c 659	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
614	44.6	4.5	1018	1	US-09-252-991A-13384	Sequence 13384, A	c 660	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 615	44.6	4.5	1018	1	US-09-252-991A-13384	Sequence 13384, A	c 660	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
616	44.6	4.5	1116	4	US-09-252-991A-4021	Sequence 4021, App	c 661	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 617	44.6	4.5	1116	4	US-09-252-991A-4021	Sequence 4021, App	c 661	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
618	44.6	4.5	1233	4	US-09-252-991A-15366	Sequence 15366, A	c 662	44.2	4.5	1254	3	US-09-359-081-2	Sequence 2, Appl
c 619	44.6												



C 686	43.8	4.4	993	4	US-09-252-991A-15615	Sequence 15615, A	Sequence 15615, A	C 764	43.4	4.4	674	3	US-09-543-106-1	Sequence 1, Appli
C 687	43.8	4.4	1008	4	US-09-252-991A-7377	Sequence 7377, Ap	Sequence 7377, Ap	C 765	43.4	4.4	753	4	US-09-252-991A-15657	Sequence 15657, A
C 688	43.8	4.4	1026	4	US-09-252-991A-12367	Sequence 12367, A	Sequence 12367, A	C 766	43.4	4.4	957	4	US-09-252-991A-3136	Sequence 3136, Ap
C 689	43.8	4.4	1047	4	US-09-252-991A-3327	Sequence 3327, Ap	Sequence 3327, Ap	C 767	43.4	4.4	1011	4	US-09-252-991A-4029	Sequence 4029, Ap
C 690	43.8	4.4	1098	4	US-09-252-991A-1354	Sequence 1354, Ap	Sequence 1354, Ap	C 768	43.4	4.4	1017	4	US-09-252-991A-3038	Sequence 3038, Ap
C 691	43.8	4.4	1098	4	US-09-252-991A-13766	Sequence 13766, A	Sequence 13766, A	C 769	43.4	4.4	1104	4	US-09-252-991A-3038	Sequence 1, Appli
C 692	43.8	4.4	1188	4	US-09-266-965-62	Sequence 62, Appl	Sequence 62, Appl	C 770	43.4	4.4	1361	4	US-09-794-534-1	Sequence 37, Appl
C 693	43.8	4.4	1188	4	US-09-252-991A-5115	Sequence 5115, Ap	Sequence 5115, Ap	C 771	43.4	4.4	1425	4	US-09-614-912-37	Sequence 2830, Ap
C 694	43.8	4.4	1280	4	US-08-483-533-38	Sequence 38, Appl	Sequence 38, Appl	C 772	43.4	4.4	1466	4	US-09-252-991A-2830	Sequence 3888, Ap
C 695	43.8	4.4	1356	4	US-09-283-471A-38	Sequence 11031, A	Sequence 11031, A	C 773	43.4	4.4	1566	4	US-09-252-991A-3888	Sequence 61, Appl
C 696	43.8	4.4	1356	4	US-09-252-991A-11031	Sequence 5005, Ap	Sequence 5005, Ap	C 774	43.4	4.4	1581	4	US-09-724-797-61	Sequence 3962, Ap
C 697	43.8	4.4	1371	4	US-09-252-991A-5005	Sequence 15670, A	Sequence 15670, A	C 775	43.4	4.4	1614	4	US-09-516-289-45	Sequence 45, Appl
C 698	43.8	4.4	1416	4	US-09-252-991A-15670	Sequence 87, Appl	Sequence 87, Appl	C 776	43.4	4.4	1614	4	US-09-616-289-45	Sequence 1, Appli
C 699	43.8	4.4	1431	4	US-09-724-797-87	Sequence 15579, A	Sequence 15579, A	C 777	43.4	4.4	2742	4	US-09-784-984B-1	Sequence 1, Appli
C 700	43.8	4.4	1521	4	US-09-252-991A-15579	Sequence 60, Appl	Sequence 60, Appl	C 778	43.4	4.4	2943	4	US-09-252-991A-349	Sequence 349, App
C 701	43.8	4.4	1536	4	US-09-266-965-60	Sequence 11089, A	Sequence 11089, A	C 779	43.4	4.4	3147	2	US-08-781-802-7	Sequence 7, Appli
C 702	43.8	4.4	1596	4	US-09-252-991A-11089	Sequence 11665, A	Sequence 11665, A	C 780	43.4	4.4	3147	3	US-08-694-078-7	Sequence 7, Appli
C 703	43.8	4.4	1608	4	US-09-252-991A-11665	Sequence 11769, A	Sequence 11769, A	C 781	43.4	4.4	3981	4	US-09-558-260-7	Sequence 1361, Ap
C 704	43.8	4.4	1608	4	US-09-252-991A-11769	Sequence 13674, A	Sequence 13674, A	C 782	43.4	4.4	4179	4	US-09-252-991A-1244	Sequence 1244, Ap
C 705	43.8	4.4	1731	4	US-09-252-991A-13674	Sequence 4120, Ap	Sequence 4120, Ap	C 783	43.4	4.4	4326	4	US-09-252-991A-11572	Sequence 11572, A
C 706	43.8	4.4	1761	4	US-09-252-991A-4120	Sequence 4085, Ap	Sequence 4085, Ap	C 784	43.4	4.4	4473	4	US-09-252-991A-11572	Sequence 11871, A
C 707	43.8	4.4	1800	4	US-09-252-991A-4085	Sequence 22, Appl	Sequence 22, Appl	C 785	43.4	4.4	4897	6	5196516-7	Patent No. 5196516
C 708	43.8	4.4	1802	4	US-09-535-315-22	Sequence 4085, Ap	Sequence 4085, Ap	C 786	43.4	4.4	4897	6	5196516-7	Patent No. 5196516
C 709	43.8	4.4	1869	4	US-09-252-991A-15737	Sequence 15737, A	Sequence 15737, A	C 787	43.4	4.4	6854	3	US-09-194-905-7	Sequence 7, Appli
C 710	43.8	4.4	2067	4	US-09-252-991A-1398	Sequence 1398, A	Sequence 1398, A	C 788	43.4	4.4	6854	3	US-09-620-312D-55	Sequence 55, Appl
C 711	43.8	4.4	2100	4	US-09-252-991A-1209	Sequence 1209, Ap	Sequence 1209, Ap	C 789	43.4	4.4	12425	4	US-09-616-289-50	Sequence 50, Appl
C 712	43.8	4.4	2127	4	US-09-252-991A-8192	Sequence 8192, Ap	Sequence 8192, Ap	C 790	43.4	4.4	20235	1	US-07-642-734C-3	Sequence 3, Appli
C 713	43.8	4.4	2127	4	US-09-818-780-75	Sequence 75, Appl	Sequence 75, Appl	C 791	43.4	4.4	20235	3	US-08-439-009A-3	Sequence 3, Appli
C 714	43.8	4.4	2304	4	US-09-252-991A-11691	Sequence 11691, A	Sequence 11691, A	C 792	43.4	4.4	68750	3	US-09-335-409-1	Sequence 1, Appli
C 715	43.8	4.4	2817	4	US-09-252-991A-7311	Sequence 7311, Ap	Sequence 7311, Ap	C 793	43.4	4.4	68750	3	US-09-568-102-1	Sequence 1, Appli
C 716	43.8	4.4	2874	4	US-09-252-991A-8112	Sequence 8112, Ap	Sequence 8112, Ap	C 794	43.4	4.4	68750	3	US-09-567-969-1	Sequence 1, Appli
C 717	43.8	4.4	2880	4	US-09-252-991A-7187	Sequence 7187, Ap	Sequence 7187, Ap	C 795	43.4	4.4	68750	3	US-09-568-480-1	Sequence 1, Appli
C 718	43.8	4.4	2889	1	US-08-537-002A-4	Sequence 4, Appli	Sequence 4, Appli	C 796	43.4	4.4	68750	3	US-09-568-480-1	Sequence 1, Appli
C 719	43.8	4.4	2889	3	US-08-863-010-4	Sequence 4, Appli	Sequence 4, Appli	C 797	43.4	4.4	68750	3	US-09-568-480-1	Sequence 1, Appli
C 720	43.8	4.4	2889	3	US-09-024-429-4	Sequence 4, Appli	Sequence 4, Appli	C 798	43.4	4.4	68750	3	US-09-568-480-1	Sequence 1, Appli
C 721	43.8	4.4	2928	4	US-09-252-991A-12178	Sequence 12178, A	Sequence 12178, A	C 799	43.4	4.4	71989	3	US-09-567-899-1	Sequence 1, Appli
C 722	43.8	4.4	3081	4	US-09-252-991A-13660	Sequence 13660, A	Sequence 13660, A	C 800	43.4	4.4	15157	4	US-09-443-501A-2	Sequence 2, Appli
C 723	43.8	4.4	3600	1	US-08-537-002A-5	Sequence 5, Appli	Sequence 5, Appli	C 801	43.2	4.4	516	3	US-09-913-514-2	Sequence 2, Appli
C 724	43.8	4.4	3600	3	US-08-863-010-5	Sequence 5, Appli	Sequence 5, Appli	C 802	43.2	4.4	516	3	US-09-183-861-34	Sequence 34, Appl
C 725	43.8	4.4	3600	3	US-09-024-429-5	Sequence 5, Appli	Sequence 5, Appli	C 803	43.2	4.4	516	4	US-09-022-765-34	Sequence 34, Appl
C 726	43.8	4.4	3678	4	US-09-252-991A-12417	Sequence 12417, A	Sequence 12417, A	C 804	43.2	4.4	516	4	US-09-551-974A-34	Sequence 34, Appl
C 727	43.8	4.4	20966	4	US-09-252-991A-3785	Sequence 3, Appli	Sequence 3, Appli	C 805	43.2	4.4	516	4	US-09-565-501A-34	Sequence 34, Appl
C 728	43.8	4.4	20966	4	US-10-377-032-3	Sequence 3, Appli	Sequence 3, Appli	C 806	43.2	4.4	516	4	US-09-639-206A-34	Sequence 34, Appl
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C 730	43.6	4.4	477	3	US-09-135-994-1	Sequence 1, Appli	Sequence 1, Appli	C 808	43.2	4.4	753	4	US-08-874-923-114	Sequence 114, App
C 731	43.6	4.4	477	4	US-09-684-843A-1	Sequence 3743, Ap	Sequence 3743, Ap	C 809	43.2	4.4	753	4	US-09-252-991A-14966	Sequence 14966, A
C 732	43.6	4.4	780	4	US-09-252-991A-3741	Sequence 3743, Ap	Sequence 3743, Ap	C 810	43.2	4.4	1023	4	US-09-252-991A-93	Sequence 93, Appl
C 733	43.6	4.4	960	4	US-09-252-991A-3730	Sequence 3785, Ap	Sequence 3785, Ap	C 811	43.2	4.4	1038	4	US-09-252-991A-14229	Sequence 14229, A
C 734	43.6	4.4	1089	4	US-09-252-991A-3785	Sequence 295, App	Sequence 295, App	C 812	43.2	4.4	1086	4	US-09-252-991A-98	Sequence 98, Appl
C 735	43.6	4.4	1509	4	US-10-140-002-295	Sequence 644, App	Sequence 644, App	C 813	43.2	4.4	1215	3	US-09-724-797-77	Sequence 77, Appl
C 736	43.6	4.4	1521	4	US-09-799-451-644	Sequence 11805, A	Sequence 11805, A	C 814	43.2	4.4	1215	3	US-08-911-853-8	Sequence 8, Appli
C 737	43.6	4.4	1722	3	US-09-385-028-15	Sequence 15, Appl	Sequence 15, Appl	C 815	43.2	4.4	1215	3	US-09-479-409-8	Sequence 8, Appli
C 738	43.6	4.4	1722	4	US-09-726-614-15	Sequence 11865, A	Sequence 11865, A	C 816	43.2	4.4	1233	4	US-09-479-409-8	Sequence 14035, A
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C 740	43.6	4.4	2004	4	US-09-252-991A-11865	Sequence 1, Appli	Sequence 1, Appli	C 818	43.2	4.4	1356	4	US-09-252-991A-14188	Sequence 14188, A
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C 742	43.6	4.4	2406	4	US-09-634-955B-3	Sequence 3, Appli	Sequence 3, Appli	C 820	43.2	4.4	1618	4	US-09-252-991A-14784	Sequence 14784, A
C 743	43.6	4.4	2406	4	US-09-816-760-3	Sequence 3, Appli	Sequence 3, Appli	C 821	43.2	4.4	2043	4	US-09-489-039A-1251	Sequence 1251, Ap
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C 745	43.6	4.4	2505	4	US-09-252-991A-11574	Sequence 1, Appli	Sequence 1, Appli	C 823	43.2	4.4	2268	4	US-09-252-991A-11815	Sequence 11815, A
C 746	43.6	4.4	2660	4	US-09-816-760-1	Sequence 1, Appli	Sequence 1, Appli	C 824	43.2	4.4	2721	4	US-09-252-991A-14887	Sequence 14887, A
C 747	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 825	43.2	4.4	2817	4	US-09-252-991A-14482	Sequence 14482, A
C 748	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 826	43.2	4.4	2817	4	US-09-252-991A-7311	Sequence 7311, Ap
C 749	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 827	43.2	4.4	2880	4	US-09-252-991A-7187	Sequence 7187, Ap
C 750	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 828	43.2	4.4	2923	6	5187076-5	Patent No. 5187076
C 751	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 829	43.2	4.4	2934	4	US-09-252-991A-84	Sequence 84, Appl
C 752	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 830	43.2	4.4	2955	4	US-09-252-991A-684	Sequence 684, Appl
C 753	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 831	43.2	4.4	3102	4	US-09-252-991A-727	Sequence 727, App
C 754	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 832	43.2	4.4	3150	4	US-09-252-991A-15560	Sequence 15560, A
C 755	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 833	43.2	4.4	3402	4	US-09-252-991A-15688	Sequence 15688, A
C 756	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 834	43.2	4.4	3606	4	US-09-252-991A-14663	Sequence 14663, A
C 757	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 835	43.2	4.4	4497	4	US-09-252-991A-14663	Sequence 5, Appli
C 758	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli	C 836	43.2	4.4	6644	4	US-08-875-435B-8	Sequence 3, Appli
C 759	43.6	4.4	2660	4	US-09-838-561-1	Sequence 1, Appli	Sequence 1, Appli							
C 760	43.6	4.4	2660	4	US-09									



837	43	4.3	342	4	US-09-252-991A-504	Sequence 604, App	Sequence 604, App	c 910	42.8	4.3	1479	4	US-09-252-991A-7048	Sequence 7048, Ap
838	43	4.3	525	4	US-09-252-991A-2828	Sequence 2828, Ap	Sequence 2828, Ap	c 911	42.8	4.3	1611	4	US-09-252-991A-16550	Sequence 16550, A
839	43	4.3	714	4	US-09-252-991A-15925	Sequence 15925, A	Sequence 15925, A	c 912	42.8	4.3	1617	4	US-09-252-991A-16528	Sequence 16528, A
840	43	4.3	720	4	US-09-252-991A-74	Sequence 74, Appl	Sequence 74, Appl	c 913	42.8	4.3	1721	1	US-08-241-766-3	Sequence 3, Appl1
841	43	4.3	780	4	US-09-252-991A-15799	Sequence 15799, A	Sequence 15799, A	c 914	42.8	4.3	1818	4	US-09-252-991A-8941	Sequence 8941, Ap
842	43	4.3	861	4	US-09-252-991A-13981	Sequence 13981, A	Sequence 13981, A	c 915	42.8	4.3	1836	4	US-09-252-991A-1026	Sequence 1026, Ap
843	43	4.3	1071	4	US-09-252-991A-14206	Sequence 14206, A	Sequence 14206, A	c 916	42.8	4.3	2003	1	US-08-036-555B-21	Sequence 21, Appl
844	43	4.3	1419	4	US-09-252-991A-10421	Sequence 10421, A	Sequence 10421, A	c 917	42.8	4.3	2003	1	US-08-469-569-21	Sequence 21, Appl
845	43	4.3	1419	4	US-09-252-991A-11636	Sequence 11636, A	Sequence 11636, A	c 918	42.8	4.3	2003	1	US-08-249-322A-21	Sequence 21, Appl
846	43	4.3	1470	4	US-09-252-991A-9286	Sequence 9286, Ap	Sequence 9286, Ap	c 919	42.8	4.3	2003	1	US-08-469-526A-21	Sequence 21, Appl
847	43	4.3	1509	4	US-09-252-991A-9286	Sequence 9286, Ap	Sequence 9286, Ap	c 920	42.8	4.3	2003	2	US-08-734-591A-21	Sequence 21, Appl
848	43	4.3	1587	4	US-09-252-991A-11720	Sequence 11720, A	Sequence 11720, A	c 921	42.8	4.3	2003	2	US-08-469-660-21	Sequence 21, Appl
849	43	4.3	1623	4	US-09-252-991A-538	Sequence 538, App	Sequence 538, App	c 922	42.8	4.3	2003	3	US-08-341-018-71	Sequence 71, Appl
850	43	4.3	1695	4	US-09-252-991A-10319	Sequence 10319, A	Sequence 10319, A	c 923	42.8	4.3	2003	3	US-08-470-335-21	Sequence 21, Appl
851	43	4.3	1803	4	US-09-252-991A-15466	Sequence 15466, A	Sequence 15466, A	c 924	42.8	4.3	2003	3	US-08-735-021-21	Sequence 21, Appl
852	43	4.3	1815	4	US-09-731-166-3	Sequence 3, Appl1	Sequence 3, Appl1	c 925	42.8	4.3	2003	3	US-08-734-664A-21	Sequence 21, Appl
853	43	4.3	1848	4	US-09-614-034-188	Sequence 188, App	Sequence 188, App	c 926	42.8	4.3	2003	3	US-08-470-339-21	Sequence 21, Appl
854	43	4.3	1890	4	US-09-252-991A-579	Sequence 579, App	Sequence 579, App	c 927	42.8	4.3	2003	3	US-08-467-602-21	Sequence 21, Appl
855	43	4.3	1977	4	US-09-252-991A-9290	Sequence 9290, Ap	Sequence 9290, Ap	c 928	42.8	4.3	2003	4	US-08-411-295F-64	Sequence 64, Appl
856	43	4.3	1995	4	US-09-252-991A-9265	Sequence 9265, Ap	Sequence 9265, Ap	c 929	42.8	4.3	2003	5	PCT-US94-05083C-21	Sequence 21, Appl
857	43	4.3	1998	6	5212296-8	Patent No. 5212296	Sequence 15771, A	c 930	42.8	4.3	2003	5	PCT-US95-06846A-21	Sequence 21, Appl
858	43	4.3	2055	4	US-09-252-991A-15771	Sequence 15771, A	Sequence 15771, A	c 931	42.8	4.3	2046	4	US-09-490-291-3	Sequence 3, Appl1
859	43	4.3	2242	1	US-08-641-627A-37	Sequence 37, Appl	Sequence 37, Appl	c 932	42.8	4.3	2076	4	US-09-490-291-5	Sequence 5, Appl1
860	43	4.3	2304	4	US-09-252-991A-11802	Sequence 11802, A	Sequence 11802, A	c 933	42.8	4.3	3051	1	US-08-241-766-10	Sequence 10, Appl1
861	43	4.3	2310	4	US-09-252-991A-3040	Sequence 3040, Ap	Sequence 3040, Ap	c 934	42.8	4.3	3195	4	US-09-252-991A-937	Sequence 937, App
862	43	4.3	2376	4	US-09-252-991A-10741	Sequence 10741, A	Sequence 10741, A	c 935	42.8	4.3	4236	4	US-09-252-991A-7057	Sequence 7057, App
863	43	4.3	2376	4	US-09-252-991A-15323	Sequence 15323, A	Sequence 15323, A	c 936	42.8	4.3	7791	3	US-08-949-386-23	Sequence 23, Appl
864	43	4.3	2388	4	US-09-252-991A-14064	Sequence 14064, A	Sequence 14064, A	c 937	42.8	4.3	7791	3	US-08-450-562-23	Sequence 23, Appl
865	43	4.3	2676	4	US-09-252-991A-15370	Sequence 15370, A	Sequence 15370, A	c 938	42.8	4.3	7791	3	US-08-984-709A-23	Sequence 23, Appl
866	43	4.3	3794	4	US-09-192-434-1	Sequence 1, Appl1	Sequence 1, Appl1	c 939	42.8	4.3	7791	3	US-08-450-272-23	Sequence 23, Appl
867	43	4.3	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	Sequence 3815, Ap	c 940	42.8	4.3	7791	3	US-08-450-273-23	Sequence 23, Appl
868	43	4.3	4059	2	US-08-485-139-1	Sequence 1, Appl1	Sequence 1, Appl1	c 941	42.8	4.3	7808	3	US-08-949-386-22	Sequence 22, Appl
869	43	4.3	4506	3	US-09-252-991A-3695	Sequence 3695, Ap	Sequence 3695, Ap	c 942	42.8	4.3	7808	3	US-08-450-562-22	Sequence 22, Appl
870	43	4.3	4800	3	US-09-106-638-1	Sequence 1, Appl1	Sequence 1, Appl1	c 943	42.8	4.3	7808	3	US-08-984-709A-22	Sequence 22, Appl
871	43	4.3	4800	3	US-08-941-445A-4	Sequence 4, Appl1	Sequence 4, Appl1	c 944	42.8	4.3	7808	3	US-08-450-272-22	Sequence 22, Appl
872	43	4.3	7527	4	US-09-252-991A-71	Sequence 71, Appl	Sequence 71, Appl	c 945	42.8	4.3	7808	4	US-08-450-273-22	Sequence 22, Appl
873	42.8	4.3	426	4	US-09-252-991A-7105	Sequence 7105, Ap	Sequence 7105, Ap	c 946	42.8	4.3	10023	4	US-09-252-991A-6997	Sequence 6997 App
874	42.8	4.3	561	4	US-09-252-991A-7275	Sequence 7275, Ap	Sequence 7275, Ap	c 947	42.6	4.3	455	4	US-09-252-991A-16394	Sequence 16394, A
875	42.8	4.3	570	4	US-09-252-991A-3834	Sequence 3834, Ap	Sequence 3834, Ap	c 948	42.6	4.3	455	4	US-09-252-991A-16030	Sequence 16030, A
876	42.8	4.3	639	4	US-09-252-991A-1078	Sequence 1078, Ap	Sequence 1078, Ap	c 949	42.6	4.3	588	4	US-09-252-991A-1995	Sequence 1995, Ap
877	42.8	4.3	745	1	US-08-036-555B-163	Sequence 163, App	Sequence 163, App	c 950	42.6	4.3	621	4	US-09-252-991A-3944	Sequence 3944, Ap
878	42.8	4.3	745	1	US-08-463-569-163	Sequence 163, App	Sequence 163, App	c 951	42.6	4.3	624	4	US-09-252-991A-12492	Sequence 12492, Ap
879	42.8	4.3	745	1	US-08-249-322A-163	Sequence 163, App	Sequence 163, App	c 952	42.6	4.3	690	4	US-09-252-991A-11336	Sequence 11336, A
880	42.8	4.3	745	1	US-08-469-526A-163	Sequence 163, App	Sequence 163, App	c 953	42.6	4.3	693	4	US-09-252-991A-15166	Sequence 15166, A
881	42.8	4.3	745	1	US-08-734-591A-163	Sequence 163, App	Sequence 163, App	c 954	42.6	4.3	747	4	US-09-252-991A-16349	Sequence 16349, A
882	42.8	4.3	745	2	US-08-469-660-163	Sequence 163, App	Sequence 163, App	c 955	42.6	4.3	750	4	US-09-252-991A-12577	Sequence 12577, A
883	42.8	4.3	745	3	US-08-341-018-51	Sequence 51, Appl	Sequence 51, Appl	c 956	42.6	4.3	771	4	US-09-252-991A-12986	Sequence 12986, A
884	42.8	4.3	745	3	US-08-470-335-163	Sequence 163, App	Sequence 163, App	c 957	42.6	4.3	840	4	US-09-252-991A-7712	Sequence 7712, Ap
885	42.8	4.3	745	3	US-08-735-021-163	Sequence 163, App	Sequence 163, App	c 958	42.6	4.3	912	4	US-09-252-991A-11313	Sequence 11313, A
886	42.8	4.3	745	3	US-08-734-664A-163	Sequence 163, App	Sequence 163, App	c 959	42.6	4.3	1050	4	US-09-252-991A-12884	Sequence 12884, A
887	42.8	4.3	745	3	US-08-470-339-163	Sequence 163, App	Sequence 163, App	c 960	42.6	4.3	1068	4	US-09-252-991A-12884	Sequence 12884, A
888	42.8	4.3	745	4	US-08-467-602-163	Sequence 163, App	Sequence 163, App	c 961	42.6	4.3	1126	3	US-09-463-702A-33	Sequence 33, Appl
889	42.8	4.3	745	4	US-08-411-295F-44	Sequence 44, Appl	Sequence 44, Appl	c 962	42.6	4.3	1126	3	US-09-819-964-5	Sequence 5, Appl1
890	42.8	4.3	745	5	PCT-US94-05083C-159	Sequence 159, App	Sequence 159, App	c 963	42.6	4.3	1154	3	US-09-347-803-15	Sequence 15, Appl
891	42.8	4.3	745	5	PCT-US95-06846A-163	Sequence 163, App	Sequence 163, App	c 964	42.6	4.3	1206	4	US-09-252-991A-519	Sequence 519, App
892	42.8	4.3	756	1	US-08-642-255-50	Sequence 50, Appl	Sequence 50, Appl	c 965	42.6	4.3	1321	4	US-09-252-991A-7850	Sequence 7850, App
893	42.8	4.3	762	4	US-09-252-991A-16176	Sequence 16176, A	Sequence 16176, A	c 966	42.6	4.3	1327	4	US-09-252-991A-11278	Sequence 11278, A
894	42.8	4.3	801	4	US-09-252-991A-9143	Sequence 9143, Ap	Sequence 9143, Ap	c 967	42.6	4.3	1269	4	US-09-252-991A-12933	Sequence 12933, A
895	42.8	4.3	849	4	US-09-252-991A-3722	Sequence 3722, Ap	Sequence 3722, Ap	c 968	42.6	4.3	1281	4	US-09-252-991A-12551	Sequence 12551, A
896	42.8	4.3	873	4	US-09-252-991A-16052	Sequence 16052, A	Sequence 16052, A	c 969	42.6	4.3	1416	4	US-09-252-991A-2625	Sequence 2625, Ap
897	42.8	4.3	939	4	US-09-252-991A-16069	Sequence 16069, A	Sequence 16069, A	c 970	42.6	4.3	1446	4	US-09-252-991A-7937	Sequence 7937, Ap
898	42.8	4.3	1035	3	US-08-858-003-30	Sequence 30, Appl	Sequence 30, Appl	c 971	42.6	4.3	1488	4	US-09-252-991A-8426	Sequence 8426, Ap
899	42.8	4.3	1035	3	US-08-176-166-30	Sequence 30, Appl	Sequence 30, Appl	c 972	42.6	4.3	1503	4	US-09-463-702A-33	Sequence 33, Appl
900	42.8	4.3	1035	3	US-08-997-467-30	Sequence 30, Appl	Sequence 30, Appl	c 973	42.6	4.3	1509	4	US-09-699-135-33	Sequence 33, Appl
901	42.8	4.3	1050	4	US-09-252-991A-8232	Sequence 8232, Ap	Sequence 8232, Ap	c 974	42.6	4.3	1551	4	US-09-252-991A-12165	Sequence 12165, A
902	42.8	4.3	1113	4	US-09-252-991A-7427	Sequence 7427, Ap	Sequence 7427, Ap	c 975	42.6	4.3	1551	4	US-09-252-991A-13148	Sequence 13148, A
903	42.8	4.3	1143	4	US-09-252-991A-1032	Sequence 1032, Ap	Sequence 1032, Ap	c 976	42.6	4.3	1569	4	US-09-252-991A-11892	Sequence 11892, A
904	42.8	4.3	1218	4	US-09-252-991A-7486	Sequence 7486, Ap	Sequence 7486, Ap	c 977	42.6	4.3	1584	4	US-09-252-991A-12888	Sequence 12888, Ap
905	42.8	4.3	1443	1	US-08-076-089-1	Sequence 1, Appl1	Sequence 1, Appl1	c 978	42.6	4.3	1562	4	US-09-252-991A-1413	Sequence 1413, Ap
906	42.8	4.3	1443	2	US-08-707-200-1	Sequence 1, Appl1	Sequence 1, Appl1	c 979	42.6	4.3	1662	4	US-09-252-991A-7894	Sequence 7894, Ap
907	42.8	4.3	1443	3	US-08-996-565-1	Sequence 1, Appl1	Sequence 1, Appl1	c 980	42.6	4.3	1692	4	US-09-252-991A-12425	Sequence 12425, A
908	42.8	4.3	1443	5	PCT-US93-05643-1	Sequence 1, Appl1	Sequence 1, Appl1	c 981	42.6	4.3	1767	4	US-09-252-991A-7614	Sequence 7614, Ap
909	42.8	4.3	1470	4	US-09-252-991A-7210	Sequence 7210, Ap	Sequence 7210, Ap	c 982	42.6	4.3	1899	4	US-09-252-991A-7664	Sequence 7664, Ap



c 983	42.6	4.3	1923	4	US-09-252-991A-3380	Sequence 3380, Ap	1056	42.6	4.3	4162	2	US-08-459-448A-26	Sequence 26, Appl
984	42.6	4.3	2049	4	US-09-252-991A-8348	Sequence 8348, Ap	1057	42.6	4.3	4162	3	US-08-459-595A-26	Sequence 26, Appl
c 985	42.6	4.3	2070	4	US-09-252-991A-15031	Sequence 15031, A	1058	42.6	4.3	4162	3	US-08-459-504B-26	Sequence 26, Appl
c 986	42.6	4.3	2181	4	US-09-252-991A-493	Sequence 493, App	1059	42.6	4.3	4162	3	US-08-459-444-26	Sequence 26, Appl
987	42.6	4.3	2186	2	US-08-878-546-9	Sequence 9, Appli	1060	42.6	4.3	4162	3	US-09-547-422-26	Sequence 26, Appl
988	42.6	4.3	2196	4	US-09-252-991A-609	Sequence 609, App	1061	42.6	4.3	4162	3	US-09-988-462-26	Sequence 26, Appl
c 989	42.6	4.3	2526	4	US-09-252-991A-12018	Sequence 12018, A	1062	42.6	4.3	4165	1	US-07-951-715A-26	Sequence 26, Appl
990	42.6	4.3	2724	4	US-09-252-991A-7543	Sequence 7543, Ap	1063	42.6	4.3	4269	4	US-09-799-451-363	Sequence 363, App
991	42.6	4.3	2742	3	US-09-233-468A-1	Sequence 1, Appli	1064	42.6	4.3	4897	6	5196516-7	Patent No. 5196516
992	42.6	4.3	2742	4	US-09-784-984B-1	Sequence 1, Appli	1065	42.6	4.3	5970	3	US-09-320-878-21	Sequence 21, Appl
c 993	42.6	4.3	2754	4	US-09-252-991A-1147	Sequence 1147, Ap	1066	42.6	4.3	5970	4	US-09-141-908-11	Sequence 11, Appl
994	42.6	4.3	3187	3	US-09-105-537-40	Sequence 40, Appl	1067	42.6	4.3	5970	4	US-09-657-440-21	Sequence 21, Appl
c 995	42.6	4.3	3147	4	US-09-252-991A-12797	Sequence 12797, A	1068	42.6	4.3	23673	3	US-09-773-816-1	Sequence 1, Appli
996	42.6	4.3	3627	4	US-09-252-991A-1324	Sequence 1324, Ap	1069	42.4	4.3	495	4	US-09-252-991A-10553	Sequence 10553, A
997	42.6	4.3	3627	4	US-09-793-594-3	Sequence 3, Appli	1070	42.4	4.3	546	4	US-09-252-991A-9911	Sequence 9911, A
998	42.6	4.3	3698	2	US-08-231-193A-43	Sequence 43, Appl	1071	42.4	4.3	561	4	US-09-252-991A-3862	Sequence 3862, Ap
999	42.6	4.3	3698	3	US-08-486-273A-43	Sequence 43, Appl	1072	42.4	4.3	657	3	US-09-527-345-3	Sequence 3, Appli
1000	42.6	4.3	3698	3	US-08-480-474-43	Sequence 43, Appl	1073	42.4	4.3	678	4	US-09-252-991A-8721	Sequence 8721, Ap
1001	42.6	4.3	3698	3	US-08-940-086A-43	Sequence 43, Appl	1074	42.4	4.3	792	4	US-09-818-780-31	Sequence 31, Appl
1002	42.6	4.3	3698	3	US-08-940-035A-43	Sequence 43, Appl	1075	42.4	4.3	810	4	US-09-252-991A-10034	Sequence 10034, A
1003	42.6	4.3	3698	3	US-08-935-105A-43	Sequence 43, Appl	1076	42.4	4.3	918	4	US-09-252-991A-16461	Sequence 16461, A
1004	42.6	4.3	3698	4	US-09-648-797-43	Sequence 43, Appl	1077	42.4	4.3	987	4	US-09-252-991A-10099	Sequence 10099, A
1005	42.6	4.3	3698	4	US-09-386-123-43	Sequence 43, Appl	1078	42.4	4.3	1005	4	US-09-252-991A-16346	Sequence 16346, A
1006	42.6	4.3	3850	3	US-09-463-702A-1	Sequence 1, Appli	1079	42.4	4.3	1026	4	US-09-252-991A-6481	Sequence 6481, Ap
1007	42.6	4.3	3850	4	US-09-699-135-1	Sequence 1, Appli	1080	42.4	4.3	1038	4	US-09-252-991A-9197	Sequence 9197, Ap
1008	42.6	4.3	4002	2	US-08-231-193A-53	Sequence 53, Appl	1081	42.4	4.3	1062	4	US-09-252-991A-6310	Sequence 6310, Ap
1009	42.6	4.3	4002	2	US-08-486-273A-53	Sequence 53, Appl	1082	42.4	4.3	1098	4	US-09-252-991A-16142	Sequence 16142, A
1010	42.6	4.3	4002	3	US-08-480-474-53	Sequence 53, Appl	1083	42.4	4.3	1137	4	US-09-724-797-53	Sequence 53, Appl
1011	42.6	4.3	4002	3	US-08-940-086A-53	Sequence 53, Appl	1084	42.4	4.3	1290	4	US-09-252-991A-5993	Sequence 5993, Ap
1012	42.6	4.3	4002	3	US-08-940-035A-53	Sequence 53, Appl	1085	42.4	4.3	1380	4	US-09-252-991A-3550	Sequence 3550, Ap
1013	42.6	4.3	4002	3	US-08-935-105A-53	Sequence 53, Appl	1086	42.4	4.3	1410	4	US-09-252-991A-8867	Sequence 8867, Ap
1014	42.6	4.3	4002	4	US-09-648-797-53	Sequence 53, Appl	1087	42.4	4.3	1546	3	US-09-303-318A-1	Sequence 1, Appli
1015	42.6	4.3	4002	4	US-09-386-123-53	Sequence 53, Appl	1088	42.4	4.3	1566	4	US-09-724-797-61	Sequence 61, Appl
1016	42.6	4.3	4017	2	US-08-231-193A-49	Sequence 49, Appl	1089	42.4	4.3	1902	4	US-09-252-991A-10005	Sequence 10005, A
1017	42.6	4.3	4017	2	US-08-486-273A-49	Sequence 49, Appl	1090	42.4	4.3	1919	4	US-09-614-912-175	Sequence 175, App
1018	42.6	4.3	4017	3	US-08-480-474-49	Sequence 49, Appl	1091	42.4	4.3	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
1019	42.6	4.3	4017	3	US-08-940-086A-49	Sequence 49, Appl	1092	42.4	4.3	1983	4	US-09-252-991A-13314	Sequence 13314, A
1020	42.6	4.3	4017	3	US-08-940-035A-49	Sequence 49, Appl	1093	42.4	4.3	1998	4	US-09-252-991A-9693	Sequence 9693, Ap
1021	42.6	4.3	4017	3	US-08-935-105A-49	Sequence 49, Appl	1094	42.4	4.3	1992	4	US-09-252-991A-13154	Sequence 13154, A
1022	42.6	4.3	4017	4	US-09-648-797-49	Sequence 49, Appl	1095	42.4	4.3	2043	4	US-09-252-991A-12652	Sequence 12652, A
1023	42.6	4.3	4017	4	US-09-386-123-49	Sequence 49, Appl	1096	42.4	4.3	2067	4	US-09-252-991A-9114	Sequence 9114, Ap
1024	42.6	4.3	4053	2	US-08-231-193A-47	Sequence 47, Appl	1097	42.4	4.3	2376	4	US-09-976-594-496	Sequence 496, App
1025	42.6	4.3	4053	2	US-08-486-273A-47	Sequence 47, Appl	1098	42.4	4.3	2634	4	US-09-252-991A-8976	Sequence 8976, Ap
1026	42.6	4.3	4053	3	US-08-480-474-47	Sequence 47, Appl	1099	42.4	4.3	2658	4	US-09-252-991A-9558	Sequence 9558, Ap
1027	42.6	4.3	4053	3	US-08-940-086A-47	Sequence 47, Appl	1100	42.4	4.3	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
1028	42.6	4.3	4053	3	US-08-940-035A-47	Sequence 47, Appl	1101	42.4	4.3	3241	3	US-09-434-288-11	Sequence 11, Appl
1029	42.6	4.3	4053	3	US-08-935-105A-47	Sequence 47, Appl	1102	42.4	4.3	4143	4	US-09-919-039-345	Sequence 345, App
1030	42.6	4.3	4053	4	US-09-648-797-47	Sequence 47, Appl	1103	42.4	4.3	4992	4	US-09-013-339-10	Sequence 10, Appl
1031	42.6	4.3	4053	4	US-09-386-123-47	Sequence 47, Appl	1104	42.4	4.3	55216	4	US-09-716-865-23	Sequence 23, Appl
1032	42.6	4.3	4068	2	US-08-231-193A-5	Sequence 5, Appli	1105	42.2	4.3	456	4	US-09-252-991A-6665	Sequence 6665, Ap
1033	42.6	4.3	4068	2	US-08-486-273A-5	Sequence 5, Appli	1106	42.2	4.3	564	4	US-09-252-991A-6557	Sequence 6557, Ap
1034	42.6	4.3	4068	3	US-08-480-474-5	Sequence 5, Appli	1107	42.2	4.3	609	4	US-09-252-991A-11904	Sequence 11904, A
1035	42.6	4.3	4068	3	US-08-940-086A-5	Sequence 5, Appli	1108	42.2	4.3	639	4	US-09-252-991A-6537	Sequence 6537, Ap
1036	42.6	4.3	4068	3	US-08-940-035A-5	Sequence 5, Appli	1109	42.2	4.3	672	4	US-09-252-991A-15696	Sequence 15696, A
1037	42.6	4.3	4068	3	US-08-935-105A-5	Sequence 5, Appli	1110	42.2	4.3	738	4	US-09-252-991A-14234	Sequence 14234, A
1038	42.6	4.3	4068	4	US-09-648-797-5	Sequence 5, Appli	1111	42.2	4.3	789	4	US-09-252-991A-9734	Sequence 9734, Ap
1039	42.6	4.3	4068	4	US-09-386-123-5	Sequence 5, Appli	1112	42.2	4.3	825	4	US-09-252-991A-7593	Sequence 7593, Ap
1040	42.6	4.3	4077	2	US-08-231-193A-51	Sequence 51, Appl	1113	42.2	4.3	861	4	US-09-252-991A-7540	Sequence 7540, Ap
1041	42.6	4.3	4077	2	US-08-486-273A-51	Sequence 51, Appl	1114	42.2	4.3	864	4	US-09-252-991A-5099	Sequence 5099, Ap
1042	42.6	4.3	4077	3	US-08-480-474-51	Sequence 51, Appl	1115	42.2	4.3	884	4	US-09-252-991A-15661	Sequence 15661, A
1043	42.6	4.3	4077	3	US-08-940-086A-51	Sequence 51, Appl	1116	42.2	4.3	882	4	US-09-252-991A-9535	Sequence 9535, Ap
1044	42.6	4.3	4077	3	US-08-940-035A-51	Sequence 51, Appl	1117	42.2	4.3	984	4	US-09-252-991A-5126	Sequence 5126, Ap
1045	42.6	4.3	4077	3	US-08-935-105A-51	Sequence 51, Appl	1118	42.2	4.3	996	4	US-09-252-991A-7732	Sequence 7732, Ap
1046	42.6	4.3	4077	4	US-09-648-797-51	Sequence 51, Appl	1119	42.2	4.3	996	4	US-09-252-991A-10775	Sequence 10775, A
1047	42.6	4.3	4077	4	US-09-386-123-51	Sequence 51, Appl	1120	42.2	4.3	1041	4	US-09-489-039A-6251	Sequence 6251, Ap
1048	42.6	4.3	4092	2	US-08-231-193A-45	Sequence 45, Appl	1121	42.2	4.3	1107	4	US-09-252-991A-14146	Sequence 14146, A
1049	42.6	4.3	4092	2	US-08-486-273A-45	Sequence 45, Appl	1122	42.2	4.3	1149	4	US-09-252-991A-5033	Sequence 5033, Ap
1050	42.6	4.3	4092	3	US-08-480-474-45	Sequence 45, Appl	1123	42.2	4.3	1176	4	US-09-252-991A-11843	Sequence 11843, A
1051	42.6	4.3	4092	3	US-08-940-086A-45	Sequence 45, Appl	1124	42.2	4.3	1194	4	US-09-252-991A-7454	Sequence 7454, Ap
1052	42.6	4.3	4092	3	US-08-940-035A-45	Sequence 45, Appl	1125	42.2	4.3	1236	4	US-09-252-991A-1087	Sequence 1087, Ap
1053	42.6	4.3	4092	3	US-08-935-105A-45	Sequence 45, Appl	1126	42.2	4.3	1245	4	US-09-252-991A-12071	Sequence 12071, A
1054	42.6	4.3	4092	4	US-09-648-797-45	Sequence 45, Appl	1127	42.2	4.3	1248	4	US-09-252-991A-8391	Sequence 8391, Ap
1055	42.6	4.3	4092	4	US-09-386-123-45	Sequence 45, Appl	1128	42.2	4.3	1266	4	US-09-252-991A-8926	Sequence 8926, Ap



1129	42.2	4.3	1269	4	US-09-252-991A-14054	Sequence 14054, A	1202	42	4.2	1683	4	US-09-724-737-21	Sequence 21, Appl
1130	42.2	4.3	1272	4	US-09-252-991A-10690	Sequence 10690, A	1203	42	4.2	1695	4	US-09-252-991A-6801	Sequence 6801, Ap
1131	42.2	4.3	1281	3	US-09-105-537-19	Sequence 19, Appl	1204	42	4.2	1930	3	US-08-987-367-1	Sequence 1, Appl
1132	42.2	4.3	1323	4	US-09-252-991A-14169	Sequence 14169, A	c1205	42	4.2	2028	4	US-09-252-991A-11416	Sequence 11416, A
1133	42.2	4.3	1422	4	US-09-252-991A-10550	Sequence 10550, A	1206	42	4.2	2689	3	US-09-105-537-34	Sequence 34, Appl
1134	42.2	4.3	1428	4	US-09-252-991A-15727	Sequence 15727, A	1207	42	4.2	5331	4	US-09-453-956-1	Sequence 1, Appl
1135	42.2	4.3	1485	4	US-09-252-991A-7612	Sequence 7612, Ap	c1208	42	4.2	5331	4	US-09-698-235-2	Sequence 2, Appl
1136	42.2	4.3	1503	4	US-09-252-991A-9482	Sequence 9482, Ap	1209	41.8	4.2	534	4	US-09-252-991A-12543	Sequence 12543, A
1137	42.2	4.3	1521	4	US-09-252-991A-13990	Sequence 13990, A	c1210	41.8	4.2	564	4	US-09-252-991A-12263	Sequence 12263, A
1138	42.2	4.3	1554	4	US-09-252-991A-15262	Sequence 15262, A	c1211	41.8	4.2	573	4	US-09-252-991A-5674	Sequence 5674, Ap
1139	42.2	4.3	1611	4	US-09-252-991A-6694	Sequence 6694, Ap	c1212	41.8	4.2	714	4	US-09-252-991A-11042	Sequence 11042, A
1140	42.2	4.3	1645	4	US-09-620-312D-807	Sequence 807, App	1213	41.8	4.2	732	4	US-09-252-991A-12697	Sequence 12697, A
1141	42.2	4.3	1671	4	US-09-252-991A-9711	Sequence 9711, Ap	c1214	41.8	4.2	759	4	US-09-252-991A-14329	Sequence 14329, A
1142	42.2	4.3	1686	4	US-09-252-991A-7673	Sequence 7673, Ap	c1215	41.8	4.2	822	4	US-09-252-991A-4946	Sequence 4946, Ap
1143	42.2	4.3	1716	4	US-09-252-991A-9577	Sequence 9577, Ap	1216	41.8	4.2	825	4	US-09-252-991A-3004	Sequence 3004, Ap
1144	42.2	4.3	1734	4	US-09-252-991A-15356	Sequence 15356, A	1217	41.8	4.2	867	4	US-09-252-991A-16236	Sequence 16236, A
1145	42.2	4.3	1782	4	US-09-252-991A-14102	Sequence 14102, A	c1218	41.8	4.2	882	4	US-09-252-991A-5644	Sequence 5644, Ap
1146	42.2	4.3	1788	4	US-09-252-991A-4632	Sequence 4632, Ap	1219	41.8	4.2	888	4	US-09-252-991A-16530	Sequence 16530, A
1147	42.2	4.3	1791	1	US-08-399-646-3	Sequence 3, Appl	c1220	41.8	4.2	942	4	US-09-252-991A-10909	Sequence 10909, A
1148	42.2	4.3	1791	1	US-08-607-321-3	Sequence 3, Appl	c1221	41.8	4.2	966	4	US-09-252-991A-8354	Sequence 8354, Ap
1149	42.2	4.3	1791	2	US-08-961-240-3	Sequence 3, Appl	1222	41.8	4.2	1020	4	US-09-252-991A-5550	Sequence 5550, Ap
1150	42.2	4.3	1791	2	US-08-605-501-3	Sequence 3, Appl	1223	41.8	4.2	1092	4	US-09-252-991A-8481	Sequence 8481, Ap
1151	42.2	4.3	1839	4	US-09-252-991A-9156	Sequence 9156, Ap	c1224	41.8	4.2	1125	4	US-09-252-991A-16066	Sequence 16066, A
1152	42.2	4.3	1848	4	US-09-252-991A-9071	Sequence 9071, Ap	1225	41.8	4.2	1200	4	US-09-252-991A-8527	Sequence 8527, Ap
1153	42.2	4.3	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	1226	41.8	4.2	1248	4	US-09-252-991A-10656	Sequence 10656, A
1154	42.2	4.3	1947	4	US-09-252-991A-1048	Sequence 1048, Ap	1227	41.8	4.2	1257	4	US-09-489-039A-5712	Sequence 5712, Ap
1155	42.2	4.3	1980	4	US-09-252-991A-8712	Sequence 8712, Ap	c1228	41.8	4.2	1260	4	US-09-252-991A-13265	Sequence 13265, A
1156	42.2	4.3	2056	1	US-08-399-646-13	Sequence 13, Appl	1229	41.8	4.2	1263	4	US-09-252-991A-2546	Sequence 2546, Ap
1157	42.2	4.3	2056	1	US-08-607-321-13	Sequence 13, Appl	1230	41.8	4.2	1278	4	US-09-252-991A-11277	Sequence 11277, A
1158	42.2	4.3	2056	2	US-08-961-240-13	Sequence 13, Appl	c1231	41.8	4.2	1296	4	US-09-252-991A-12123	Sequence 12123, A
1159	42.2	4.3	2056	2	US-08-605-501-13	Sequence 13, Appl	1232	41.8	4.2	1326	4	US-09-252-991A-12394	Sequence 12394, A
1160	42.2	4.3	2103	4	US-09-252-991A-11773	Sequence 11773, A	1233	41.8	4.2	1608	4	US-09-252-991A-9091	Sequence 9091, Ap
1161	42.2	4.3	2103	4	US-09-252-991A-13604	Sequence 13604, A	1234	41.8	4.2	1626	4	US-09-252-991A-4934	Sequence 4934, Ap
1162	42.2	4.3	2126	2	US-08-789-354-1	Sequence 1, Appl	c1235	41.8	4.2	1665	4	US-09-252-991A-9011	Sequence 9011, Ap
1163	42.2	4.3	2126	3	US-09-110-937-1	Sequence 1, Appl	1236	41.8	4.2	1710	2	US-08-933-821-5	Sequence 5, Appl
1164	42.2	4.3	2126	3	US-09-058-725B-1	Sequence 1, Appl	1237	41.8	4.2	1780	2	US-08-960-507-5	Sequence 5, Appl
1165	42.2	4.3	2126	3	US-09-232-857-1	Sequence 1, Appl	1238	41.8	4.2	1780	3	US-09-136-828-5	Sequence 5, Appl
1166	42.2	4.3	2250	4	US-09-252-991A-4181	Sequence 4181, Ap	1239	41.8	4.2	1780	3	US-09-332-928A-5	Sequence 5, Appl
1167	42.2	4.3	2259	4	US-09-252-991A-13396	Sequence 13396, A	1240	41.8	4.2	1780	3	US-09-136-801-5	Sequence 5, Appl
1168	42.2	4.3	2313	4	US-09-252-991A-11939	Sequence 11939, A	1241	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
1169	42.2	4.3	2361	4	US-09-252-991A-15781	Sequence 15781, A	1242	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
1170	42.2	4.3	2577	4	US-09-252-991A-6607	Sequence 6607, Ap	1243	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
1171	42.2	4.3	2640	4	US-09-252-991A-15419	Sequence 15419, A	1244	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
1172	42.2	4.3	2679	4	US-09-252-991A-15623	Sequence 15623, A	1245	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
1173	42.2	4.3	2952	4	US-09-252-991A-5096	Sequence 5096, Ap	1246	41.8	4.2	1806	4	US-09-252-991A-11213	Sequence 11213, A
1174	42.2	4.3	3222	4	US-09-252-991A-13746	Sequence 13746, Ap	c1247	41.8	4.2	1920	4	US-09-252-991A-8999	Sequence 8999, Ap
1175	42.2	4.3	4095	4	US-09-252-991A-10309	Sequence 10309, A	c1248	41.8	4.2	1944	4	US-09-252-991A-16245	Sequence 16245, A
1176	42.2	4.3	4143	4	US-09-252-991A-9151	Sequence 9151, Ap	c1249	41.8	4.2	1956	4	US-09-724-737-57	Sequence 57, Appl
1177	42.2	4.3	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	1250	41.8	4.2	2031	4	US-09-252-991A-9572	Sequence 9572, Ap
1178	42.2	4.3	4767	4	US-09-410-551B-28	Sequence 28, Appl	c1251	41.8	4.2	2064	1	US-08-343-428-1	Sequence 1, Appl
1179	42.2	4.3	4767	4	US-09-940-316B-28	Sequence 28, Appl	1252	41.8	4.2	2079	4	US-09-252-991A-5584	Sequence 5584, Ap
1180	42.2	4.3	4818	4	US-09-410-551B-32	Sequence 32, Appl	1253	41.8	4.2	2349	4	US-09-252-991A-4983	Sequence 4983, Ap
1181	42.2	4.3	4818	4	US-09-940-316B-32	Sequence 32, Appl	1254	41.8	4.2	2367	4	US-09-252-991A-726	Sequence 726, App
1182	42.2	4.3	13613	3	US-09-105-537-3	Sequence 3, Appl	c1255	41.8	4.2	2379	4	US-09-252-991A-686	Sequence 686, App
1183	42.2	4.3	35300	4	US-09-266-965-76	Sequence 76, Appl	1256	41.8	4.2	2475	3	US-09-624-693A-20	Sequence 20, Appl
1184	42.2	4.3	369	3	US-09-422-487-5	Sequence 5, Appl	1257	41.8	4.2	2499	4	US-09-252-991A-696	Sequence 696, App
1185	42.2	4.3	369	3	US-09-378-088A-127	Sequence 127, App	1258	41.8	4.2	2592	4	US-09-252-991A-9528	Sequence 9528, Ap
1186	42.2	4.3	369	4	US-09-643-596B-127	Sequence 127, App	c1259	41.8	4.2	2808	4	US-09-252-991A-16466	Sequence 16466, A
1187	42.2	4.3	432	4	US-09-252-991A-11821	Sequence 11821, A	c1260	41.8	4.2	3006	4	US-09-252-991A-9720	Sequence 9720, Ap
1188	42.2	4.3	750	4	US-09-724-737-91	Sequence 91, Appl	1261	41.8	4.2	3387	4	US-09-194-640A-2	Sequence 2, Appl
1189	42.2	4.3	816	4	US-09-252-991A-2684	Sequence 2684, Ap	1262	41.8	4.2	3678	4	US-09-252-991A-8447	Sequence 8447, Ap
1190	42.2	4.3	927	4	US-09-252-991A-6846	Sequence 6846, Ap	1263	41.8	4.2	3868	3	US-09-357-070-1	Sequence 1, Appl
1191	42.2	4.3	927	4	US-09-252-991A-15420	Sequence 15420, A	1264	41.8	4.2	4078	4	US-09-016-434-1152	Sequence 1152, Ap
1192	42.2	4.3	1107	4	US-09-252-991A-2872	Sequence 2872, Ap	1265	41.8	4.2	4553	2	US-09-023-655-975	Sequence 975, App
1193	42.2	4.3	1254	4	US-09-252-991A-11478	Sequence 11478, A	1266	41.8	4.2	4695	2	US-08-231-193A-57	Sequence 57, Appl
1194	42.2	4.3	1335	4	US-09-252-991A-2994	Sequence 2994, Ap	1267	41.8	4.2	4695	2	US-08-486-273A-57	Sequence 57, Appl
1195	42.2	4.3	1336	4	US-09-252-991A-11563	Sequence 11563, A	1268	41.8	4.2	4695	3	US-08-940-086A-57	Sequence 57, Appl
1196	42.2	4.3	1386	4	US-09-252-991A-15531	Sequence 15531, A	1269	41.8	4.2	4695	3	US-08-940-035A-57	Sequence 57, Appl
1197	42.2	4.3	1416	4	US-09-252-991A-11499	Sequence 11499, A	1270	41.8	4.2	4695	3	US-08-935-105A-57	Sequence 57, Appl
1198	42.2	4.3	1431	4	US-09-252-991A-11886	Sequence 11886, A	1271	41.8	4.2	4695	4	US-09-648-797-57	Sequence 57, Appl
1199	42.2	4.3	1461	4	US-09-252-991A-15308	Sequence 15308, A	1272	41.8	4.2	4695	4	US-09-386-123-57	Sequence 57, Appl
1200	42.2	4.3	1524	4	US-09-252-991A-11455	Sequence 11455, A	1273	41.8	4.2	5045	3	US-09-390-721-1	Sequence 1, Appl
1201	42.2	4.3	1626	4	US-09-252-991A-3266	Sequence 3266, Ap	1274	41.8	4.2	5045	3	US-09-390-721-1	Sequence 3, Appl



1275	41.8	4.2	5045	4	US-09-713-893-1	Sequence 1, Appli	1348	41.6	4.2	4478	4	US-09-940-316B-16	Sequence 16, Appli
1276	41.8	4.2	5045	4	US-09-713-893-3	Sequence 3, Appli	1349	41.6	4.2	4547	4	US-09-410-551B-22	Sequence 22, Appli
1277	41.8	4.2	5220	2	US-08-777-405A-1	Sequence 1, Appli	1350	41.6	4.2	4547	4	US-09-940-316B-22	Sequence 22, Appli
1278	41.8	4.2	5220	2	US-08-777-871A-1	Sequence 1, Appli	1351	41.6	4.2	4571	4	US-09-410-551B-18	Sequence 18, Appli
1279	41.8	4.2	5220	2	US-09-225-951-1	Sequence 1, Appli	1352	41.6	4.2	4571	4	US-09-940-316B-18	Sequence 18, Appli
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- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
34	989	100.0	989	15	US-10-210-951-21
35	989	100.0	989	15	US-10-211-884-21
36	989	100.0	989	15	US-10-211-884-21
37	989	100.0	989	15	US-10-013-909A-305
38	989	100.0	989	15	US-10-211-858-21
39	989	100.0	989	15	US-10-211-858-21
40	989	100.0	989	15	US-10-307-817-121
41	989	100.0	989	15	US-10-307-817-121
42	989	100.0	989	15	US-10-307-817-125
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	79	257	26.0	257	15	US-10-102-524-1360	Sequence 1360, Ap
	80	254.4	25.7	257	15	US-10-102-524-1452	Sequence 1452, Ap
c	81	185.8	18.8	84428	16	US-10-229-1488-1	Sequence 1, Appli
	82	182.4	18.4	85692	16	US-10-461-194-1	Sequence 1, Appli
	83	179.2	18.1	86941	16	US-10-461-194-2	Sequence 2, Appli
	84	171	17.3	693	18	US-10-425-115-49671	Sequence 49671, A
	85	161.8	16.4	953	9	US-09-452-239-45	Sequence 45, Appl
	86	159.2	16.1	1049	9	US-09-452-239-43	Sequence 43, Appl
c	87	152.2	16.1	3759	17	US-10-437-963-23149	Sequence 23149, A
	88	158.6	16.0	997	9	US-09-452-239-13	Sequence 13, Appl
	89	157.6	15.9	813	18	US-10-425-115-108865	Sequence 108865
	90	157.2	15.9	1078	9	US-09-452-239-41	Sequence 41, Appl
	91	155.6	15.7	1018	9	US-09-452-239-35	Sequence 35, Appl
	92	154	15.6	891	9	US-09-452-239-1	Sequence 1, Appli
	93	153.4	15.5	888	18	US-10-425-115-53820	Sequence 53820, A
	94	153	15.5	77536	10	US-09-940-3168-1	Sequence 1, Appli
	95	152.4	15.4	901	16	US-10-425-114-27082	Sequence 27082, A
	96	152.4	15.4	991	18	US-10-425-115-53827	Sequence 53827, A
	97	152.4	15.4	1159	16	US-10-425-114-2777	Sequence 2777, Ap
	98	152.4	15.4	1218	15	US-10-361-460-77	Sequence 77, Appl
	99	152.4	15.4	2381	18	US-10-425-115-138013	Sequence 138013,
	100	150.8	15.2	849	16	US-10-425-114-25410	Sequence 25410, A
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	102	149.6	15.1	1060	16	US-10-425-114-28379	Sequence 28379, A
	103	149.6	15.1	1090	17	US-10-767-701-12827	Sequence 12827, A
	104	149.6	15.1	1377	18	US-10-425-115-138007	Sequence 138007,
	105	149.2	15.1	1003	15	US-10-361-460-33	Sequence 33, Appl
	106	148	15.0	1088	16	US-10-425-114-12284	Sequence 12284, A
	107	148	15.0	1097	16	US-10-425-114-3691	Sequence 3691, Ap
	108	148	15.0	1097	16	US-10-425-114-16291	Sequence 16291, A
	109	148	15.0	1118	9	US-09-452-239-37	Sequence 37, Appl
	110	148	15.0	1146	9	US-09-452-239-3	Sequence 3, Appli
	111	146.4	14.8	1160	15	US-10-361-460-31	Sequence 31, Appl
	112	146.4	14.8	1200	18	US-10-425-115-138010	Sequence 138010,
	113	146.4	14.8	1890	18	US-10-739-930-2642	Sequence 2642, Ap
	114	145.8	14.7	840	18	US-10-425-115-138002	Sequence 138002,
	115	145.2	14.7	1114	16	US-10-425-114-3140	Sequence 3140, Ap
	116	145.2	14.7	1287	18	US-10-425-115-113175	Sequence 113175,
	117	145	14.7	905	17	US-10-437-963-41715	Sequence 41715, A
	118	144.4	14.6	1057	9	US-09-452-239-5	Sequence 5, Appli
	119	143.2	14.5	1152	16	US-10-425-114-26100	Sequence 26100, A
	120	143.2	14.5	1152	16	US-10-425-115-53821	Sequence 53821, A
	121	143.2	14.5	1443	17	US-10-767-701-14336	Sequence 14336, A
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	123	142.8	14.4	1089	16	US-10-425-114-2526	Sequence 2526, Ap
	124	140.8	14.2	1060	17	US-10-437-963-62449	Sequence 62449, A
	125	140.6	14.2	1058	9	US-09-452-239-11	Sequence 11, Appl
	126	139.6	14.1	1506	18	US-10-425-115-113176	Sequence 113176,
	127	139.4	14.1	792	18	US-10-425-115-140246	Sequence 140246,
	128	135.4	13.7	1281	18	US-10-425-115-138015	Sequence 138015,
	129	134.6	13.6	1052	16	US-10-425-114-24738	Sequence 24738, A
	130	134.6	13.6	1107	18	US-10-425-115-138003	Sequence 138003,
	131	129.6	13.1	1146	18	US-10-425-115-53825	Sequence 53825, A
	132	127.8	12.9	985	16	US-10-425-114-23965	Sequence 23965, A
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	134	127.4	12.9	109519	11	US-09-758-759-1	Sequence 1, Appli
	135	126	12.7	923	9	US-09-452-239-7	Sequence 7, Appli
	136	126	12.7	944	15	US-10-361-460-32	Sequence 32, Appl
	137	126	12.7	1066	18	US-10-425-115-179664	Sequence 179664,
	138	125.4	12.7	1006	16	US-10-425-114-27818	Sequence 27818, A
	139	125	12.6	1051	15	US-10-289-757-146	Sequence 146, App
	140	123.4	12.5	1059	15	US-10-289-757-37	Sequence 36, Appl
	141	122.6	12.4	1063	15	US-10-289-757-37	Sequence 37, Appl
	142	122.2	12.4	1073	18	US-10-425-115-113171	Sequence 113171,
	143	113.4	11.5	781	18	US-10-425-115-53814	Sequence 53814, A
	144	106.4	10.8	343	9	US-09-917-800A-275	Sequence 275, App
c	145	103.6	10.5	343	16	US-10-152-319A-298	Sequence 298, App
c	146	103.6	10.5	343	15	US-10-152-319A-298	Sequence 298, App
	147	101.4	10.3	672	15	US-10-156-761-5814	Sequence 5814, Ap
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	149	97.4	9.8	593	18	US-10-425-115-106605	Sequence 106605,
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443	52.4	5.3	1891	15	US-10-007-926A-234	Sequence 234, App	516	51.8	5.2	4469	18	US-10-788-792-21	Sequence 21, Appl
444	52.4	5.3	1891	18	US-10-684-422-210	Sequence 210, App	517	51.8	5.2	4469	18	US-10-473-974-203	Sequence 203, App
445	52.4	5.3	3114	17	US-10-437-963-28971	Sequence 28971, A	518	51.8	5.2	4469	18	US-10-817-525-1	Sequence 1, Appl
446	52.4	5.3	5117	15	US-10-172-118-24	Sequence 24, Appl	519	51.6	5.2	786	15	US-10-156-761-4529	Sequence 4529, App
447	52.4	5.3	5117	16	US-10-342-887-24	Sequence 24, Appl	520	51.6	5.2	893	15	US-10-180-375-107	Sequence 107, App
448	52.4	5.3	5204	16	US-10-037-417-7	Sequence 7, Appl	521	51.6	5.2	893	15	US-10-183-687-123	Sequence 123, App
449	52.4	5.3	5403	16	US-10-112-344-583	Sequence 583, App	522	51.6	5.2	1177	17	US-10-437-963-12093	Sequence 12093, A
450	52.4	5.3	5640	15	US-10-037-270-41	Sequence 41, Appl	523	51.6	5.2	1242	16	US-10-282-122A-25883	Sequence 25883, A
451	52.4	5.3	5640	15	US-10-117-722-41	Sequence 41, Appl	524	51.6	5.2	2055	15	US-10-369-493-35729	Sequence 35729, A
452	52.4	5.3	8296	14	US-10-037-182-35	Sequence 35, Appl	525	51.6	5.2	2211	17	US-10-437-963-63253	Sequence 63253, A
453	52.4	5.3	11091	15	US-10-312-088-9	Sequence 9, Appl	526	51.6	5.2	2283	16	US-10-109-048-1143	Sequence 1143, App
454	52.4	5.3	11118	15	US-10-312-088-8	Sequence 8, Appl	527	51.6	5.2	2865	17	US-10-156-761-6107	Sequence 6107, App
455	52.4	5.3	12338	14	US-10-205-032-15	Sequence 15, Appl	528	51.6	5.2	2973	15	US-10-200-562-13968	Sequence 13968, A
456	52.4	5.3	13350	14	US-10-037-182-1	Sequence 1, Appl	529	51.6	5.2	9369	15	US-10-437-963-63253	Sequence 63253, A
457	52.4	5.3	13367	16	US-10-112-352-58	Sequence 58, Appl	530	51.6	5.2	9369	15	US-10-237-551-190	Sequence 247, App
458	52.4	5.3	13640	16	US-10-112-944-103	Sequence 103, App	531	51.6	5.2	9369	15	US-10-237-551-247	Sequence 247, App
459	52.4	5.3	14520	15	US-10-156-761-2885	Sequence 2885, App	532	51.6	5.2	9369	15	US-10-425-115-15006	Sequence 165006, A
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461	52.4	5.3	897	17	US-10-156-761-15102	Sequence 15102, A	534	51.4	5.2	1130	17	US-10-437-963-79440	Sequence 5404, App
462	52.2	5.3	897	17	US-10-437-963-54305	Sequence 54305, A	535	51.4	5.2	1230	15	US-10-156-761-5404	Sequence 6586, App
463	52.2	5.3	1126	17	US-10-767-701-13291	Sequence 13291, A	536	51.4	5.2	1359	15	US-10-156-761-6586	Sequence 6587, App
464	52.2	5.3	1193	16	US-10-425-114-24011	Sequence 24011, A	537	51.4	5.2	1359	15	US-10-156-761-6587	Sequence 60807, A
465	52.2	5.3	1308	18	US-10-425-115-49576	Sequence 49576, A	538	51.4	5.2	1510	17	US-10-437-963-60807	Sequence 3330, App
466	52.2	5.3	1671	17	US-10-437-963-65581	Sequence 65581, A	539	51.4	5.2	1629	15	US-10-156-761-3330	Sequence 99040, A
467	52.2	5.3	1687	18	US-10-425-115-71979	Sequence 71979, A	540	51.4	5.2	2021	17	US-10-437-963-99040	Sequence 81510, A
468	52.2	5.3	1746	15	US-10-156-761-4388	Sequence 4388, App	541	51.4	5.2	2031	17	US-10-437-963-81510	Sequence 11169, A
469	52.2	5.3	2505	15	US-10-369-493-31754	Sequence 31754, A	542	51.4	5.2	2526	18	US-10-723-860-818	Sequence 818, App
470	52.2	5.3	2757	16	US-10-282-122A-26027	Sequence 26027, A	543	51.4	5.2	2526	18	US-10-723-860-5422	Sequence 5422, App
471	52.2	5.3	6297	15	US-10-132-134-37	Sequence 37, Appl	544	51.4	5.2	4725	15	US-10-205-032-17	Sequence 17, Appl
472	52	5.3	1062	17	US-10-767-701-9233	Sequence 9233, App	545	51.4	5.2	6891	17	US-10-437-963-54940	Sequence 5940, App
473	52	5.3	1065	15	US-10-156-761-6270	Sequence 6270, App	546	51.4	5.2	7847	16	US-10-302-172-591	Sequence 2884, App
474	52	5.3	1159	17	US-10-437-963-54428	Sequence 54428, A	547	51.4	5.2	11817	15	US-10-156-761-2884	Sequence 2, Appl
475	52	5.3	1218	15	US-10-214-446-37	Sequence 37, Appl	548	51.4	5.2	30000	12	US-09-980-217-2	Sequence 4334, App
476	52	5.3	1230	15	US-10-156-761-6139	Sequence 6139, App	549	51.4	5.2	447	11	US-09-732-627A-4334	Sequence 3105, App
477	52	5.3	1449	18	US-10-425-115-161558	Sequence 161558, A	550	51.2	5.2	507	17	US-10-437-963-12968	Sequence 1739, App
478	52	5.3	1459	17	US-10-437-963-26984	Sequence 26984, A	551	51.2	5.2	507	17	US-10-437-963-12968	Sequence 841, App
479	52	5.3	1491	10	US-09-899-575-99	Sequence 99, Appl	552	51.2	5.2	522	15	US-10-156-761-3105	Sequence 12968, A
480	52	5.3	1556	16	US-10-425-114-19808	Sequence 19808, A	553	51.2	5.2	522	15	US-10-156-761-3105	Sequence 2043, App
481	52	5.3	1586	16	US-10-425-114-14339	Sequence 14339, A	554	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 14710, A
482	52	5.3	1707	15	US-10-156-761-47239	Sequence 4723, App	555	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 1946, App
483	52	5.3	3597	15	US-10-156-761-1751	Sequence 1751, App	556	51.2	5.2	792	9	US-09-770-445-841	Sequence 421, App
484	52	5.3	672	15	US-10-156-761-1819	Sequence 1819, App	557	51.2	5.2	898	17	US-10-437-963-12968	Sequence 15750, A
485	51.8	5.2	918	15	US-10-156-761-6700	Sequence 15076, A	558	51.2	5.2	1002	15	US-10-156-761-421	Sequence 2577, App
486	51.8	5.2	1227	16	US-10-282-132A-15076	Sequence 1322, App	559	51.2	5.2	1107	16	US-10-282-122A-14710	Sequence 89570, A
487	51.8	5.2	1253	13	US-10-087-192-1322	Sequence 43202, A	560	51.2	5.2	1134	15	US-10-156-761-3946	Sequence 73981, A
488	51.8	5.2	1344	15	US-10-156-761-1108	Sequence 1108, App	561	51.2	5.2	1188	15	US-10-425-115-15750	Sequence 3, Appl
489	51.8	5.2	1347	15	US-10-369-493-43202	Sequence 43202, A	562	51.2	5.2	1267	18	US-10-437-963-89571	Sequence 89571, A
490	51.8	5.2	1593	15	US-10-156-761-5226	Sequence 5226, App	563	51.2	5.2	1493	18	US-10-739-930-3025	Sequence 3025, App
491	51.8	5.2	1640	16	US-10-425-114-32254	Sequence 32254, A	564	51.2	5.2	2034	9	US-09-815-242-8002	Sequence 8002, App
492	51.8	5.2	1645	16	US-10-425-114-30266	Sequence 30266, A	565	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6391, App
493	51.8	5.2	1659	15	US-10-369-493-39901	Sequence 39901, A	566	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 15103, App
494	51.8	5.2	1677	15	US-10-369-493-39150	Sequence 39150, A	567	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 2553, App
495	51.8	5.2	1677	15	US-10-369-493-39150	Sequence 39150, A	568	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 101015, A
496	51.8	5.2	1677	15	US-10-369-493-39150	Sequence 39150, A	569	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 2948, App
497	51.8	5.2	1704	18	US-10-739-930-2739	Sequence 2739, App	570	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 16086, A
498	51.8	5.2	1779	15	US-10-156-761-1559	Sequence 1559, App	571	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 2979, App
499	51.8	5.2	1796	17	US-10-437-963-43317	Sequence 43317, A	572	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 1045, App
500	51.8	5.2	1803	18	US-10-425-115-133999	Sequence 133999, A	573	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6041, App
501	51.8	5.2	1880	17	US-10-437-963-23751	Sequence 23751, A	574	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 25509, A
502	51.8	5.2	1894	17	US-10-437-963-89370	Sequence 89370, A	575	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 1244, App
503	51.8	5.2	2075	15	US-10-138-434A-2	Sequence 2, Appl	576	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 39, Appl
504	51.8	5.2	2075	15	US-10-425-586-1	Sequence 1, Appl	577	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 32171, A
505	51.8	5.2	2075	16	US-10-466-136-1	Sequence 1, Appl	578	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 42117, A
506	51.8	5.2	2145	16	US-10-282-122A-31855	Sequence 2737, App	579	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 5063, App
507	51.8	5.2	2322	18	US-10-739-930-2737	Sequence 2737, App	580	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 130993, A
508	51.8	5.2	2847	15	US-10-156-761-2404	Sequence 2404, App	581	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 4813, App
509	51.8	5.2	4462	9	US-09-974-298-28	Sequence 28, Appl	582	51.2	5.2	2067	15	US-10-156-761-6391	
510	51.8	5.2	4469	9	US-09-796-008-1	Sequence 1, Appl	583	51.2	5.2	2067	15	US-10-156-761-6391	
511	51.8	5.2	4469	15	US-10-133-937-42	Sequence 42, Appl	584	51.2	5.2	2067	15	US-10-156-761-6391	
512	51.8	5.2	4469	15	US-10-172-118-857	Sequence 857, App	585	51.2	5.2	2067	15	US-10-156-761-6391	
513	51.8	5.2	4469	16	US-10-159-563-42	Sequence 42, App	586	51.2	5.2	2067	15	US-10-156-761-6391	
514	51.8	5.2	4469	16	US-10-342-887-857	Sequence 857, App	587	51.2	5.2	2067	15	US-10-156-761-6391	
515	51.8	5.2	4469	18	US-10-786-720-15	Sequence 15, Appl	588	51.2	5.2	2067	15	US-10-156-761-6391	



589	51	5.2	2561	9	US-09-976-740-48	Sequence 48, Appl	662	50.2	5.1	4826	17	US-10-717-381-1	Sequence 1, Appl
590	51	5.2	2561	13	US-10-023-529-48	Sequence 48, Appl	c 663	50	5.1	390	9	US-09-960-352-14023	Sequence 14023, A
591	51	5.2	2561	13	US-10-023-523-48	Sequence 48, Appl	c 664	50	5.1	1020	17	US-10-437-963-98512	Sequence 98512, A
592	51	5.2	2561	16	US-10-616-187-48	Sequence 48, Appl	665	50	5.1	1057	18	US-10-425-114-24158	Sequence 24158, A
593	51	5.2	2561	16	US-10-671-242-48	Sequence 48, Appl	666	50	5.1	1213	18	US-10-425-115-122558	Sequence 122558, A
594	51	5.2	2601	17	US-10-437-963-72883	Sequence 72883, A	667	50	5.1	1217	17	US-10-437-963-37456	Sequence 37456, A
595	51	5.2	2710	16	US-10-250-613-33	Sequence 33, Appl	668	50	5.1	1317	15	US-10-369-493-31645	Sequence 31645, A
596	51	5.2	2765	17	US-10-437-963-2941	Sequence 2941, Appl	669	50	5.1	1337	15	US-10-369-493-42992	Sequence 42992, A
597	51	5.2	3606	15	US-10-156-761-3063	Sequence 3063, Appl	670	50	5.1	1365	16	US-10-282-122A-13750	Sequence 13750, A
598	50.8	5.1	819	15	US-10-156-761-4765	Sequence 4765, Appl	c 671	50	5.1	1582	18	US-10-739-930-2333	Sequence 2333, Appl
599	50.8	5.1	1125	16	US-10-282-122A-31378	Sequence 31378, A	672	50	5.1	1806	15	US-10-329-079-28	Sequence 28, Appl
600	50.8	5.1	1155	15	US-10-193-002-12	Sequence 12, Appl	673	50	5.1	1806	15	US-10-329-079-29	Sequence 29, Appl
601	50.8	5.1	1155	15	US-10-084-843-12	Sequence 12, Appl	674	50	5.1	1860	15	US-10-156-761-6889	Sequence 6889, Appl
602	50.8	5.1	1178	16	US-10-260-238-706	Sequence 706, Appl	675	50	5.1	2148	15	US-10-369-493-42943	Sequence 42943, A
603	50.8	5.1	1188	15	US-10-156-761-421	Sequence 421, Appl	676	50	5.1	3012	17	US-10-437-963-78726	Sequence 78726, A
604	50.8	5.1	1230	17	US-10-437-963-96421	Sequence 96421, A	677	50	5.1	3135	15	US-10-156-761-2721	Sequence 2721, A
605	50.8	5.1	1317	9	US-09-815-242-4148	Sequence 4148, Appl	678	50	5.1	3374	17	US-10-437-963-10004	Sequence 10004, A
606	50.8	5.1	1317	16	US-10-282-122A-7337	Sequence 7337, Appl	679	50	5.1	5061	17	US-10-437-963-9832	Sequence 9832, Appl
607	50.8	5.1	1479	9	US-09-887-576-820	Sequence 820, Appl	c 680	50	5.1	10692	15	US-10-156-761-414	Sequence 414, Appl
608	50.8	5.1	1551	15	US-10-156-761-1622	Sequence 1622, Appl	681	50	5.1	13842	9	US-09-861-289-30	Sequence 30, Appl
609	50.8	5.1	1682	18	US-10-479-638-10	Sequence 10, Appl	682	50	5.1	13842	9	US-09-860-846-30	Sequence 30, Appl
610	50.8	5.1	2230	17	US-10-437-963-65821	Sequence 65821, A	683	50	5.1	13842	10	US-09-988-3848-30	Sequence 30, Appl
611	50.8	5.1	5760	14	US-10-152-886-14	Sequence 14, Appl	684	50	5.1	13842	10	US-09-836-821-30	Sequence 30, Appl
612	50.8	5.1	10000	15	US-10-156-761-15103	Sequence 15103, A	685	50	5.1	13842	15	US-10-271-889-30	Sequence 30, Appl
613	50.6	5.1	508	9	US-09-452-239-15	Sequence 15, Appl	686	50	5.1	15738	15	US-10-329-079-12	Sequence 12, Appl
614	50.6	5.1	940	18	US-10-425-115-176490	Sequence 176490, A	687	50	5.1	32329	16	US-10-374-903A-1	Sequence 1, Appl
615	50.6	5.1	1032	17	US-10-437-963-36005	Sequence 36005, A	688	50	5.1	36778	9	US-09-861-289-5	Sequence 5, Appl
616	50.6	5.1	1041	15	US-10-156-761-7418	Sequence 7418, Appl	689	50	5.1	36778	9	US-09-860-846-5	Sequence 5, Appl
617	50.6	5.1	1371	16	US-10-282-122A-25436	Sequence 25436, A	690	50	5.1	36778	10	US-09-836-821-5	Sequence 5, Appl
618	50.6	5.1	1400	18	US-10-425-115-20597	Sequence 20597, A	691	50	5.1	36778	15	US-10-271-889-48	Sequence 48, Appl
619	50.6	5.1	1449	17	US-10-437-963-64629	Sequence 64629, A	692	50	5.1	37360	15	US-10-329-079-6	Sequence 6, Appl
620	50.6	5.1	1695	15	US-10-156-761-3949	Sequence 3949, Appl	693	50	5.1	37948	10	US-09-988-3848-5	Sequence 5, Appl
621	50.6	5.1	1848	17	US-10-437-963-22612	Sequence 22612, A	694	50	5.1	38506	15	US-09-793-708-19	Sequence 19, Appl
622	50.6	5.1	2300	18	US-10-425-115-134362	Sequence 134362, A	695	50	5.1	38506	15	US-10-201-365-1	Sequence 1, Appl
623	50.6	5.1	2477	18	US-10-425-115-170055	Sequence 170055, A	696	50	5.1	38506	15	US-10-160-539-19	Sequence 19, Appl
624	50.6	5.1	2741	18	US-10-425-115-148395	Sequence 148395, A	c 697	50	5.1	29354	9	US-09-785-400-84	Sequence 9, Appl
625	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, A	698	49.8	5.0	856	9	US-09-823-245A-99	Sequence 99, Appl
626	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, A	699	49.8	5.0	880	16	US-10-425-114-32836	Sequence 32836, A
627	50.6	5.1	4233	18	US-10-723-860-4143	Sequence 4143, Appl	c 700	49.8	5.0	915	15	US-10-156-761-2013	Sequence 2013, Appl
628	50.6	5.1	4244	16	US-10-723-860-8016	Sequence 8016, Appl	701	49.8	5.0	940	16	US-10-425-114-35300	Sequence 35300, A
629	50.4	5.1	549	16	US-10-260-238-239	Sequence 239, Appl	702	49.8	5.0	948	18	US-10-425-115-43218	Sequence 43218, A
630	50.4	5.1	645	15	US-10-156-761-6059	Sequence 6059, Appl	703	49.8	5.0	1227	15	US-10-156-761-6074	Sequence 6074, Appl
631	50.4	5.1	662	17	US-10-437-963-74146	Sequence 74146, A	704	49.8	5.0	1245	11	US-09-758-759-22	Sequence 22, Appl
632	50.4	5.1	669	15	US-10-107-431-166	Sequence 166, Appl	705	49.8	5.0	1272	15	US-10-107-431-32	Sequence 32, Appl
633	50.4	5.1	777	18	US-10-425-115-83763	Sequence 83763, A	706	49.8	5.0	1293	14	US-10-145-415-17	Sequence 17, Appl
634	50.4	5.1	838	18	US-10-425-115-127687	Sequence 127687, A	707	49.8	5.0	1374	16	US-10-282-122A-14455	Sequence 14455, A
635	50.4	5.1	891	17	US-10-437-963-41595	Sequence 41595, A	708	49.8	5.0	1410	17	US-10-437-963-97868	Sequence 97868, A
636	50.4	5.1	1062	17	US-10-437-963-34793	Sequence 34793, A	709	49.8	5.0	1440	15	US-10-156-761-5216	Sequence 5216, Appl
637	50.4	5.1	1159	16	US-10-374-780A-879	Sequence 879, Appl	710	49.8	5.0	1572	15	US-10-156-761-113	Sequence 113, Appl
638	50.4	5.1	1454	18	US-10-425-115-68094	Sequence 68094, A	711	49.8	5.0	1581	16	US-10-464-368-113	Sequence 42666, A
639	50.4	5.1	1587	15	US-10-156-761-5134	Sequence 5134, Appl	712	49.8	5.0	1694	17	US-10-437-963-42666	Sequence 42666, A
640	50.4	5.1	1848	15	US-10-156-761-3850	Sequence 3850, Appl	713	49.8	5.0	1791	15	US-10-156-761-2352	Sequence 2352, Appl
641	50.4	5.1	1910	17	US-10-437-963-23941	Sequence 23941, A	714	49.8	5.0	1814	14	US-10-060-036-182	Sequence 182, Appl
642	50.4	5.1	1951	17	US-10-437-963-31078	Sequence 31078, A	715	49.8	5.0	1929	9	US-09-761-534A-9	Sequence 9, Appl
643	50.4	5.1	2082	15	US-10-156-761-6082	Sequence 6082, Appl	716	49.8	5.0	2031	15	US-10-156-761-2451	Sequence 2451, Appl
644	50.4	5.1	3048	15	US-10-156-761-3146	Sequence 3146, Appl	717	49.8	5.0	2115	15	US-10-156-761-5640	Sequence 5640, Appl
645	50.4	5.1	3456	17	US-10-437-963-50711	Sequence 50711, A	718	49.8	5.0	2136	17	US-10-437-963-49142	Sequence 49142, A
646	50.4	5.1	5003	17	US-10-437-963-18350	Sequence 18350, A	719	49.8	5.0	2520	17	US-09-873-367C-159	Sequence 159, Appl
647	50.4	5.1	6375	16	US-10-389-647-144	Sequence 144, Appl	c 720	49.8	5.0	2535	17	US-10-437-963-11953	Sequence 11953, A
648	50.4	5.1	14427	15	US-10-156-761-1540	Sequence 1540, Appl	721	49.8	5.0	2664	15	US-10-156-761-1241	Sequence 1241, Appl
649	50.4	5.1	45055	15	US-10-107-431-277	Sequence 277, Appl	722	49.8	5.0	3066	15	US-10-156-761-1742	Sequence 1742, Appl
650	50.2	5.1	595	16	US-10-260-238-3262	Sequence 3262, Appl	723	49.8	5.0	3113	14	US-09-894-998-52	Sequence 52, Appl
651	50.2	5.1	740	17	US-10-437-963-67956	Sequence 67956, A	724	49.8	5.0	3113	15	US-10-121-988-52	Sequence 52, Appl
652	50.2	5.1	841	16	US-10-282-122A-14618	Sequence 14618, A	725	49.8	5.0	3113	15	US-10-200-562-52	Sequence 52, Appl
653	50.2	5.1	1002	15	US-10-156-761-696	Sequence 696, Appl	726	49.8	5.0	3113	15	US-10-237-551-52	Sequence 52, Appl
654	50.2	5.1	1093	18	US-10-425-115-106454	Sequence 106454, A	727	49.8	5.0	3345	9	US-09-894-998-49	Sequence 49, Appl
655	50.2	5.1	1426	17	US-10-437-963-1435	Sequence 1435, Appl	728	49.8	5.0	3345	14	US-10-121-988-49	Sequence 49, Appl
656	50.2	5.1	1586	17	US-10-437-963-59660	Sequence 59660, A	729	49.8	5.0	3345	15	US-10-200-562-49	Sequence 49, Appl
657	50.2	5.1	1896	15	US-10-156-761-5658	Sequence 5658, Appl	730	49.8	5.0	3345	15	US-10-200-562-189	Sequence 189, Appl
658	50.2	5.1	2856	17	US-10-437-963-61943	Sequence 61943, A	731	49.8	5.0	3345	15	US-10-237-551-49	Sequence 49, Appl
659	50.2	5.1	3032	17	US-10-437-963-16502	Sequence 16502, A	732	49.8	5.0	3345	15	US-10-237-551-189	Sequence 189, Appl
660	50.2	5.1	3039	15	US-10-369-493-42391	Sequence 42391, A	733	49.8	5.0	4323	16	US-10-282-122A-26577	Sequence 26577, A
661	50.2	5.1	4826	9	US-09-772-304A-1	Sequence 1, Appl	c 734	49.8	5.0	37116	15	US-10-107-431-279	Sequence 279, Appl



735	49.8	5.0	65140	17	US-10-203-295-1	Sequence 1, Appli	808	49.4	5.0	2091	15	US-10-237-551-78	Sequence 78, Appl
736	49.6	5.0	125401	17	US-10-203-295-35	Sequence 35, Appl	809	49.4	5.0	2091	15	US-10-237-551-226	Sequence 226, App
737	49.6	5.0	242	9	US-09-923-876-781	Sequence 781, App	810	49.4	5.0	2118	14	US-10-121-988-87	Sequence 87, Appl
738	49.6	5.0	242	10	US-09-923-876-781	Sequence 781, App	811	49.4	5.0	2118	15	US-10-200-562-87	Sequence 87, Appl
739	49.6	5.0	746	16	US-10-425-114-12136	Sequence 12136, A	812	49.4	5.0	2118	15	US-10-200-562-87	Sequence 87, Appl
740	49.6	5.0	806	17	US-10-425-114-12136	Sequence 12136, A	813	49.4	5.0	2211	14	US-10-121-988-86	Sequence 86, Appl
C 740	49.6	5.0	806	17	US-10-425-114-12136	Sequence 12136, A	813	49.4	5.0	2211	15	US-10-200-562-86	Sequence 86, Appl
C 741	49.6	5.0	876	18	US-10-425-114-13780	Sequence 13780, A	814	49.4	5.0	2211	15	US-10-200-562-86	Sequence 86, Appl
742	49.6	5.0	976	16	US-10-425-114-13780	Sequence 13780, A	815	49.4	5.0	2211	15	US-10-200-562-86	Sequence 86, Appl
743	49.6	5.0	976	16	US-10-425-114-13780	Sequence 13780, A	815	49.4	5.0	2211	15	US-10-200-562-86	Sequence 86, Appl
744	49.6	5.0	978	15	US-10-156-761-6381	Sequence 6381, Ap	C 816	49.4	5.0	2270	17	US-10-437-963-53336	Sequence 53336, A
745	49.6	5.0	981	17	US-10-437-963-58326	Sequence 58326, A	817	49.4	5.0	2502	16	US-10-282-122A-17902	Sequence 17902, A
746	49.6	5.0	1089	15	US-10-156-761-2655	Sequence 2655, Ap	818	49.4	5.0	2517	15	US-10-437-963-53336	Sequence 53336, A
C 746	49.6	5.0	1089	15	US-10-156-761-2655	Sequence 2655, Ap	818	49.4	5.0	2517	15	US-10-437-963-53336	Sequence 53336, A
C 747	49.6	5.0	1176	16	US-10-425-114-21556	Sequence 21556, A	819	49.4	5.0	3038	15	US-10-251-661-11	Sequence 11, Appl
748	49.6	5.0	1194	17	US-10-425-114-21556	Sequence 21556, A	820	49.4	5.0	3038	15	US-10-251-661-11	Sequence 11, Appl
749	49.6	5.0	1205	17	US-10-437-963-102262	Sequence 102262, A	821	49.4	5.0	3331	10	US-09-373-658-31	Sequence 31, Appl
750	49.6	5.0	1329	15	US-10-437-963-84924	Sequence 84924, A	822	49.4	5.0	3331	11	US-09-373-658-31	Sequence 31, Appl
751	49.6	5.0	1329	15	US-10-437-963-84924	Sequence 84924, A	823	49.4	5.0	3352	18	US-10-425-115-84048	Sequence 84048, A
752	49.6	5.0	1362	15	US-10-156-761-5851	Sequence 5851, Ap	824	49.4	5.0	3489	11	US-09-894-273-1	Sequence 1, Appli
753	49.6	5.0	1404	16	US-10-282-122A-33594	Sequence 33594, A	C 825	49.4	5.0	3489	15	US-10-294-804-1	Sequence 1, Appli
754	49.6	5.0	1651	17	US-10-369-493-31750	Sequence 31750, A	C 826	49.4	5.0	3489	15	US-10-294-804-1	Sequence 1, Appli
755	49.6	5.0	1743	15	US-10-437-963-23386	Sequence 23386, A	827	49.4	5.0	4255	16	US-10-282-122A-14875	Sequence 14875, A
756	49.6	5.0	1743	15	US-10-437-963-23386	Sequence 23386, A	828	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
757	49.6	5.0	1761	16	US-10-342-887-1387	Sequence 1387, Ap	829	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
758	49.6	5.0	1765	15	US-10-342-887-1387	Sequence 1387, Ap	C 830	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
C 758	49.6	5.0	1765	15	US-10-342-887-1387	Sequence 1387, Ap	C 830	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
759	49.6	5.0	1929	17	US-10-156-761-1503	Sequence 1503, Ap	831	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
760	49.6	5.0	2040	9	US-10-237-551-225	Sequence 225, App	C 832	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
761	49.6	5.0	2040	9	US-10-237-551-225	Sequence 225, App	C 832	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
762	49.6	5.0	2059	17	US-10-437-963-70663	Sequence 70663, A	C 833	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
763	49.6	5.0	2059	17	US-10-437-963-70663	Sequence 70663, A	C 833	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
764	49.6	5.0	2271	15	US-10-437-963-88743	Sequence 88743, A	C 834	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
C 764	49.6	5.0	2271	15	US-10-437-963-88743	Sequence 88743, A	C 834	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
C 765	49.6	5.0	2471	15	US-09-815-242-4027	Sequence 4027, Ap	C 835	49.2	5.0	955	16	US-10-425-114-17203	Sequence 17203, A
C 766	49.6	5.0	2471	15	US-09-815-242-4027	Sequence 4027, Ap	C 835	49.2	5.0	955	16	US-10-425-114-17203	Sequence 17203, A
C 767	49.6	5.0	2487	15	US-10-282-122A-7316	Sequence 7316, Ap	836	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
C 768	49.6	5.0	2487	15	US-10-282-122A-7316	Sequence 7316, Ap	836	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
C 769	49.6	5.0	2700	15	US-10-437-963-59377	Sequence 59377, A	C 837	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
770	49.6	5.0	2700	15	US-10-437-963-59377	Sequence 59377, A	C 837	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
771	49.6	5.0	2742	9	US-10-437-963-31244	Sequence 31244, A	C 838	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
772	49.6	5.0	2742	9	US-10-437-963-31244	Sequence 31244, A	C 838	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
773	49.6	5.0	3459	15	US-10-101-510-133	Sequence 101-510-133	C 839	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
774	49.6	5.0	3459	15	US-10-101-510-133	Sequence 101-510-133	C 839	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
775	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
776	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
777	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
778	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
779	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
780	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
781	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
782	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
783	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
784	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
785	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
786	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
787	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
788	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
789	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
790	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
791	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
792	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
793	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
794	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
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796	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
797	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
798	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
799	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
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801	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
802	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
803	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
804	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
805	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
806	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App
807	49.6	5.0	3459	15	US-10-437-963-62969	Sequence 62969, A	840	49.2	5.0	1051	18	US-10-332-859-324	Sequence 324, App



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882	49	5.0	2067	17	US-10-437-963-18405	Sequence 18405, A	955	48.6	4.9	847	18	US-10-425-115-41717	Sequence 41717, A
883	49	5.0	2143	16	US-10-425-114-23617	Sequence 23617, A	956	48.6	4.9	934	16	US-10-425-114-17266	Sequence 17266, A
C 884	49	5.0	2204	17	US-10-437-963-11022	Sequence 11022, A	957	48.6	4.9	974	16	US-10-425-114-18881	Sequence 18881, A
885	49	5.0	2239	16	US-10-425-114-5232	Sequence 5232, Ap	958	48.6	4.9	1107	18	US-10-425-115-18817	Sequence 18817, A
886	49	5.0	2271	17	US-10-437-963-74809	Sequence 74809, A	959	48.6	4.9	1143	15	US-10-425-115-162747	Sequence 162747, A
C 887	49	5.0	2439	15	US-10-156-761-2569	Sequence 2569, Ap	960	48.6	4.9	1170	18	US-10-425-115-162747	Sequence 162747, A
888	49	5.0	2536	18	US-10-425-115-91117	Sequence 91117, A	961	48.6	4.9	1203	15	US-10-369-493-34414	Sequence 34414, A
C 889	49	5.0	2939	17	US-10-437-963-58050	Sequence 58050, A	962	48.6	4.9	1302	18	US-10-425-115-164928	Sequence 164928, A
C 890	49	5.0	12425	9	US-09-976-740-50	Sequence 50, Appl	963	48.6	4.9	1366	18	US-10-425-115-28293	Sequence 28293, A
C 891	49	5.0	12425	13	US-10-023-529-50	Sequence 50, Appl	964	48.6	4.9	1453	17	US-10-437-963-78719	Sequence 78719, A
C 892	49	5.0	12425	13	US-10-023-523-50	Sequence 50, Appl	965	48.6	4.9	1461	15	US-10-156-761-2205	Sequence 2205, Ap
C 893	49	5.0	12425	16	US-10-616-187-50	Sequence 50, Appl	966	48.6	4.9	1479	13	US-10-016-283-35	Sequence 35, Appl
C 894	49	5.0	12425	16	US-10-671-242-50	Sequence 50, Appl	967	48.6	4.9	1533	18	US-09-814-353-20197	Sequence 20197, A
C 895	49	5.0	77536	10	US-09-940-316B-1	Sequence 1, Appl	968	48.6	4.9	1637	18	US-10-425-115-164014	Sequence 164014, A
896	48.8	4.9	363	15	US-10-156-761-5224	Sequence 5224, Ap	969	48.6	4.9	1685	16	US-10-425-114-27558	Sequence 27558, A
C 897	48.8	4.9	389	18	US-10-425-115-178702	Sequence 178702, A	970	48.6	4.9	1783	17	US-10-437-963-340	Sequence 340, App
C 898	48.8	4.9	458	17	US-10-437-963-3998	Sequence 3998, Ap	971	48.6	4.9	1839	11	US-09-758-759-150	Sequence 150, App
C 899	48.8	4.9	513	15	US-10-156-761-5057	Sequence 5057, Ap	972	48.6	4.9	1962	17	US-10-437-963-89753	Sequence 89753, A
900	48.8	4.9	516	17	US-10-437-963-75898	Sequence 75898, A	973	48.6	4.9	2040	9	US-09-874-923-5	Sequence 5, Appl
901	48.8	4.9	602	18	US-10-425-115-172234	Sequence 172234, A	974	48.6	4.9	2040	9	US-09-991-496-5	Sequence 72, Appl
902	48.8	4.9	618	15	US-10-156-761-4061	Sequence 4061, Ap	975	48.6	4.9	2040	15	US-10-098-732A-72	Sequence 35019, A
903	48.8	4.9	728	16	US-10-425-114-14002	Sequence 14002, A	976	48.6	4.9	2238	17	US-10-437-963-35019	Sequence 68, Appl
904	48.8	4.9	827	16	US-10-425-114-18832	Sequence 18832, A	977	48.6	4.9	2279	15	US-10-021-660-68	Sequence 212, App
905	48.8	4.9	828	15	US-10-156-761-1422	Sequence 1422, Ap	978	48.6	4.9	2279	16	US-10-211-462-212	Sequence 9, Appl
906	48.8	4.9	933	15	US-10-156-761-1758	Sequence 1758, Ap	979	48.6	4.9	2577	17	US-10-332-413-9	Sequence 4, Appl
907	48.8	4.9	1068	15	US-10-156-761-1861	Sequence 1861, Ap	980	48.6	4.9	2712	17	US-09-748-033-4	Sequence 4, Appl
908	48.8	4.9	1094	16	US-10-425-114-3	Sequence 3, Appl	981	48.6	4.9	3298	16	US-10-362-247-4	Sequence 4, Appl
909	48.8	4.9	1095	17	US-10-767-701-13435	Sequence 13435, A	982	48.6	4.9	3872	17	US-10-437-963-57556	Sequence 57556, A
910	48.8	4.9	1125	16	US-10-425-114-14054	Sequence 14054, A	983	48.6	4.9	3975	15	US-10-156-761-4112	Sequence 4112, Ap
C 911	48.8	4.9	1164	17	US-10-425-115-109968	Sequence 109968, A	984	48.6	4.9	5065	14	US-10-067-457-4	Sequence 4, Appl
912	48.8	4.9	1164	17	US-10-767-701-12837	Sequence 12837, A	985	48.6	4.9	5499	16	US-10-276-774-973	Sequence 973, App
913	48.8	4.9	1194	15	US-10-214-446-33	Sequence 33, Appl	986	48.4	4.9	562	15	US-10-174-693-53	Sequence 53, Appl
914	48.8	4.9	1224	16	US-10-425-114-21138	Sequence 21138, A	987	48.4	4.9	642	15	US-10-156-761-6149	Sequence 6149, Ap
915	48.8	4.9	1272	15	US-10-107-431-262	Sequence 262, App	988	48.4	4.9	651	15	US-10-156-761-6890	Sequence 6890, Ap
916	48.8	4.9	1290	17	US-10-767-701-9008	Sequence 9008, Ap	989	48.4	4.9	800	18	US-10-425-115-25676	Sequence 25676, A
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918	48.8	4.9	1392	15	US-10-156-761-4350	Sequence 4350, Ap	991	48.4	4.9	1059	16	US-10-259-165-215	Sequence 215, App
919	48.8	4.9	1455	16	US-10-425-114-31249	Sequence 31249, A	992	48.4	4.9	1164	16	US-10-425-114-21717	Sequence 21717, A
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931	48.8	4.9	9167	16	US-10-359-120-171	Sequence 171, App	1004	48.4	4.9	2892	15	US-10-156-761-3066	Sequence 3066, Ap
932	48.8	4.9	9169	16	US-10-359-120-169	Sequence 169, App	1005	48.4	4.9	3377	17	US-10-437-963-92668	Sequence 92668, A
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934	48.8	4.9	9189	16	US-10-359-120-155	Sequence 155, App	1007	48.4	4.9	4833	16	US-10-282-122A-25605	Sequence 25605, A
935	48.8	4.9	9194	16	US-10-359-120-163	Sequence 163, App	1008	48.4	4.9	6779	17	US-10-437-963-29812	Sequence 29812, A
936	48.8	4.9	9194	16	US-10-359-120-164	Sequence 164, App	1009	48.4	4.9	24081	15	US-10-132-134-13	Sequence 13, Appl
937	48.8	4.9	9407	16	US-10-359-120-173	Sequence 173, App	1010	48.4	4.9	31263	16	US-10-282-122A-25447	Sequence 25447, A
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939	48.8	4.9	9783	16	US-10-359-120-172	Sequence 172, App	1012	48.2	4.9	480	17	US-10-437-963-48143	Sequence 48143, A
940	48.8	4.9	9785	16	US-10-359-120-176	Sequence 176, App	1013	48.2	4.9	553	18	US-10-425-115-82149	Sequence 82149, A
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942	48.8	4.9	9792	15	US-10-359-120-170	Sequence 170, App	1015	48.2	4.9	729	18	US-10-425-115-154823	Sequence 154823, A
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944	48.8	4.9	12411	16	US-10-359-120-165	Sequence 165, App	1017	48.2	4.9	786	16	US-10-260-238-458	Sequence 458, App
945	48.8	4.9	18435	15	US-10-156-761-412	Sequence 156, App	1018	48.2	4.9	789	16	US-10-425-114-27917	Sequence 27917, A
946	48.8	4.9	135638	15	US-10-314-657-1	Sequence 412, App	1019	48.2	4.9	811	18	US-10-489-372-40	Sequence 40, Appl
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948	48.6	4.9	528	9	US-09-452-239-33	Sequence 33, Appl	1021	48.2	4.9	823	14	US-10-153-668-54	Sequence 56, Appl
949	48.6	4.9	623	17	US-10-437-963-5272	Sequence 5272, Ap	1022	48.2	4.9	825	16	US-10-282-122A-25820	Sequence 25820, A
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C 951	48.6	4.9	687	16	US-10-282-122A-26299	Sequence 26299, A	1024	48.2	4.9	861	15	US-10-156-761-3921	Sequence 3921, Ap
C 952	48.6	4.9	690	16	US-10-282-122A-28509	Sequence 28509, A	1025	48.2	4.9	920	15	US-10-037-270-132	Sequence 132, App
953	48.6	4.9	761	18	US-10-425-115-127921	Sequence 127921, A	1026	48.2	4.9	920	15	US-10-117-722-132	Sequence 132, App



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1030	48.2	4.9	969	10	US-09-789-831-3	Sequence 3, Appli	1103	48	4.9	1128	17	US-10-782-596-15	Sequence 15, Appl
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1032	48.2	4.9	1038	10	US-09-789-831-2	Sequence 2, Appli	1105	48	4.9	1155	15	US-10-369-493-42888	Sequence 42888, A
1033	48.2	4.9	1038	15	US-10-251-661-9	Sequence 9, Appli	1106	48	4.9	1158	16	US-10-425-114-22832	Sequence 22832, A
1034	48.2	4.9	1038	16	US-10-410-888-3	Sequence 3, Appli	1107	48	4.9	1164	16	US-10-425-114-22171	Sequence 21171, A
1035	48.2	4.9	1038	16	US-10-159-563-166	Sequence 166, App	1108	48	4.9	1175	16	US-10-425-114-1930	Sequence 1930, Ap
1036	48.2	4.9	1038	17	US-10-415-325-22	Sequence 22, Appl	1109	48	4.9	1186	18	US-10-425-115-84443	Sequence 84443, A
1037	48.2	4.9	1042	10	US-09-789-831-17	Sequence 17, Appl	1110	48	4.9	1188	15	US-10-246-330-9	Sequence 9, Appli
1038	48.2	4.9	1059	16	US-10-389-647-304	Sequence 304, App	1111	48	4.9	1232	16	US-10-425-114-17219	Sequence 17219, A
1039	48.2	4.9	1151	18	US-10-425-115-175028	Sequence 175028, A	1112	48	4.9	1236	17	US-10-437-963-95996	Sequence 95996, A
1040	48.2	4.9	1215	15	US-10-156-761-2811	Sequence 2811, Ap	1113	48	4.9	1257	17	US-10-767-701-11943	Sequence 11943, A
1041	48.2	4.9	1347	15	US-10-156-761-6038	Sequence 6038, Ap	1114	48	4.9	1275	16	US-10-282-122A-25779	Sequence 25779, A
1042	48.2	4.9	1566	18	US-10-817-483-30	Sequence 30, Appl	1115	48	4.9	1297	18	US-10-425-115-14015	Sequence 14015, A
1043	48.2	4.9	1638	17	US-10-437-963-82416	Sequence 82416, A	1116	48	4.9	1313	16	US-10-425-114-33638	Sequence 33638, A
1044	48.2	4.9	1670	17	US-10-767-701-13989	Sequence 13989, A	1117	48	4.9	1392	15	US-10-156-761-2601	Sequence 2601, Ap
1045	48.2	4.9	1710	15	US-10-156-761-2318	Sequence 2318, Ap	1118	48	4.9	1433	15	US-10-369-493-42370	Sequence 42370, A
1046	48.2	4.9	1818	17	US-10-437-963-55757	Sequence 55757, A	1119	48	4.9	1533	18	US-10-425-115-161561	Sequence 161561, A
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1057	48.2	4.9	1994	10	US-09-851-673-1	Sequence 1, Appli	1130	48	4.9	3435	11	US-09-758-759-166	Sequence 166, App
1058	48.2	4.9	1994	16	US-10-628-841-3	Sequence 3, Appli	1131	48	4.9	3489	9	US-09-815-242-7731	Sequence 7731, Ap
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1061	48.2	4.9	2034	18	US-10-761-370-2	Sequence 2, Appli	1134	48	4.9	487	16	US-10-374-780A-1253	Sequence 1253, Ap
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1063	48.2	4.9	2130	18	US-10-425-115-114288	Sequence 114288, A	1136	47.8	4.8	627	15	US-10-156-761-6579	Sequence 6579, Ap
1064	48.2	4.9	2595	16	US-10-282-122A-14998	Sequence 14998, A	1137	47.8	4.8	702	17	US-10-437-963-14724	Sequence 14724, A
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1067	48.2	4.9	3350	15	US-10-200-562-48	Sequence 48, Appl	1140	47.8	4.8	888	15	US-10-156-761-5898	Sequence 5898, Ap
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1071	48.2	4.9	4542	16	US-10-282-122A-28674	Sequence 28674, A	1144	47.8	4.8	1075	18	US-10-425-115-5563	Sequence 5563, Ap
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1073	48.2	4.9	6979	15	US-10-132-134-11	Sequence 11, Appl	1146	47.8	4.8	1179	16	US-10-425-114-14395	Sequence 14395, A
1074	48.2	4.9	20922	10	US-09-942-025-14	Sequence 14, Appl	1147	47.8	4.8	1191	18	US-10-425-115-79775	Sequence 79775, A
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1078	48.2	4.9	67311	10	US-09-942-025-1	Sequence 1, Appli	1151	47.8	4.8	1404	16	US-10-282-122A-25706	Sequence 25706, A
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1081	48	4.9	353	18	US-10-425-115-98452	Sequence 98452, A	1154	47.8	4.8	1527	16	US-10-282-122A-25749	Sequence 25749, A
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1083	48	4.9	579	17	US-09-758-759-174	Sequence 174, App	1156	47.8	4.8	1612	17	US-10-437-963-15030	Sequence 15030, A
1084	48	4.9	652	17	US-10-767-701-5497	Sequence 5497, Ap	1157	47.8	4.8	1671	11	US-09-758-759-102	Sequence 102, App
1085	48	4.9	712	18	US-10-363-345A-27449	Sequence 27449, A	1158	47.8	4.8	1711	18	US-10-425-115-58741	Sequence 58741, A
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1087	48	4.9	753	11	US-09-758-759-193	Sequence 193, App	1160	47.8	4.8	1771	9	US-09-991-496-7	Sequence 7, Appli
1088	48	4.9	756	15	US-10-107-431-132	Sequence 132, App	1161	47.8	4.8	2256	17	US-10-437-963-86656	Sequence 86656, A
1089	48	4.9	833	16	US-10-369-493-33233	Sequence 33233, A	1162	47.8	4.8	2387	17	US-10-437-963-38072	Sequence 38072, A
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1091	48	4.9	888	17	US-10-425-115-24687	Sequence 24687, A	1164	47.8	4.8	2895	17	US-10-437-963-66971	Sequence 66971, A
1092	48	4.9	954	15	US-10-437-963-98299	Sequence 98299, A	1165	47.8	4.8	3824	15	US-10-116-275-197	Sequence 197, App
1093	48	4.9	954	15	US-10-156-761-4757	Sequence 4757, Ap	1166	47.8	4.8	3824	16	US-10-159-563-307	Sequence 307, App
1094	48	4.9	1128	10	US-09-875-076-15	Sequence 15, Appl	1167	47.8	4.8	3824	16	US-10-723-860-2600	Sequence 2600, Ap
1095	48	4.9	1128	10	US-09-875-076-15	Sequence 15, Appl	1168	47.8	4.8	3824	18	US-10-723-860-6734	Sequence 6734, Ap
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1098	48	4.9	1128	15	US-10-272-983-15	Sequence 15, Appl	1171	47.8	4.8	71989	9	US-10-727-889-2	Sequence 2, Appli
1099	48	4.9	1128	15	US-10-393-807-15	Sequence 15, Appl	1172	47.8	4.8	71989	18	US-10-849-462-2	Sequence 2, Appli



c1173	47.6	4.8	524	17	US-10-437-963-873	Sequence 873, App	1258	47.4	4.8	670	15	US-10-132-350-31	Sequence 31, Appl
1174	47.6	4.8	633	15	US-10-369-493-4191	Sequence 4191, A	1259	47.4	4.8	693	15	US-10-156-761-1183	Sequence 1183, Ap
1175	47.6	4.8	780	15	US-10-156-761-6288	Sequence 6288, Ap	1260	47.4	4.8	862	17	US-10-767-701-10425	Sequence 10425, A
1176	47.6	4.8	878	16	US-10-425-114-15378	Sequence 15378, A	1261	47.4	4.8	931	17	US-10-437-963-91705	Sequence 91705, A
1177	47.6	4.8	891	15	US-10-156-761-7285	Sequence 7285, Ap	1262	47.4	4.8	958	17	US-10-437-963-86145	Sequence 86145, A
c1178	47.6	4.8	921	16	US-10-282-122A-7524	Sequence 7524, Ap	1263	47.4	4.8	996	15	US-10-156-761-7396	Sequence 7396, Ap
c1179	47.6	4.8	967	18	US-10-425-115-66497	Sequence 66497, A	c1264	47.4	4.8	1050	17	US-10-767-701-12642	Sequence 12642, A
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c1181	47.6	4.8	1002	16	US-10-259-194A-618	Sequence 618, App	1266	47.4	4.8	1203	15	US-10-156-761-4664	Sequence 4664, Ap
c1182	47.6	4.8	1026	16	US-10-242-535A-53529	Sequence 53529, A	1267	47.4	4.8	1256	18	US-10-425-115-73921	Sequence 73921, Ap
c1183	47.6	4.8	1026	16	US-10-085-783A-53529	Sequence 53529, A	1268	47.4	4.8	1345	16	US-10-425-114-24692	Sequence 24692, A
1184	47.6	4.8	1049	14	US-10-123-155-358	Sequence 358, App	1269	47.4	4.8	1404	16	US-10-282-122A-15189	Sequence 15189, A
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1198	47.6	4.8	1110	15	US-10-156-761-4246	Sequence 4246, Ap	1271	47.4	4.8	1438	18	US-10-425-115-84149	Sequence 84149, A
1199	47.6	4.8	1176	15	US-10-369-493-40494	Sequence 40494, A	1272	47.4	4.8	1443	15	US-10-156-761-3397	Sequence 3397, Ap
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c1201	47.6	4.8	1257	17	US-10-437-963-64185	Sequence 64185, A	1274	47.4	4.8	1649	17	US-10-437-963-89113	Sequence 89113, A
c1202	47.6	4.8	1282	16	US-10-425-114-23644	Sequence 23644, A	1275	47.4	4.8	1672	17	US-10-437-963-81182	Sequence 81182, A
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1204	47.6	4.8	1344	16	US-10-425-114-16346	Sequence 16346, A	c1277	47.4	4.8	1723	17	US-10-437-963-11515	Sequence 11515, A
c1205	47.6	4.8	1376	17	US-10-437-963-10544	Sequence 10544, A	1278	47.4	4.8	1734	16	US-10-282-122A-25721	Sequence 25721, A
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1207	47.6	4.8	1410	15	US-10-369-493-42819	Sequence 42819, A	1280	47.4	4.8	1848	15	US-10-156-761-3041	Sequence 3041, Ap
1208	47.6	4.8	1469	16	US-10-425-114-31292	Sequence 31292, A	1281	47.4	4.8	1900	17	US-10-437-963-28228	Sequence 28228, A
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c1211	47.6	4.8	1661	17	US-10-437-963-12797	Sequence 12797, A	1284	47.4	4.8	2076	15	US-10-156-761-5585	Sequence 5585, Ap
1212	47.6	4.8	1689	16	US-10-425-114-17162	Sequence 17162, A	1285	47.4	4.8	2124	17	US-10-437-963-57642	Sequence 57642, A
1213	47.6	4.8	1713	17	US-10-324-967-33	Sequence 33, Appl	c1286	47.4	4.8	2181	17	US-10-437-963-102020	Sequence 102020, A
1214	47.6	4.8	1956	15	US-10-156-761-5591	Sequence 5591, Ap	1287	47.4	4.8	2316	15	US-10-156-761-4416	Sequence 4416, Ap
1215	47.6	4.8	1970	16	US-10-425-114-22993	Sequence 22993, A	1288	47.4	4.8	2354	16	US-10-425-114-28070	Sequence 28070, A
1216	47.6	4.8	1971	15	US-10-190-435-49	Sequence 49, Appl	1289	47.4	4.8	2354	18	US-10-425-115-33746	Sequence 33746, A
1217	47.6	4.8	1971	15	US-10-241-009-38	Sequence 38, Appl	1290	47.4	4.8	2354	18	US-10-715-872-155	Sequence 155, App
1218	47.6	4.8	1971	15	US-10-190-434B-38	Sequence 38, Appl	1291	47.4	4.8	2463	16	US-10-282-122A-13810	Sequence 13810, A
1219	47.6	4.8	1971	15	US-10-190-305A-48	Sequence 48, Appl	1292	47.4	4.8	2565	15	US-10-425-114-3437	Sequence 3437, Ap
1220	47.6	4.8	1971	15	US-10-190-305A-54	Sequence 54, Appl	c1293	47.4	4.8	2699	17	US-10-437-963-1877	Sequence 1877, Ap
c1221	47.6	4.8	2111	17	US-10-437-963-31473	Sequence 31473, A	1294	47.4	4.8	2883	16	US-10-282-122A-11335	Sequence 11335, A
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1223	47.6	4.8	2305	15	US-10-387-336-80	Sequence 80, Appl	1296	47.4	4.8	3633	15	US-10-289-757-130	Sequence 130, App
1224	47.6	4.8	2306	15	US-10-387-336-82	Sequence 82, Appl	1297	47.4	4.8	8244	15	US-10-402-842-3	Sequence 3, Appl
1225	47.6	4.8	2337	16	US-10-282-122A-25485	Sequence 25485, A	1298	47.4	4.8	8244	15	US-10-402-842-1	Sequence 1, Appl
1226	47.6	4.8	2424	16	US-10-282-122A-15037	Sequence 15037, A	1299	47.4	4.8	8798	15	US-09-808-880-1	Sequence 1, Appl
1227	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl	c1300	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl
1228	47.6	4.8	2457	15	US-10-190-305A-38	Sequence 38, Appl	c1301	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl
1229	47.6	4.8	2463	10	US-089-575-31	Sequence 31, Appl	c1302	47.4	4.8	137560	18	US-10-481-112-1	Sequence 1, Appl
1230	47.6	4.8	2466	15	US-10-241-009-31	Sequence 31, Appl	1303	47.2	4.8	564	17	US-10-437-963-72922	Sequence 72922, A
1231	47.6	4.8	2466	15	US-10-190-434B-31	Sequence 31, Appl	1304	47.2	4.8	619	18	US-10-425-115-183789	Sequence 183789, A
1232	47.6	4.8	2466	15	US-10-190-305A-33	Sequence 33, Appl	1305	47.2	4.8	852	16	US-10-282-122A-11557	Sequence 11557, A
c1233	47.6	4.8	2466	15	US-09-894-998-35	Sequence 35, Appl	1306	47.2	4.8	867	18	US-10-425-115-105816	Sequence 105816, A
c1234	47.6	4.8	2481	14	US-10-121-988-35	Sequence 35, Appl	1307	47.2	4.8	918	15	US-10-156-761-5990	Sequence 5990, Ap
c1235	47.6	4.8	2481	15	US-10-200-562-35	Sequence 35, Appl	1308	47.2	4.8	962	17	US-10-767-701-9413	Sequence 9413, Ap
c1236	47.6	4.8	2481	15	US-10-237-551-35	Sequence 35, Appl	1309	47.2	4.8	1011	18	US-10-425-115-135441	Sequence 135441, A
1237	47.6	4.8	2652	15	US-10-369-493-42921	Sequence 42921, A	1310	47.2	4.8	1014	15	US-10-156-761-5551	Sequence 5551, Ap
c1238	47.6	4.8	3066	14	US-10-121-988-152	Sequence 152, App	1311	47.2	4.8	1017	15	US-10-156-761-4338	Sequence 4338, Ap
c1239	47.6	4.8	3066	15	US-10-200-562-152	Sequence 152, App	1312	47.2	4.8	1134	16	US-10-282-122A-14824	Sequence 14824, A
c1240	47.6	4.8	3066	15	US-10-237-551-152	Sequence 152, App	c1313	47.2	4.8	1152	15	US-10-156-761-1776	Sequence 1776, Ap
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1244	47.6	4.8	5886	18	US-10-152-886-84	Sequence 84, Appl	1317	47.2	4.8	1237	18	US-10-425-115-137466	Sequence 137466, A
1245	47.6	4.8	6008	17	US-10-798-037-3	Sequence 3, Appl	1318	47.2	4.8	1266	15	US-10-156-761-6436	Sequence 6436, Ap
1246	47.6	4.8	6008	17	US-10-336-472-21	Sequence 21, Appl	1319	47.2	4.8	1374	16	US-10-425-115-119307	Sequence 119307, A
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1248	47.6	4.8	10692	15	US-10-156-761-414	Sequence 414, App	1321	47.2	4.8	1382	18	US-10-425-115-120130	Sequence 120130, A
1249	47.6	4.8	12801	18	US-10-798-037-5	Sequence 5, Appl	1322	47.2	4.8	1386	15	US-10-369-493-42300	Sequence 42300, A
c1250	47.6	4.8	2541	17	US-10-203-295-2	Sequence 2, Appl	1323	47.2	4.8	1395	16	US-10-282-122A-14398	Sequence 14398, A
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1253	47.4	4.8	463	17	US-10-767-701-559	Sequence 559, App	1326	47.2	4.8	1431	15	US-10-156-761-7327	Sequence 7327, Ap
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c1485	46.6	4.7	1855	17	US-10-437-963-78779	Sequence 78779, A
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1488	46.6	4.7	1992	15	US-10-156-761-7241	Sequence 7241, Ap
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1494	46.6	4.7	3876	17	US-10-437-963-61988	Sequence 61988, A
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1496	46.6	4.7	5721	15	US-10-156-761-2880	Sequence 2880, Ap
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Maximum Match 100%

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Database :

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9: gb\_pr.\*

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11: gb\_ro.\*

12: gb\_sy.\*

13: gb\_sy.\*

14: gb\_vl.\*

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# SUMMARIES

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2	989	100.0	989	6	AX697237 Sequence
3	989	100.0	989	9	AX358476 Homo sapi
4	985.8	99.7	1037	6	AX338454 Sequence
5	985.8	99.7	1041	9	BC047774 Homo sapi
6	981.8	99.3	985	6	BD22712 Homo sapi
7	938.2	94.9	988	9	AK074421 Human sig
8	907.8	91.8	913	9	BC023663 Homo sapi
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11	625	63.2	946	10	BC049670 Mus muscu
12	312	31.5	326	6	AX407985 Sequence
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18	200	20.2	14100	1	MX024657 U24657 Myxococcus
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20	193.8	19.6	675	6	CQ801150 Sequence
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23	185.8	18.8	2381	6	E06690
24	185.4	18.7	304282	1	AE016910 Chromobac
25	185	18.7	663	12	AY657514 Synthetic
26	182.4	18.4	69644	1	AY179507 Streptomy
27	161.8	16.4	953	6	AR236716 Sequence
28	161.8	16.4	953	8	BT009394 Trifitum
29	159.6	16.1	976	8	AB110168 Oryza sat
30	159.6	16.1	996	8	AK104326 Oryza sat
31	159.6	16.1	1096	8	AK104801 Oryza sat
32	159.6	16.1	1098	8	AK071482 Oryza sat
33	159.2	16.1	1049	6	AR236715 Sequence
34	158.6	16.0	997	6	AR236700 Sequence
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36	157.2	15.9	1078	6	AR236714 Sequence
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38	155.6	15.7	1018	6	AR236711 Sequence
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41	153	15.5	77534	1	AF235504 Streptomy
42	153	15.5	77536	6	BD235937 Polyketid
43	153	15.5	77536	6	AR271638 Sequence
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45	152.4	15.4	1218	6	AX146637 Sequence
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47	150.2	15.2	1158	8	AY644637 Oryza sat
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49	150.2	15.2	137354	8	AP000364 Oryza sat
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52	148	15.0	1118	8	BT009186 Trifitum
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54	148	15.0	1145	6	AR236695 Sequence
55	146.8	14.8	10882	1	AE002493 Neisseria
56	146.8	14.8	34980	6	AX044032 Sequence
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58	146.2	14.8	1018	8	BT009093 Trifitum
59	145	14.7	959	8	AK108479 Oryza sat
60	144.6	14.6	329861	1	NNA522491 Neisseria
61	144.4	14.6	1057	6	AR236696 Sequence
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63	141.8	14.3	783	6	AX654528 Sequence
64	141.8	14.3	1149	8	AK061757 Oryza sat
65	140.6	14.2	1058	6	AR236699 Sequence
66	140	14.2	783	6	AX654276 Sequence
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69	128.2	13.0	237221	1	AP003599 Nostoc sp
70	127.4	12.9	651	6	AX196012 Sequence
71	127.4	12.9	109519	6	AX195929 Sequence
72	126	12.7	923	6	AR236697 Sequence
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74	123.2	12.5	300465	1	AE016962 Coccidia
75	122.8	12.4	1810	6	E09625 Streptomyce
76	122.8	12.4	3267	1	STMACYA
77	118.6	12.0	201	11	BV202015 sqm20798
78	118.6	12.0	8988	2	AY294423 Continuation (4 of
79	118.6	12.0	161371	10	AC132590 Mus muscu
80	116.8	11.8	188267	2	AC137230 Rattus no
81	116.8	11.8	228354	2	AC137429 Rattus no
82	116.8	11.8	266634	2	AC123487 Rattus no
83	110	11.1	1013	8	AF168780 Eucalyptu
84	110	11.1	1944	1	AF145250 Rhodother
85	109.8	11.1	1006	8	AF046122 Eucalyptu
86	109.8	11.1	1068	8	EG12228 Continuation (4 of
87	109.6	11.1	110000	2	AC105718 Continuation (4 of
88	107.8	10.9	486	8	AY651026 Boehmeria
89	107.4	10.9	304282	1	AE016910 Chromobac
90	106.2	10.7	976	8	VVCCOAMT Z54233 V.vinifera
91	103.6	10.5	343	6	AX400599 Sequence
92	102	10.3	134199	1	SYCSLRF D64004 Synechocyst



c	93	101.4	10.3	300425	1	AP005044	Streptomy	166	82.2	8.3	105815	8	AP002536	Oryza sat
	94	99.4	10.1	300800	1	SC0939112	Al939112	167	82.2	8.3	156054	8	AB023482	Oryza sat
	95	98.4	9.9	772	8	FVAJ1447	Al001447	168	81	8.2	622	8	AB076979	Avena sat
	96	96.8	9.8	1012	6	B2243370	B2243370	169	79.6	8.0	1258	6	A22706	Caffeoyl-Co
	97	96.8	9.8	1012	6	B2243370	B2243370	170	79.2	8.0	1258	6	A22706	Caffeoyl-Co
	98	96.8	9.8	1012	6	AR216420	AR216420	171	78	7.9	1098	8	AY128822	Arabidops
	99	96.8	9.8	1026	6	AR432822	AR432822	172	78	7.9	1185	8	AY087981	Arabidops
	100	96.8	9.8	1026	6	AR066484	AR066484	173	78	7.9	1201	8	AY093172	Arabidops
	101	96.8	9.8	1026	6	AR074097	AR074097	174	77.4	7.8	837	8	AY094008	Arabidops
	102	96.8	9.8	1026	6	AR143609	AR143609	175	77.4	7.8	837	8	AY070483	Arabidops
	103	96.8	9.8	1026	6	BD224282	BD224282	176	76.2	7.7	760	6	AR074116	Sequence
	104	96.8	9.8	1026	6	AR432734	AR432734	177	76.2	7.7	760	6	BD224301	Materials
	105	96.8	9.8	1026	6	BD005645	BD005645	178	76.2	7.7	760	6	BD224301	Materials
	106	96.8	9.8	1172	8	AV279007	AV279007	179	76.2	7.7	760	6	AR432753	Sequence
	107	96.4	9.7	1136	8	AV279011	AV279011	180	76.2	7.7	760	6	BD005664	Materials
	108	96.4	9.7	1136	8	AV279011	AV279011	181	76.2	7.7	760	6	BD005664	Materials
	109	96.4	9.7	1150	8	AV279012	AV279012	182	75.8	7.7	1046	8	PTU27116	Populus tre
	110	96.4	9.7	1150	8	AV279013	AV279013	183	74.8	7.6	816	8	AF022775	Populus tre
	111	96.4	9.7	1150	8	AV279030	AV279030	184	74.4	7.5	929	6	AR236703	Sequence
	112	96.4	9.7	1150	8	AV279033	AV279033	185	74.4	7.5	1104	8	AF053553	Meembrya
	113	96.4	9.7	1150	8	AV279035	AV279035	186	74.2	7.5	726	8	AF240466	Populus t
	114	95.2	9.6	1172	8	AV279006	AV279006	187	73.8	7.5	920	4	AY340812	Canis fam
	115	95.2	9.6	1172	8	AV279025	AV279025	188	73.8	7.5	1834	8	AK105550	Oryza sat
	116	95.2	9.6	1172	8	AV279027	AV279027	189	73.8	7.5	2768	8	AK109619	Oryza sat
	117	95.2	9.6	1180	6	AX798857	AX798857	190	73.8	7.5	170021	8	AP003256	Oryza sat
	118	95.2	9.6	1182	8	AV279009	AV279009	191	73.8	7.5	176261	8	AP003274	Oryza sat
	119	95.2	9.6	1438	8	AV279021	AV279021	192	73.4	7.4	145828	8	AP005392	Oryza sat
	120	95.2	9.6	1442	8	AV279019	AV279019	193	73.4	7.4	154188	8	AP005633	Oryza sat
	121	95.2	9.6	1444	8	AV279017	AV279017	194	73.2	7.4	870	6	AR225246	Sequence
	122	95.2	9.6	1445	8	AV279018	AV279018	195	72.8	7.4	706	8	PBA130811	Populus b
	123	95.2	9.6	1445	8	AV279022	AV279022	196	72.6	7.3	1213	9	BC011935	Populus b
	124	95.2	9.6	1451	8	AV279004	AV279004	197	71.8	7.3	280558	1	AE017301	Thermus t
	125	95.2	9.6	1451	8	AV279020	AV279020	198	71.6	7.2	744	8	AF327458	Populus a
	126	95.2	9.6	1463	8	AV279016	AV279016	199	71.2	7.2	601	11	BV167609	sgm95100
	127	95.2	9.6	1464	8	AV279015	AV279015	200	71.2	7.2	2084	11	BV177509	sgm95100
	128	94.6	9.6	1152	8	AV279032	AV279032	201	71.2	7.2	2084	11	BV177509	sgm95100
	129	94.6	9.6	1152	8	AV279032	AV279032	202	71.2	7.2	2084	11	BV177509	sgm95100
	130	93.4	9.4	675	6	AR390021	AR390021	203	71	7.2	816	9	CR456997	Homo sapi
	131	93	9.4	1136	8	AV279034	AV279034	204	71	7.2	1025	8	PBTJ4894	Populus b
	132	93	9.4	1136	8	AV279010	AV279010	205	71	7.2	1107	6	CO812330	Sequence
	133	93	9.4	1181	8	AV279005	AV279005	206	71	7.2	1291	6	CO716680	Sequence
	134	93	9.4	1181	8	AV279024	AV279024	207	70.6	7.1	918	8	ZEU13151	Zinnia eleg
	135	93	9.4	1181	8	AV279026	AV279026	208	70.6	7.1	2084	11	BV177077	Rattus no
	136	93	9.4	1206	8	AV279008	AV279008	209	70.4	7.1	189038	2	AC120323	Sequence
	137	93	9.4	1206	8	AV279028	AV279028	210	70	7.1	811	6	AR225247	Sequence
	138	93	9.4	1209	8	AV279028	AV279028	211	69.8	7.1	5222	1	DRU52145	Deinococcus
	139	93	9.4	1222	8	AV279029	AV279029	212	69.6	7.0	60090	1	U30252	Synechococc
	140	93	9.4	1232	8	AF036095	AF036095	213	69.4	7.0	873	9	CR456422	Homo sapi
	141	93	9.4	1434	8	AV279014	AV279014	214	69.4	7.0	1206	6	AX774876	Sequence
	142	88	8.9	931	6	AR236702	AR236702	215	69.4	7.0	1206	6	AX774876	Sequence
	143	87.8	8.9	534	6	AR236717	AR236717	216	69.2	7.0	297850	1	AP006577	Homo sapien
	144	87.4	8.8	1210	8	AK063541	AK063541	217	68	6.9	976	11	PM12D6G	Populus b
	145	87.2	8.8	2955	1	AF075724	AF075724	218	67.8	6.9	1217	9	BC000419	Homo sapi
	146	86.2	8.7	347660	1	AP002994	AP002994	219	67.8	6.9	1217	9	BC005867	Homo sapi
	147	85.6	8.7	962	6	AR236705	AR236705	220	67.8	6.9	239130	2	AC079420	Mus muscu
	148	85.6	8.7	1023	6	AR236706	AR236706	221	67.6	6.8	930	8	AB000408	Populus k
	149	85.4	8.6	6020	8	AY098515	AY098515	222	67.4	6.8	890	8	AY145521	Meembrya
	150	85.4	8.6	125020	9	AF429315	AF429315	223	67.4	6.8	12454	1	AE002019	Deinococc
	151	84.4	8.5	939	8	PBTJ4896	PBTJ4896	224	67.2	6.8	132151	8	AC144491	Oryza sat
	152	84.4	8.5	963	8	AY620245	AY620245	225	67.2	6.8	160738	8	AC073556	Oryza sat
	153	84.4	8.5	1049	8	PBTJ4895	PBTJ4895	226	67	6.8	160738	8	AC073556	Oryza sat
	154	84	8.5	780	6	CO805684	CO805684	227	67	6.8	110000	2	LMFLCHR32_06	Coffea ca
	155	84	8.5	780	6	CO805684	CO805684	228	67	6.8	110000	2	LMFLCHR32_06	Continuation (7 of
	156	84	8.5	780	8	AY143979	AY143979	229	67	6.8	110000	2	LMFLCHR32_06	Continuation (32 of
	157	84	8.5	815	8	AY081457	AY081457	230	67	6.8	110000	2	LMFLCHR32_06	Continuation (32 of
	158	84	8.5	999	8	AY062630	AY062630	231	66.8	6.8	1023	8	AB061268	Homo sapi
	159	84	8.5	1033	8	AY057554	AY057554	232	66.8	6.8	1074	6	AR074145	Solanum t
	160	83.6	8.5	1033	8	AY088577	AY088577	233	66.8	6.8	1074	6	AR074145	Solanum t
	161	82.8	8.4	1258	6	IR2681	IR2681	234	66.8	6.8	1074	6	AR216380	Sequence
	162	82.8	8.4	1258	6	IR2681	IR2681	235	66.8	6.8	1074	6	AR432782	Sequence
	163	82.8	8.4	1258	6	IR2681	IR2681	236	66.8	6.8	1074	6	BD005693	Materials
	164	82.6	8.4	125020	9	PUMCCOAMT	PUMCCOAMT	237	66.8	6.8	1074	6	BD005693	Materials
	165	82.2	8.3	1272	8	AY644636	AY644636	238	66.8	6.8	1075	6	BD224331	Materials



239	66.8	6.8	1075	6	AR216381	Sequence	AR216381	Sequence	312	60.8	6.1	1578	6	A38265	A38265 Sequence 1
240	66.8	6.8	1075	6	AR432783	Sequence	AR432783	Sequence	313	60.8	6.1	1578	6	AR001081	AR001081 Sequence
241	66.8	6.8	1075	6	BD005694	Materials	BD005694	Materials	c 314	60.8	6.1	2357	14	AY363172	AY363172 Pseudorab
242	66.8	6.8	33950	1	SC0939108	Streptomy	AL939108	Streptomy	315	60.8	6.1	2510	14	SH1UL2XA	M95285 Suid herpes
243	66.6	6.7	13533	1	AF257324	Streptomy	AF257324	Streptomy	c 316	60.8	6.1	9182	14	SH1ULGNS	L00676 Pseudorabie
244	66.4	6.7	744	6	C0760958	Sequence	C0760958	Sequence	c 317	60.8	6.1	300316	8	AE016894	AE016894 Eremothec
245	66.4	6.7	744	6	AX259371	Sequence	AX259371	Sequence	c 318	60.6	6.1	9117	8	AY087244	AY087244 Arabidops
246	66.4	6.7	966	8	MS020736	Sequence	U20736	Medicago sa	319	60.6	6.1	7413	1	PAAPRAPG	X64558 Pseudomonas
247	66.4	6.7	1906	6	C0760964	Sequence	C0760964	Sequence	320	60.6	6.1	11588	1	AE004554	AE004554 Pseudomon
248	66.4	6.7	8600	2	AC136951	Sequence	AC136951	Leighmani	c 321	60.6	6.1	201050	1	AL646064	AL646064 Ralstonia
249	66.4	6.7	346301	1	BX640432	Bordetell	BX640432	Bordetell	322	60.6	6.1	298550	1	AP005029	AP005029 Streptomy
250	66.4	6.7	348642	1	BX640446	Bordetell	BX640446	Bordetell	323	60.6	6.1	301068	1	AE017231	AE017231 Mycobacte
251	66.2	6.7	912	6	AR236707	Sequence	AR236707	Sequence	c 324	60.6	6.1	1094	11	EW7GL1B	AL685196 Penicilli
252	66	6.7	300425	1	AP005041	Streptomy	AP005041	Streptomy	325	60.4	6.1	10445	1	AE014716	AE014716 Bifidobac
253	66	6.7	300800	1	SC0939112	Streptomy	AL939112	Streptomy	c 326	60.4	6.1	25883	1	AB008466	AB008466 Streptomy
254	65.8	6.7	6375	1	AY632768	Sequence	AY632768	Sequence	c 327	60.4	6.1	136753	2	AC149968	AC149968 Strongylo
255	65.4	6.6	101	11	BV185588	sqm14856	BV185588	sqm14856	328	60.4	6.1	349980	6	AX553951	AX553951 Sequence
256	64.8	6.6	908	8	AY500159	Corchorus	AY500159	Corchorus	329	60.4	6.1	34980	6	AX553951	AX553951 Sequence
257	64.8	6.6	967	6	AR225249	Sequence	AR225249	Sequence	330	60.2	6.1	1007	11	PM3H11G	AL685749 Penicilli
258	64.8	6.6	283100	1	SC0939110	Streptomy	AL939110	Streptomy	331	60.2	6.1	1062	6	BD180422	BD180422 Highly th
259	64.6	6.5	2832	8	AY452532	Chlamydom	AY452532	Chlamydom	c 332	60.2	6.1	3797	14	FVULSGENE	X87247 Pseudorabie
260	64.6	6.5	110000	2	LMFLCHR36_07	Continuation (8 of	Continuation (8 of	Continuation (8 of	333	60.2	6.1	6653	1	AY162971	AY162971 Micromono
261	64.6	6.5	311000	1	SC0939122	Streptomy	AL939122	Streptomy	334	60.2	6.1	211161	2	AC098271	AC098271 Rattus no
262	64.4	6.5	143	6	AX899499	Sequence	AX899499	Sequence	335	60	6.1	729	6	AX507705	AX507705 Sequence
263	64.4	6.5	143	6	BD035032	Sequence	BD035032	Sequence	336	60	6.1	730	8	AY056313	AY056313 Arabidops
264	64.2	6.5	600	6	AR236713	Sequence	AR236713	Sequence	337	60	6.1	956	8	AF360317	AF360317 Arabidops
265	64.2	6.5	346362	1	BX640439	Bordetell	BX640439	Bordetell	c 338	60	6.1	982	6	AR236709	AR236709 Sequence
266	64.2	6.5	346362	1	BX640439	Bordetell	BX640439	Bordetell	c 339	60	6.1	1065	11	PM2B12B	AL684695 Penicilli
267	64	6.5	954	8	AK073585	Oryza sat	AK073585	Oryza sat	340	60	6.1	1227	8	NT282982	Z82982 Nicotina ta
268	64	6.5	1543	8	AK058441	Oryza sat	AK058441	Oryza sat	c 341	60	6.1	1279	11	PM2H12G	AL684840 Penicilli
269	64	6.5	85130	2	AC074054	Sequence	AC074054	Sequence	342	60	6.1	123019	9	AC111006	AC111006 Homo sapi
270	64	6.5	135876	8	AC113337	Genomic s	AC113337	Genomic s	c 343	60	6.1	277000	1	SC0939109	AL939109 Streptomy
271	64	6.5	145110	2	AC074355	Oryza sat	AC074355	Oryza sat	344	59.8	6.0	1242	6	BD180349	BD180349 Highly th
272	64	6.5	181419	8	AC148515	Sus scrof	AC148515	Sus scrof	345	59.6	6.0	399	6	BD224470	BD224470 Materiala
273	64	6.5	299986	1	AE017240	Mycobacte	AE017240	Mycobacte	346	59.6	6.0	399	6	AR216520	AR216520 Sequence
274	64	6.5	305096	8	AE017062	Oryza sat	AE017062	Oryza sat	c 347	59.6	6.0	956	11	PM2B12B	AL684743 Penicilli
275	63.8	6.4	12541	1	AE001956	Deinococc	AE001956	Deinococc	348	59.6	6.0	1980	14	AC2NKR24	M18041 Avian trans
276	63.6	6.4	510	6	AR236698	Sequence	AR236698	Sequence	349	59.6	6.0	2253	5	CHKCFOSA	M37000 Chicken c-f
277	63.6	6.4	1279	11	PM2H12G	Sequence	AL684840	Penicilli	350	59.6	6.0	2253	5	CHKCFOSA	M37000 Chicken c-f
278	63.6	6.4	2039	9	AK130031	Homo sapi	AK130031	Homo sapi	351	59.6	6.0	7185	6	AX803764	AX803764 Sequence
279	63.4	6.4	296300	1	AP005035	Streptomy	AP005035	Streptomy	c 352	59.6	6.0	48177	7	AY369265	AY369265 Burkholde
280	63.2	6.4	1016	8	NTCCOAMT	Sequence	Z58282	N.tabacum m	353	59.6	6.0	61944	6	AX803750	AX803750 Sequence
281	63.2	6.4	1065	11	PM2B12B	Sequence	AL684695	Penicilli	c 354	59.6	6.0	110000	1	AE016822_23	Continuation (25 o
282	63.2	6.4	136753	2	AC149968	Streptomy	AL939122	Streptomy	c 355	59.6	6.0	110000	1	AE016822_24	Continuation (25 o
283	63.2	6.4	299425	1	AP005037	Streptomy	AP005037	Streptomy	c 356	59.6	6.0	283100	1	SC0939110	AL939110 Streptomy
284	63.2	6.4	301068	1	AE017231	Mycobacte	AE017231	Mycobacte	c 357	59.6	6.0	295150	1	SC0939125	AL939125 Streptomy
285	63.2	6.4	349672	1	BX640419	Bordetell	BX640419	Bordetell	358	59.6	6.0	308015	1	AE015783	AE015783 Pseudomon
286	63	6.4	135005	9	H8860F19	Human DNA	AL035460	Human DNA	c 359	59.4	6.0	116305	8	AP003992	AP003992 Oryza sat
287	62.8	6.3	2595	10	RATTREX	Sequence	M60647	Rat tropoel	360	59.4	6.0	122615	8	AP005456	AP005456 Oryza sat
288	62.8	6.3	75216	6	AX704275	Sequence	AX704275	Sequence	c 361	59.4	6.0	170051	8	AP005772	AP005772 Oryza sat
289	62.8	6.3	110000	1	AE000516_13	Continuation (14 o	Continuation (14 o	Continuation (14 o	c 362	59.4	6.0	189910	2	AC148233	AC148233 Oryctolag
290	62.8	6.3	299450	1	BX248338	Mycobacte	BX248338	Mycobacte	363	59.4	6.0	197050	1	AL646081	AL646081 Ralstonia
291	62.8	6.3	349306	1	BX842575	Mycobacte	BX842575	Mycobacte	c 364	59.4	6.0	296500	1	SC0939128	AL939128 Streptomy
292	62.6	6.3	1014	8	NTU62734	Sequence	U62734	Nicotiana t	365	59.2	6.0	1791	6	BD179866	BD179866 Highly th
293	62.6	6.3	216050	1	AL646076	Ralstonia	AL646076	Ralstonia	366	59.2	6.0	273285	1	AE017304	AE017304 Thermus t
294	62.6	6.3	348257	1	BX640425	Bordetell	BX640425	Bordetell	367	59.2	6.0	298450	1	SC0939107	AL939107 Streptomy
295	62.4	6.3	110000	1	AE000516_02	Continuation (3 of	Continuation (3 of	Continuation (3 of	368	59	6.0	2531	8	AY341851	AY341851 Oryza sat
296	62.4	6.3	219952	2	AC084804	Mus muscu	AC084804	Mus muscu	369	59	6.0	3152	8	AY341843	AY341843 Oryza sat
297	62.4	6.3	341957	1	BX842572	Mycobacte	BX842572	Mycobacte	370	59	6.0	10800	6	AX512249	AX512249 Sequence
298	62.4	6.3	343050	1	BX248334	Mycobacte	BX248334	Mycobacte	371	59	6.0	10809	6	AX512245	AX512245 Sequence
299	62.2	6.3	300029	1	AE017178	Sequence	AE017178	Sequence	c 372	59	6.0	110000	2	LMFLCHR36_03	Continuation (4 of
300	62.2	6.3	301332	2	AC148913	Streptomy	AL939126	Streptomy	373	59	6.0	139298	8	OSJN00012	AL606441 Oryza sat
301	62	6.3	181718	2	AC148913	Sus scrof	AC148913	Sus scrof	374	59	6.0	277000	1	SC0939109	AL939109 Streptomy
302	62	6.3	295150	1	SC0939126	Streptomy	AL939126	Streptomy	375	58.8	5.9	1393	11	PM11H12G	AL684264 Penicilli
303	61.8	6.2	186752	9	AC111200	Homo sapi	AC111200	Homo sapi	c 376	58.8	5.9	2320	8	AK069799	AK069799 Oryza sat
304	61.8	6.2	281450	1	AP005032	Streptomy	AP005032	Streptomy	c 377	58.8	5.9	2793	8	AK067140	AK067140 Oryza sat
305	61.6	6.2	845	6	AR225248	Sequence	AR225248	Sequence	378	58.8	5.9	3849	6	AX058889	AX058889 Sequence
306	61.6	6.2	276289	1	AE017306	Thermus t	AE017306	Thermus t	379	58.8	5.9	5858	3	AF350276	AF350276 Nephila m
307	61.4	6.2	146111	10	AC132340	Mus muscu	AC132340	Mus muscu	380	58.8	5.9	12744	1	AF204401	AF204401 Streptomy
308	61.2	6.2	302325	1	AE017236	Mycobacte	AE017236	Mycobacte	381	58.8	5.9	187517	5	AY519500	AY519500 Gallus ga
309	61	6.2	976	11	PM1206G	Penicilli	AL684370	Penicilli	c 382	58.8	5.9	247910	1	AE017307	AE017307 Thermus t
310	61	6.2	151085	8	AP003239	Oryza sat	AP003239	Oryza sat	c 383	58.8	5.9	299800	1	AP005040	AP005040 Streptomy
311	61	6.2	292100	1	SC0939121	Streptomy	AL939121	Streptomy	c 384	58.8	5.9	311000	1	SC0939122	AL939122 Streptomy



C 385	58.6	5.9	48024	7	AV368235	AV368235 Burkholder	C 458	57.2	5.8	272101	1	AE017302	AE017302 Thermus t
C 386	58.6	5.9	274676	1	AE017305	AE017305 Thermus t	459	57	5.8	10136	1	AF546156	AF546156 Micromonospora
C 387	58.6	5.9	283308	1	AE017242	AE017242 Mycobacte	460	57	5.8	11219	1	SERERYAA	M63676 Sereny
C 388	58.6	5.9	293050	1	SC0939116	SC0939116 Streptomy	461	57	5.8	11219	6	AR049367	AR049367 Sequence
C 389	58.6	5.9	299925	1	AF005045	AF005045 Streptomy	462	57	5.8	11219	6	AR095528	AR095528 Sequence
C 390	58.6	5.9	300327	1	AE017228	AE017228 Mycobacte	463	57	5.8	38494	6	AR345349	AR345349 Sequence
C 391	58.4	5.9	1288	6	AR007563	AR007563 Sequence	464	57	5.8	38503	1	MSGB1912CS	L01536 M. leprae g
C 392	58.4	5.9	3958	5	CHKROS	CHKROS	465	57	5.8	38675	1	MLU15180	U15180 Mycobacteri
C 393	58.4	5.9	7413	14	PVL50S	PVL50S	466	57	5.8	38675	6	AR345367	AR345367 Sequence
C 394	58.4	5.9	127304	2	AC119051	AC119051 Gallus ga	467	57	5.8	281450	1	AP005032	AP005032 Streptomy
C 395	58.4	5.9	309050	1	SC0939117	SC0939117 Streptomy	468	57	5.8	384450	1	MLEPRTN4	BL583920 Mycobacte
C 396	58.2	5.9	1970	5	GGY17794	GGY17794 Gallus gall	469	57	5.7	990	6	BD179631	BD179631 Highly th
C 397	58.2	5.9	4237	8	D84400	D84400 Oryza sativ	470	57	5.7	1003	8	NTU62735	U62735 Nicotiana t
C 398	58.2	5.9	89976	1	AF363270	AF363270 Actinopla	471	57	5.7	1182	6	AR352531	AR352531 Sequence
C 399	58.2	5.9	94839	2	AC098688	AC098688 Bos tauru	472	57	5.7	1306	8	AY323238	AY323238 Zea mays
C 400	58.2	5.9	197805	2	AC105307	AC105307 Bos tauru	473	57	5.7	1306	8	AY323240	AY323240 Zea mays
C 401	58.2	5.9	295150	1	SC0939125	SC0939125 Streptomy	474	57	5.7	1306	8	AY323262	AY323262 Zea mays
C 402	58.2	5.9	299925	1	AP005039	AP005039 Streptomy	475	57	5.7	1306	8	AY323270	AY323270 Zea mays
C 403	58	5.9	897	6	AX654732	AX654732 Sequence	476	57	5.7	1308	8	AY323269	AY323269 Zea mays
C 404	58	5.9	2329	1	SGHRDT	SGHRDT	477	57	5.7	1309	8	AY323239	AY323239 Zea mays
C 405	58	5.9	2396	1	AF425994	AF425994 Streptomy	478	57	5.7	1309	8	AY323256	AY323256 Zea mays
C 406	58	5.9	10444	14	PVI422133	PVI422133 Suid herp	479	57	5.7	1311	8	AY323267	AY323267 Zea mays
C 407	58	5.9	88421	6	AX417445	AX417445 Sequence	480	57	5.7	1311	8	AY323267	AY323267 Zea mays
C 408	58	5.9	186752	9	AC111200	AC111200 Homo sapi	481	57	5.7	1314	8	AY323253	AY323253 Zea mays
C 409	58	5.9	290850	1	SC0939127	SC0939127 Streptomy	482	57	5.7	1314	8	AY323268	AY323268 Zea mays
C 410	58	5.9	308050	1	SC0939124	SC0939124 Streptomy	483	57	5.7	1320	8	AY323271	AY323271 Zea mays
C 411	57.8	5.8	9678	1	AB110645	AB110645 Streptomy	484	57	5.7	1544	8	AY323246	AY323246 Zea mays
C 412	57.8	5.8	245210	2	AC137771	AC137771 Homo sapi	485	57	5.7	1546	8	AY323244	AY323244 Zea mays
C 413	57.8	5.8	299550	1	AP005031	AP005031 Streptomy	486	57	5.7	2000	6	AX655393	AX655393 Sequence
C 414	57.8	5.8	347894	1	BX640431	BX640431 Bordetell	487	57	5.7	2000	6	AF262754	AF262754 Amycolato
C 415	57.6	5.8	3297	6	BD180129	BD180129 Highly th	488	57	5.7	2000	1	AF262754	AF262754 Amycolato
C 416	57.6	5.8	106873	14	AB096160	AB096160 Cercopith	489	57	5.7	2569	1	AF262754	AF262754 Amycolato
C 417	57.6	5.8	166789	14	AF533768	AF533768 Cercopith	490	57	5.7	2569	1	AF262754	AF262754 Amycolato
C 418	57.6	5.8	166254	2	AC145332	AC145332 Felis cat	491	57	5.7	6584	1	SCPAHCAS	SCPAHCAS
C 419	57.6	5.8	299050	1	SC0939119	SC0939119 Streptomy	492	57	5.7	11604	6	AR352525	AR352525 Sequence
C 420	57.6	5.8	321250	1	SC0939111	SC0939111 Streptomy	493	57	5.7	15079	6	AR352525	AR352525 Sequence
C 421	57.4	5.8	1029	6	BD174410	BD174410 DNA resto	494	57	5.7	15120	1	SCU87786	SCU87786 Streptomyce
C 422	57.4	5.8	1298	8	AY323254	AY323254 Zea mays	495	57	5.7	15120	6	AR352523	AR352523 Sequence
C 423	57.4	5.8	1298	8	AY323255	AY323255 Zea mays	496	57	5.7	22976	6	AX000035	AX000035 Sequence
C 424	57.4	5.8	1298	8	AY323258	AY323258 Zea mays	497	57	5.7	22976	6	AX000035	AX000035 Sequence
C 425	57.4	5.8	1298	8	AY323259	AY323259 Zea mays	498	57	5.7	22976	6	AX000035	AX000035 Sequence
C 426	57.4	5.8	1298	8	AY323260	AY323260 Zea mays	499	57	5.7	22976	6	AX000035	AX000035 Sequence
C 427	57.4	5.8	1298	8	AY323261	AY323261 Zea mays	500	57	5.7	22976	6	AX000035	AX000035 Sequence
C 428	57.4	5.8	1298	8	AY323263	AY323263 Zea mays	501	57	5.7	22976	6	AX000035	AX000035 Sequence
C 429	57.4	5.8	1298	8	AY323265	AY323265 Zea mays	502	57	5.7	22976	6	AX000035	AX000035 Sequence
C 430	57.4	5.8	1311	8	AY323252	AY323252 Zea mays	503	57	5.7	22976	6	AX000035	AX000035 Sequence
C 431	57.4	5.8	1311	8	AY323257	AY323257 Zea mays	504	57	5.7	22976	6	AX000035	AX000035 Sequence
C 432	57.4	5.8	1311	8	AY323264	AY323264 Zea mays	505	57	5.7	22976	6	AX000035	AX000035 Sequence
C 433	57.4	5.8	1311	8	AY323264	AY323264 Zea mays	506	57	5.7	22976	6	AX000035	AX000035 Sequence
C 434	57.4	5.8	1311	8	AY323241	AY323241 Zea mays	507	57	5.7	22976	6	AX000035	AX000035 Sequence
C 435	57.4	5.8	1311	8	AY323243	AY323243 Zea mays	508	57	5.7	22976	6	AX000035	AX000035 Sequence
C 436	57.4	5.8	1311	8	AY323243	AY323243 Zea mays	509	57	5.7	22976	6	AX000035	AX000035 Sequence
C 437	57.4	5.8	1311	8	AY323247	AY323247 Zea mays	510	57	5.7	22976	6	AX000035	AX000035 Sequence
C 438	57.4	5.8	1311	8	AY323248	AY323248 Zea mays	511	57	5.7	22976	6	AX000035	AX000035 Sequence
C 439	57.4	5.8	1311	8	AY323250	AY323250 Zea mays	512	57	5.7	22976	6	AX000035	AX000035 Sequence
C 440	57.4	5.8	1311	8	AY323251	AY323251 Zea mays	513	57	5.7	22976	6	AX000035	AX000035 Sequence
C 441	57.4	5.8	1311	8	AY323252	AY323252 Zea mays	514	57	5.7	22976	6	AX000035	AX000035 Sequence
C 442	57.4	5.8	1311	8	AY323253	AY323253 Zea mays	515	57	5.7	22976	6	AX000035	AX000035 Sequence
C 443	57.4	5.8	1311	8	AY323254	AY323254 Zea mays	516	57	5.7	22976	6	AX000035	AX000035 Sequence
C 444	57.4	5.8	1311	8	AY323255	AY323255 Zea mays	517	57	5.7	22976	6	AX000035	AX000035 Sequence
C 445	57.4	5.8	1311	8	AY323256	AY323256 Zea mays	518	57	5.7	22976	6	AX000035	AX000035 Sequence
C 446	57.4	5.8	1311	8	AY323257	AY323257 Zea mays	519	57	5.7	22976	6	AX000035	AX000035 Sequence
C 447	57.4	5.8	1311	8	AY323258	AY323258 Zea mays	520	57	5.7	22976	6	AX000035	AX000035 Sequence
C 448	57.4	5.8	1311	8	AY323259	AY323259 Zea mays	521	57	5.7	22976	6	AX000035	AX000035 Sequence
C 449	57.4	5.8	1311	8	AY323260	AY323260 Zea mays	522	57	5.7	22976	6	AX000035	AX000035 Sequence
C 450	57.4	5.8	1311	8	AY323261	AY323261 Zea mays	523	57	5.7	22976	6	AX000035	AX000035 Sequence
C 451	57.4	5.8	1311	8	AY323262	AY323262 Zea mays	524	57	5.7	22976	6	AX000035	AX000035 Sequence
C 452	57.2	5.8	1311	8	AY323263	AY323263 Zea mays	525	57	5.7	22976	6	AX000035	AX000035 Sequence
C 453	57.2	5.8	1311	8	AY323264	AY323264 Zea mays	526	57	5.7	22976	6	AX000035	AX000035 Sequence
C 454	57.2	5.8	1311	8	AY323265	AY323265 Zea mays	527	57	5.7	22976	6	AX000035	AX000035 Sequence
C 455	57.2	5.8	1311	8	AY323266	AY323266 Zea mays	528	57	5.7	22976	6	AX000035	AX000035 Sequence
C 456	57.2	5.8	1311	8	AY323267	AY323267 Zea mays	529	57	5.7	22976	6	AX000035	AX000035 Sequence
C 457	57.2	5.8	1311	8	AY323268	AY323268 Zea mays	530	57	5.7	22976	6	AX000035	AX000035 Sequence







c 677	55.4	5.6	299800	1	AP005028	Streptomy	750	54.6	5.5	2830	3	AF027972	Nephila c
c 678	55.4	5.6	314100	1	SC0933106	Streptomy	751	54.6	5.5	2830	6	AR091362	AR091362 Sequence
c 679	55.4	5.6	986	8	AF377753	Zea mays	c 752	54.6	5.5	3866	1	D31792	D31792 Streptomyce
c 680	55.2	5.6	1182	8	AK105138	AK105138	c 753	54.6	5.5	4761	1	SCO244019	AJ244019 Streptomy
c 681	55.2	5.6	1324	8	OSLIP19	X57325 Rice lip19	c 754	54.6	5.5	5520	3	AC084329	AC084329 Leishmani
c 682	55.2	5.6	1344	8	AK104844	AK104844 Oryza sat	c 755	54.6	5.5	9811	14	AF449714	AF449714 Cercopith
c 683	55.2	5.6	1375	8	AK065180	AK065180 Oryza sat	756	54.6	5.5	12277	1	AF340166	AF340166 Streptomy
c 684	55.2	5.6	1679	9	AB001835	AB001835 Homo sapi	757	54.6	5.5	22449	1	SPSNCBCE	Y1548 S.pristinae
c 685	55.2	5.6	2208	1	STMWRWGT	M74717 Streptomyce	758	54.6	5.5	22449	1	SPSNCBCE	X98690 S.pristinae
c 686	55.2	5.6	9589	1	SC0001205	AE005037 Halobacte	c 759	54.6	5.5	110086	8	AP003373	AP003373 Oryza sat
c 687	55.2	5.6	13508	1	AE005037	AE005037 Halobacte	760	54.6	5.5	112144	8	AP003758	AP003758 Oryza sat
c 688	55.2	5.6	14219	1	AB070957	AB070957 Streptomy	c 761	54.6	5.5	127348	8	AC134769	AC134769 Genomic s
c 689	55.2	5.6	66351	2	AC139773	AC139773 Homo sapi	c 762	54.6	5.5	142549	2	AP004271	AP004271 Oryza sat
c 690	55.2	5.6	66669	1	AME16952	Y16952 Amycolatops	c 763	54.6	5.5	158405	10	NMHC310M6	AF109906 Mus muscu
c 691	55.2	5.6	85163	1	AY048670	AY048670 Streptomy	c 764	54.6	5.5	161326	9	AC004067	AC004067 Homo sapi
c 692	55.2	5.6	95209	2	AP004323	AP004323 Oryza sat	c 765	54.6	5.5	163490	8	CNS08CD4	AL954828 Oryza sat
c 693	55.2	5.6	110000	2	LMFLCHR16_02	Continuation (3 of	c 766	54.6	5.5	170666	8	AP003845	AP003845 Oryza sat
c 694	55.2	5.6	110000	2	LMFLCHR16_03	Continuation (4 of	c 767	54.6	5.5	189050	1	AL646077	AL646077 Ralstonia
c 695	55.2	5.6	137860	10	AC122407	AC122407 Mus muscu	c 768	54.6	5.5	212050	1	AL646060	AL646060 Ralstonia
c 696	55.2	5.6	145796	8	AC130598	AC130598 Oryza sat	c 769	54.6	5.5	212899	10	AC087117	AC087117 Mus Muscu
c 697	55.2	5.6	146408	8	AC130610	AC130610 Oryza sat	770	54.4	5.5	1443	6	BD180149	BD180149 Highly th
c 698	55.2	5.6	154728	9	AC018730	AC018730 Homo sapi	771	54.4	5.5	1608	5	LFL308119	AJ308119 Lampetra
c 699	55.2	5.6	187782	8	AC135425	AC135425 Oryza sat	772	54.4	5.5	4117	14	AF074327	AF074327 Tupaia he
c 700	55.2	5.6	299300	1	AP005026	AP005026 Streptomy	773	54.4	5.5	4120	14	AF074328	AF074328 Tupaia he
c 701	55.2	5.6	300794	8	AE016884	AE016884 Erenothec	774	54.4	5.5	6620	1	AB164631	AB164631 Streptomy
c 702	55.2	5.6	348257	1	BX640425	BX640425 Bordetell	775	54.4	5.5	13461	14	AF084543	AF084543 Tupaia he
c 703	55.2	5.6	349497	1	BX640440	BX640440 Bordetell	776	54.4	5.5	13889	10	AF292939	AF292939 Mus muscu
c 704	55	5.6	2205	9	BC009438	BC009438 Homo sapi	c 777	54.4	5.5	54587	2	AC146908_3	Continuation (4 of
c 705	55	5.6	2490	8	AK100050	AK100050 Oryza sat	778	54.4	5.5	132981	8	AC147802	AC147802 Oryza sat
c 706	55	5.6	2559	6	AR488839	AR488839 Sequence	779	54.4	5.5	163732	8	OSJN000033	AL606632 Oryza sat
c 707	55	5.6	2562	6	CQ720385	CQ720385 Sequence	c 780	54.4	5.5	195859	14	AF281817	AF281817 Tupaia he
c 708	55	5.6	28890	1	AF512431	AF512431 Saccharot	781	54.4	5.5	213050	1	AL646079	AL646079 Ralstonia
c 709	55	5.6	30943	6	CQ801140	CQ801140 Sequence	782	54.4	5.5	300810	8	AE016896	AE016896 Erenothec
c 710	55	5.6	3784	1	MM223012	AJ223012 Amycolato	783	54.4	5.5	302007	1	SCO939132	AL939132 Streptomy
c 711	55	5.6	53789	6	AG9720	AG9720 Sequence 3	784	54.4	5.5	302898	1	AE017238	AE017238 Mycobacte
c 712	55	5.6	66280	1	AF195122	AF195122 Rhodobact	785	54.4	5.5	344321	1	BX640429	BX640429 Bordetell
c 713	55	5.6	103576	8	YUP8H12	AC000098 Arabidops	c 786	54.4	5.5	348624	1	BX640441	BX640441 Bordetell
c 714	55	5.6	109528	2	AF040570	AF040570 Amycolato	787	54.4	5.5	349876	1	BX640442	BX640442 Bordetell
c 715	55	5.6	110000	2	BX255276_15	Continuation (16 o	788	54.2	5.5	825	8	AY533122	AY533122 Oryza sat
c 716	55	5.6	181206	2	AC110907	AC110907 Mus muscu	789	54.2	5.5	1300	8	AK102889	AK102889 Oryza sat
c 717	55	5.6	188050	1	AL646072	AL646072 Ralstonia	790	54.2	5.5	1433	8	AF168779	AF168779 Eucalyptu
c 718	55	5.6	292200	1	SC0939129	AL939129 Streptomy	791	54.2	5.5	1602	1	SLU12007	U12007 Streptomyce
c 719	55	5.6	295150	1	SC0939126	AL939126 Streptomy	792	54.2	5.5	1910	8	AK104793	AK104793 Oryza sat
c 720	54.8	5.5	594	6	BD224381	BD224381 Materials	793	54.2	5.5	1910	8	AK106154	AK106154 Oryza sat
c 721	54.8	5.5	594	6	AR216431	AR216431 Sequence	794	54.2	5.5	1934	8	AK098925	AK098925 Oryza sat
c 722	54.8	5.5	594	6	AR432833	AR432833 Sequence	795	54.2	5.5	1964	8	AK064950	AK064950 Oryza sat
c 723	54.8	5.5	607	6	AR074114	AR074114 Sequence	796	54.2	5.5	2202	8	AK067226	AK067226 Oryza sat
c 724	54.8	5.5	607	6	BD224299	BD224299 Materials	797	54.2	5.5	3202	1	AF157829	AF157829 Myxococcu
c 725	54.8	5.5	607	6	BD273001	BD273001 Materials	798	54.2	5.5	4858	1	AF162663	AF162663 Myxococcu
c 726	54.8	5.5	607	6	AR216349	AR216349 Sequence	799	54.2	5.5	8046	1	AF049107	AF049107 Myxococcu
c 727	54.8	5.5	607	6	AR432751	AR432751 Sequence	c 800	54.2	5.5	15141	14	SH1PROIE	M34651 Pseudorabie
c 728	54.8	5.5	607	6	BD005662	BD005662 Materials	801	54.2	5.5	25315	1	AY204472	AY204472 Myxococcu
c 729	54.8	5.5	1795	1	AF118856	AF118856 Streptomy	802	54.2	5.5	32748	1	AB070951	AB070951 Streptomy
c 730	54.8	5.5	2142	1	CCU42203	U42203 Caulobacter	c 803	54.2	5.5	65140	6	AX211705	AX211705 Sequence
c 731	54.8	5.5	2365	8	AK102809	AK102809 Oryza sat	c 804	54.2	5.5	106562	2	AP004055	AP004055 Oryza sat
c 732	54.8	5.5	2783	1	STMFMET	D13170 Streptomyce	c 805	54.2	5.5	110098	8	AP004144	AP004144 Oryza sat
c 733	54.8	5.5	3030	8	VCA429230	AJ429230 Volvox ca	806	54.2	5.5	122218	8	AC093939	AC093939 Oryza sat
c 734	54.8	5.5	5500	8	ATGLVSP	X58338 A.thaliana	c 807	54.2	5.5	123580	1	AF263912	AF263912 Streptomy
c 735	54.8	5.5	10894	1	AE005785	AE005785 Caulobact	c 808	54.2	5.5	125401	6	AX211739	AX211739 Sequence
c 736	54.8	5.5	12528	1	AE005826	AE005826 Caulobact	809	54.2	5.5	136150	8	AP002485	AP002485 Oryza sat
c 737	54.8	5.5	58638	7	AY576796	AY576796 Actinopla	c 810	54.2	5.5	142010	8	AP003928	AP003928 Oryza sat
c 738	54.8	5.5	92620	2	BM26636	AB026636 Arabidops	811	54.2	5.5	189043	8	AP004366	AP004366 Oryza sat
c 739	54.8	5.5	110000	2	BX255276_07	Continuation (8 of	c 812	54.2	5.5	196050	1	AL646058	AL646058 Ralstonia
c 740	54.8	5.5	156789	14	AF533768	AF533768 Cercopith	c 813	54.2	5.5	202301	1	AE017286	AE017286 Desulfovi
c 741	54.8	5.5	166182	10	AC084391	AC084391 Mus muscu	814	54.2	5.5	245233	2	AC130123	AC130123 Rattus no
c 742	54.8	5.5	218310	10	AC034265	AC034265 Mus muscu	c 815	54.2	5.5	301443	1	AE017239	AE017239 Mycobacte
c 743	54.8	5.5	231001	2	AC130981	AC130981 Rattus no	816	54.2	5.5	339972	8	OSA307662	AJ307662 Oryza sat
c 744	54.8	5.5	258319	2	AC127770	AC127770 Rattus no	817	54	5.5	885	11	PM7F8G	AL685189 Penicilli
c 745	54.8	5.5	292100	1	SC0939121	AL939121 Streptomy	818	54	5.5	1065	6	BD180086	BD180086 Highly th
c 746	54.6	5.5	955	8	NTU62736	U62736 Nicotiana t	819	54	5.5	1217	1	AF038408	AF038408 Streptoal
c 747	54.6	5.5	980	6	AX652989	AX652989 Sequence	820	54	5.5	1380	6	E17152	E17152 Micrococcu
c 748	54.6	5.5	1261	8	AK112011	AK112011 Oryza sat	821	54	5.5	1485	6	BD180362	BD180362 Highly th
c 749	54.6	5.5	1308	6	BD217906	BD217906 Gene fami	822	54	5.5	2900	1	TTHS16007	AJ516007 Thermus t



C 823	54	5.5	3444	1	SAU75434	U75434 Streptomyce	C 896	53.4	5.4	63082	2	AC022663	AC022663 Homo sapi
C 824	54	5.5	4507	9	BC053392	BC053392 Homo sapi	C 897	53.4	5.4	81767	2	AC021929	AC021929 Homo sapi
C 825	54	5.5	4308	9	AK024444	AK024444 Homo sapi	C 898	53.4	5.4	136254	8	CNS071P29	AL713941 Oryza sat
C 826	54	5.5	10274	1	AE005893	AE005893 Caulobact	C 899	53.4	5.4	136551	2	AC048354	AC048354 Homo sapi
C 827	54	5.5	18497	9	AF254411	AF254411 Homo sapi	C 900	53.4	5.4	141066	8	AP005188	AP005188 Oryza sat
C 828	54	5.5	143298	8	AC134240	AC134240 Oryza sat	C 901	53.4	5.4	151699	8	AP003916	AP003916 Oryza sat
C 829	54	5.5	153431	8	AC134235	AC134235 Oryza sat	C 902	53.4	5.4	155337	2	AC116408	AC116408 Mus muscu
C 830	54	5.5	172876	9	AC114489	AC114489 Homo sapi	C 903	53.4	5.4	163778	9	AL391005	AL391005 Human DNA
C 831	54	5.5	174992	2	AC025422	AC025422 Homo sapi	C 904	53.4	5.4	187410	8	AP005579	AP005579 Oryza sat
C 832	54	5.5	179451	2	AC148581	AC148581 Gasterost	C 905	53.4	5.4	226155	2	AC136740	AC136740 Mus muscu
C 833	54	5.5	208936	2	AC010821	AC010821 Homo sapi	C 906	53.4	5.4	233405	2	AC126733	AC126733 Rattus no
C 834	54	5.5	209844	9	AC011495	AC011495 Homo sapi	C 907	53.4	5.4	236502	2	AC098186	AC098186 Rattus no
C 835	54	5.5	210614	1	AB088224	AB088224 Streptomy	C 908	53.4	5.4	272101	1	AE017302	AE017302 Thermus c
C 836	54	5.5	250046	2	AC113592	AC113592 Mus muscu	C 909	53.4	5.4	296500	1	SC0939128	AL393128 Streptomy
C 837	54	5.5	298550	1	AP005047	AP005047 Streptomy	C 910	53.4	5.4	308050	1	SC0939124	AL393124 Streptomy
C 838	54	5.5	299425	1	AP005049	AP005049 Streptomy	C 911	53.4	5.4	308050	1	SC0939124	AL393124 Streptomy
C 839	54	5.5	300239	8	AE016881	AE016881 Erenothec	C 912	53.4	5.4	344805	1	EX640434	EX640434 Bordetell
C 840	54	5.5	300239	8	AE016881	AE016881 Erenothec	C 913	53.2	5.4	348074	1	EX640449	EX640449 Bordetell
C 841	54	5.5	303550	1	SC0939131	AL3939131 Streptomy	C 914	53.2	5.4	1183	8	AK109116	AK109116 Oryza sat
C 842	53.8	5.4	1872	6	CQ801144	CQ801144 Sequence	C 915	53.2	5.4	1283	8	AK058442	AK058442 Oryza sat
C 843	53.8	5.4	2007	14	CHV10C	Z492225 Caprine her	C 916	53.2	5.4	1341	1	AY337515	AY337515 Myxococcu
C 844	53.8	5.4	2082	6	AR452220	AR452220 Sequence	C 917	53.2	5.4	1405	8	AK108620	AK108620 Oryza sat
C 845	53.8	5.4	2082	6	AR452220	AR452220 Sequence	C 918	53.2	5.4	1509	6	BD180173	BD180173 Highly th
C 846	53.8	5.4	11171	6	CQ801141	AX262311 Sequence	C 919	53.2	5.4	2672	1	AF159692	AF159692 Myxococcu
C 847	53.8	5.4	15141	14	SHIPROIE	CQ801141 Sequence	C 920	53.2	5.4	2767	8	SL1224970	AF159692 Myxococcu
C 848	53.8	5.4	24613	1	AY116644	M34651 Pseudorabie	C 921	53.2	5.4	10161	1	AF546153	AF546153 Micromono
C 849	53.8	5.4	64492	1	AY116644	AY116644 Streptomy	C 922	53.2	5.4	13325	1	AE005016	AE005016 Halobacte
C 850	53.8	5.4	85268	2	AC022648	AE086653 Streptomy	C 923	53.2	5.4	110400	8	AP005919	AE005919 Oryza sat
C 851	53.8	5.4	114793	9	AP217796	AC022648 Homo sapi	C 924	53.2	5.4	116887	10	AL929153	AL929153 Mouse DNA
C 852	53.8	5.4	138390	14	AX261359	AF217796 Homo sapi	C 925	53.2	5.4	135638	1	AF484556	AF484556 Streptomy
C 853	53.8	5.4	139544	8	AP004048	AX261359 Bovine he	C 926	53.2	5.4	137468	8	AP003269	AP003269 Oryza sat
C 854	53.8	5.4	145014	8	AP004048	AP004048 Oryza sat	C 927	53.2	5.4	181676	10	AC124194	AC124194 Mus muscu
C 855	53.8	5.4	166565	2	AC146324	AP004048 Oryza sat	C 928	53.2	5.4	197411	10	AC135961	AC135961 Mus muscu
C 856	53.8	5.4	299300	1	AP005026	AC146324 Canis fam	C 929	53.2	5.4	232605	1	AE017222	AE017222 Mycobacte
C 857	53.8	5.4	301457	1	SC0939123	AP005026 Streptomy	C 930	53.2	5.4	309267	1	AE017235	AE017235 Mycobacte
C 858	53.8	5.4	301457	1	SC0939123	AL93123 Streptomy	C 931	53.2	5.4	348525	1	EX640428	EX640428 Bordetell
C 859	53.8	5.4	321250	1	SC0939111	AE016924 Chromobac	C 932	53.2	5.4	349354	1	EX640416	EX640416 Bordetell
C 860	53.8	5.4	340900	1	SME591791	AL939111 Streptomy	C 933	53.2	5.4	349672	1	EX640419	EX640419 Bordetell
C 861	53.6	5.4	6252	8	AY039003	AL939111 Streptomy	C 934	53	5.4	632	6	AR227195	AR227195 Sequence
C 862	53.6	5.4	10554	1	AE005956	AY039003 Hordeum v	C 935	53	5.4	765	6	BD180096	BD180096 Highly th
C 863	53.6	5.4	15274	1	AE004994	AE005956 Caulobact	C 936	53	5.4	1929	6	AX811491	AX811491 Sequence
C 864	53.6	5.4	32463	8	CNS08C9W	AE004994 Halobacte	C 937	53	5.4	2304	6	BD179527	BD179527 Highly th
C 865	53.6	5.4	38734	6	BD129566	AL772418 Oryza sat	C 938	53	5.4	2953	10	BC054782	BC054782 Mus muscu
C 866	53.6	5.4	110000	2	BX255376_01	BD129566 Polynucle	C 939	53	5.4	3518	10	MUSHSP7A2	M35021 Mouse heat
C 867	53.6	5.4	146585	8	CNS08C9W	Continuation (2 of	C 940	53	5.4	3701	1	AF172724	AF172724 Caulobact
C 868	53.6	5.4	198873	2	AC022811	AL831809 Oryza sat	C 941	53	5.4	8113	14	HSB81C4A	LI4320 Bovine herp
C 869	53.6	5.4	204050	1	AL646073	AC022811 Homo sapi	C 942	53	5.4	10029	1	AE012236	AE012236 Xanthomon
C 870	53.6	5.4	21050	1	AL646060	AL646073 Ralstonia	C 943	53	5.4	10513	1	AE004792	AE004792 Pseudomon
C 871	53.6	5.4	236054	2	AC114393	AL646060 Ralstonia	C 944	53	5.4	11283	1	AE005710	AE005710 Caulobact
C 872	53.6	5.4	270418	1	AE017303	AE014393 Rattus no	C 945	53	5.4	11923	1	AE005972	AE005972 Caulobact
C 873	53.6	5.4	302325	1	AE017236	AE017236 Mycobacte	C 946	53	5.4	32668	1	MEU575934	AY524043 Micromono
C 874	53.6	5.4	303855	1	AP005033	AE017230 Streptomy	C 947	53	5.4	38146	1	AY524043	AY524043 Micromono
C 875	53.6	5.4	320150	1	AP005033	AP005033 Streptomy	C 948	53	5.4	100773	8	AF466201	AF466201 Sorghum b
C 876	53.6	5.4	348134	1	EX640420	EX640420 Bordetell	C 949	53	5.4	102591	9	AC002978	AC002978 Homo sapi
C 877	53.6	5.4	348642	1	EX640446	EX640446 Bordetell	C 950	53	5.4	110000	2	LMFLCHR12_13	Continuation (14 o
C 878	53.4	5.4	1706	8	AK058859	BX640446 Bordetell	C 951	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he
C 879	53.4	5.4	1707	8	AK058859	AK058859 Oryza sat	C 952	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he
C 880	53.4	5.4	1754	8	AF165181	AF165181 Zea mays	C 953	53	5.4	144093	10	AC109193	AC109193 Mus muscu
C 881	53.4	5.4	2248	6	BD249574	BD249574 Modificat	C 954	53	5.4	178620	10	AC121865	AC121865 Mus muscu
C 882	53.4	5.4	2248	6	AK340022	AK340022 Sequence	C 955	53	5.4	194387	10	AC105989	AC105989 Mus muscu
C 883	53.4	5.4	2336	3	NEPDSF	M37137 N.clavipes	C 956	53	5.4	301925	1	AP005046	AP005046 Streptomy
C 884	53.4	5.4	2338	6	AR088543	AR088543 Sequence	C 957	53	5.4	303642	1	AE016923	AE016923 Chromobac
C 885	53.4	5.4	2338	6	AR088543	I92789 Sequence 1	C 958	53	5.4	347071	1	EX640415	BX640415 Bordetell
C 886	53.4	5.4	2798	3	AF448524	AF448524 Mytilus g	C 959	52.8	5.3	348706	1	BX640445	BX640445 Bordetell
C 887	53.4	5.4	3177	9	AF055989	AF055989 Homo sapi	C 960	52.8	5.3	1094	11	PM7G11B	AL685196 Penicilli
C 888	53.4	5.4	10091	1	AE011852	AE011852 Xanthomon	C 961	52.8	5.3	1236	6	AR007558	AR007558 Sequence
C 889	53.4	5.4	10256	1	AE004894	AE004894 Pseudomon	C 962	52.8	5.3	3157	1	MSGPOLA	LI1920 Mycobacteri
C 890	53.4	5.4	11626	1	AE011704	AE011704 Xanthomon	C 963	52.8	5.3	4423	10	MMUSF217	X77602 M.musculu
C 891	53.4	5.4	11905	1	APU33059	U33059 Actinosynne	C 964	52.8	5.3	11842	1	AE005053	AE005053 Halobacte
C 892	53.4	5.4	12111	1	AE010422	AE010422 Methanopy	C 965	52.8	5.3	92509	1	AL646086	AL646086 Ralstonia
C 893	53.4	5.4	13750	1	AY260903	AY260903 Rhodospir	C 966	52.8	5.3	114996	8	AY485643	AY485643 Hordeum v
C 894	53.4	5.4	18424	1	AF163841	AF163841 Myxococcu	C 967	52.8	5.3	172647	2	AC130732	AC130732 Oryza sat
C 895	53.4	5.4	39250	1	SVI011500	AJ0111500 Streptomy	C 968	52.8	5.3	239571	2	AC150509	AC150509 Bos tauru



c 969	52.8	5.3	299925	1	AP005039	Streptomy	c1042	52.4	5.3	168861	2	AC130786	AC130786 Papio anu
c 970	52.8	5.3	300050	1	BE248339	Mycobacte	c1043	52.4	5.3	169162	8	AP004267	AP004267 Oryza sat
c 971	52.8	5.3	305584	1	AE016920	Chromobac	c1044	52.4	5.3	176647	2	AC130188	AC130188 Papio anu
c 972	52.8	5.3	314100	1	SC0933106	Streptomy	c1045	52.4	5.3	196558	10	AC073946	AC073946 Mus muscu
c 973	52.8	5.3	347137	1	BE640448	Bordetell	1046	52.4	5.3	202270	2	AC102341	AC102341 Mus muscu
c 974	52.8	5.3	347496	1	BE842577	Mycobacte	1047	52.4	5.3	242662	2	AC080020	AC080020 Mus muscu
c 975	52.8	5.3	348934	1	BE640417	Bordetell	1048	52.4	5.3	247910	1	AE017307	AE017307 Thermus t
c 976	52.8	5.3	349028	1	BE640413	Bordetell	1049	52.4	5.3	300550	1	AP005030	AP005030 Streptomy
c 977	52.8	5.3	349497	1	BE640440	Bordetell	c1050	52.4	5.3	320150	1	AP005033	AP005033 Streptomy
c 978	52.8	5.3	349726	1	BE640421	Bordetell	1051	52.4	5.3	320150	1	AP005033	AP005033 Streptomy
c 979	52.8	5.3	349726	1	BE640421	Bordetell	1052	52.4	5.3	705	6	BD179549	BD179549 Highly th
c 980	52.6	5.3	948	6	BD180185	Highly th	1053	52.2	5.3	833	8	AY088274	AY088274 Arabidops
c 981	52.6	5.3	1569	5	AY518690	Gallus ga	c1054	52.2	5.3	996	6	BD179727	BD179727 Highly th
c 982	52.6	5.3	2466	6	CQ759736	Sequence	1055	52.2	5.3	1140	11	PM12C4G	PM12C4G Penicilli
c 983	52.6	5.3	2560	4	AY453841	Oryctolag	1056	52.2	5.3	1611	8	AK071964	AK071964 Oryza sat
c 984	52.6	5.3	2561	6	AR409339	Sequence	1057	52.2	5.3	1719	6	BD180543	BD180543 Highly th
c 985	52.6	5.3	2561	6	AR409339	Sequence	1058	52.2	5.3	1766	8	AF325915	AF325915 Euglena g
c 986	52.6	5.3	2619	6	CQ759734	Sequence	1059	52.2	5.3	2085	8	AK119580	AK119580 Oryza sat
c 987	52.6	5.3	2778	9	AK128815	Homo sapi	1060	52.2	5.3	2529	1	AE060536	AE060536 Streptomy
c 988	52.6	5.3	3342	1	AF200819	Streptomy	1061	52.2	5.3	2760	1	SRSNRS	Y14336 Streptomyce
c 989	52.6	5.3	3705	6	CQ759732	Sequence	1062	52.2	5.3	6297	6	AX598629	AX598629 Sequence
c 990	52.6	5.3	4881	1	AME318385	AMycolato	1063	52.2	5.3	7155	14	BHV1ULX	U64519 Rhodospirill
c 991	52.6	5.3	7985	14	AB098202	Cercopith	1064	52.2	5.3	9353	14	BHV1ULX	249078 Bovine herp
c 992	52.6	5.3	11064	5	D63799	Thermus the	1065	52.2	5.3	10460	1	AE011791	AE011791 Xanthomon
c 993	52.6	5.3	12162	1	AY034175	Streptomy	c1066	52.2	5.3	10696	1	AE012103	AE012103 Xanthomon
c 994	52.6	5.3	13803	1	AE011784	Xanthomon	1067	52.2	5.3	14355	3	AF218623	AF218623 Nepila m
c 995	52.6	5.3	13901	1	AY258009	Streptomy	1068	52.2	5.3	31444	14	BVH1FT31	254206 Bovine herp
c 996	52.6	5.3	29132	1	STH575648	Streptomy	1069	52.2	5.3	66808	1	SAU421825	SAU421825 Stigmatel
c 997	52.6	5.3	47090	9	AC092310	Homo sapi	1070	52.2	5.3	76196	1	AY354515	AY354515 Streptomy
c 998	52.6	5.3	81767	2	AC021929	Homo sapi	c1071	52.2	5.3	82868	6	CQ792587	CQ792587 Sequence
c 999	52.6	5.3	110000	1	AE000516	Continuation (22 o	1072	52.2	5.3	128098	6	CQ792587	CQ792587 Sequence
c1000	52.6	5.3	110000	1	AE016822	Continuation (22 o	c1073	52.2	5.3	133387	2	AP004309	AP004309 Oryza sat
c1001	52.6	5.3	110000	1	AE000516	Continuation (14 o	1074	52.2	5.3	143200	8	AP004380	AP004380 Oryza sat
c1002	52.6	5.3	135357	8	AP003896	Oryza sat	c1075	52.2	5.3	159860	8	AP005647	AP005647 Oryza sat
c1003	52.6	5.3	138390	14	AY261359	Arz61359 Bovine he	1076	52.2	5.3	159860	8	AP005647	AP005647 Oryza sat
c1004	52.6	5.3	163328	8	AP004865	AP004865 Oryza sat	c1077	52.2	5.3	205144	4	AY495827	AY495827 Oryctolag
c1005	52.6	5.3	185495	8	AP005620	Oryza sat	c1078	52.2	5.3	273285	1	SC0939115	SC0939115 Streptomy
c1006	52.6	5.3	230715	2	AC140280	Rattus no	c1079	52.2	5.3	276800	1	AE017304	AE017304 Thermus t
c1007	52.6	5.3	237362	2	AC140280	Mus muscu	c1080	52.2	5.3	300327	1	AE017228	AE017228 Mycobacte
c1008	52.6	5.3	277363	2	AC134745	Rattus no	c1081	52.2	5.3	300425	1	AP005038	AP005038 Chromobac
c1009	52.6	5.3	299425	1	AP005049	Streptomy	1082	52.2	5.3	305584	1	AE016920	AE016920 Chromobac
c1010	52.6	5.3	303550	1	SC0939118	Streptomy	1083	52.2	5.3	309050	1	SC0939117	SC0939117 Streptomy
c1011	52.6	5.3	306550	1	BE248342	Mycobacte	1084	52.2	5.3	991	11	PM12H12B	PM12H12B Penicilli
c1012	52.6	5.3	346051	1	BE248342	Mycobacte	1085	52.2	5.3	992	8	AF377751	AF377751 Zea mays
c1013	52.4	5.3	1175	5	CMH1SHS	X01065 Duck (C. mo	1086	52.2	5.3	1000	8	AY513932	AY513932 Zea mays
c1014	52.4	5.3	1227	8	AK467205	Sequence	1087	52.2	5.3	1155	8	AY513932	AY513932 Zea mays
c1015	52.4	5.3	1485	8	AK107516	Oryza sat	1088	52.2	5.3	1255	8	AK073667	AK073667 Oryza sat
c1016	52.4	5.3	1891	6	AX337108	Sequence	1089	52.2	5.3	1410	1	AME277083	AME277083 Amycolato
c1017	52.4	5.3	1891	6	AX587764	Sequence	1090	52.2	5.3	1491	6	AX455983	AX455983 Sequence
c1018	52.4	5.3	1891	9	HSJUNDR	X56681 Human jund	1091	52.2	5.3	1703	8	AK120673	AK120673 Oryza sat
c1019	52.4	5.3	2796	3	AF043944	AF043944 Mytilus e	1092	52.2	5.3	1711	1	AF347026	AF347026 Streptomy
c1020	52.4	5.3	3139	8	D63955	D63955 Oryza sativ	1093	52.2	5.3	2800	1	PSNOSZR	Z13988 P. stutzeri
c1021	52.4	5.3	3978	6	BOVADC	M25579 Bovine aden	1094	52.2	5.3	3113	8	SS95BASAL	AJ001438 Spermatoz
c1022	52.4	5.3	3978	6	AR106654	AR106654 Sequence	1095	52.2	5.3	3114	12	AY192356	AY192356 Synthetic
c1023	52.4	5.3	3980	1	AF546147S1	AF546147 Streptomy	1096	52.2	5.3	3135	12	AY192357	AY192357 Synthetic
c1024	52.4	5.3	5117	9	AB0118240	AB0118240 Sequence	1097	52.2	5.3	3150	12	AY192358	AY192358 Synthetic
c1025	52.4	5.3	5117	9	AB011105	AB011105 Homo sapi	1098	52.2	5.3	10352	1	AF546152	AF546152 Streptomy
c1026	52.4	5.3	5204	6	AR338550	AR338550 Sequence	1099	52.2	5.3	10854	1	AE001886	AE001886 Deinococc
c1027	52.4	5.3	5640	6	AR338550	AR338550 Sequence	1100	52.2	5.3	11506	1	AE004793	AE004793 Pseudomon
c1028	52.4	5.3	8296	6	AX463772	AX463772 Sequence	1101	52.2	5.3	43269	8	AC135499	AC135499 Oryza sat
c1029	52.4	5.3	10911	6	CQ730457	CQ730457 Sequence	1102	52.2	5.3	110000	1	AE016822	AE016822 Continuation (23 o
c1030	52.4	5.3	11238	9	AF443072	AF443072 Homo sapi	1103	52.2	5.3	142081	8	AP004572	AP004572 Oryza sat
c1031	52.4	5.3	11329	9	AF443072	AF443072 Homo sapi	1104	52.2	5.3	152974	8	AC135497	AC135497 Oryza sat
c1032	52.4	5.3	11350	6	AX463738	AX463738 Sequence	1105	52.2	5.3	186090	2	AC097352	AC097352 Canis fam
c1033	52.4	5.3	11367	6	AX704754	AX704754 Sequence	1106	52.2	5.3	191916	2	AC095027	AC095027 Canis fam
c1034	52.4	5.3	16197	1	AE002072	AE002072 Sequence	1107	52.2	5.3	191996	9	AC092275	AC092275 Homo sapi
c1035	52.4	5.3	60196	6	AX697977	AX697977 Sequence	1108	52.2	5.3	193119	8	AC025907	AC025907 Oryza sat
c1036	52.4	5.3	85434	2	AC066610	AC066610 Homo sapi	1109	52.2	5.3	200968	8	AP005516	AP005516 Oryza sat
c1037	52.4	5.3	101075	8	CNS08CBU	AB070940 Streptomy	1110	52.2	5.3	211657	10	AL732564	AL732564 Mouse DNA
c1038	52.4	5.3	104326	1	AB070940	AB070940 Streptomy	1111	52.2	5.3	299925	1	AP005045	AP005045 Streptomy
c1039	52.4	5.3	138203	1	AY310323	AY310323 Streptomy	1112	52.2	5.3	300029	8	AE017099	AE017099 Oryza sat
c1040	52.4	5.3	149098	9	AL445209	AL445209 Human	1113	52.2	5.3	301846	1	AE016913	AE016913 Chromobac
c1041	52.4	5.3	157302	9	AL445209	AL445209 Human	1114	52.2	5.3	307435	1	AE016914	AE016914 Chromobac



1115	51.8	5.2	974	8	AF377768	Zea mays	cl188	51.6	5.2	113193	1	AF357202	Streptomy
1116	51.8	5.2	975	8	AF377745	Zea mays	cl189	51.6	5.2	113193	6	AX703543	Sequence
1117	51.8	980	8	AF377759	Zea mays	1190	51.6	5.2	114051	8	OSUN00036	Sequence	
1118	51.8	981	8	AF377761	Zea mays	cl191	51.6	5.2	169064	2	AC115699	Mus muscu	
1119	51.8	981	8	AY513914	Zea luxur	1192	51.6	5.2	174139	2	AC116700	Mus muscu	
1120	51.8	981	8	AY513920	Zea mays	1193	51.6	5.2	192857	8	AP005605	Oryza sat	
1121	51.8	981	8	AY513928	Zea mays	1194	51.6	5.2	192857	1	AL646067	Ralsconia	
1122	51.8	982	8	AF377767	Zea mays	1195	51.6	5.2	226889	14	AC146905	Human Her	
1123	51.8	983	8	AY513929	Zea mays	cl196	51.6	5.2	229483	14	AC146851	Human Her	
1124	51.8	988	8	AY513923	Zea mays	cl197	51.6	5.2	231236	14	AY315197	Human Her	
1125	51.8	995	8	AY513927	Zea mays	cl198	51.6	5.2	234881	14	AC146906	Human Her	
1126	51.8	1262	10	BC010402	Mus muscu	cl199	51.6	5.2	290850	1	SC0939127	Streptomy	
1127	51.8	1673	8	AY600140	Broussone	1200	51.6	5.2	291000	1	SC0939105	Streptomy	
1128	51.8	1705	8	AK069785	Oryza sat	1201	51.6	5.2	299050	1	SC0939104	Streptomy	
1129	51.8	1926	6	AR217867	Sequence	cl202	51.6	5.2	299425	1	AP005037	Streptomy	
1130	51.8	1931	6	AR083152	Sequence	1203	51.6	5.2	299550	1	AP005031	Streptomy	
1131	51.8	2036	8	AF050631	Zea mays	cl204	51.6	5.2	301399	1	AE017233	Mycobacte	
1132	51.8	2075	6	AR253206	Sequence	1205	51.6	5.2	348934	1	AX640417	Bordetell	
1133	51.8	2075	6	AR361924	Sequence	cl206	51.6	5.2	348997	1	AX640427	Bordetell	
1134	51.8	2075	6	AR433000	Sequence	cl207	51.6	5.2	349008	1	AX640444	Bordetell	
1135	51.8	2075	6	AX482567	Sequence	1208	51.6	5.2	349116	1	AP003003	Mesorhizo	
1136	51.8	2075	6	AX482567	Sequence	1209	51.6	5.2	349640	1	AX572600	Rhodopseu	
1137	51.8	2075	6	AX565707	Sequence	1210	51.4	5.2	985	8	AK058890	Oryza sat	
1138	51.8	2075	6	AX597107	Sequence	1211	51.4	5.2	1746	1	AF425992	Streptomy	
1139	51.8	2075	6	AX701365	Sequence	1212	51.4	5.2	1926	6	AX811493	Sequence	
1140	51.8	2075	9	AF001900	Homo sapi	1213	51.4	5.2	2454	8	AF022816	Chlamydom	
1141	51.8	2525	6	CQ782831	Sequence	1214	51.4	5.2	2526	9	HSCEBPA	Y11525 H.eapiens m	
1142	51.8	2525	6	BD127336	Primer fo	1215	51.4	5.2	3292	10	MUSHP7A2	Mouse heat	
1143	51.8	2525	9	AK074866	Homo sapi	1216	51.4	5.2	3520	5	AY008972	Gallus ga	
1144	51.8	2597	6	AX600203	Sequence	1217	51.4	5.2	4725	6	AX697993	Sequence	
1145	51.8	2714	9	AF327056	Homo sapi	1218	51.4	5.2	7916	1	ASY18523	Actinoplane	
1146	51.8	2725	9	BC069327	Homo sapi	1219	51.4	5.2	10968	1	AY204471	Myxococcu	
1147	51.8	4469	6	AX236302	Sequence	1220	51.4	5.2	12855	5	AF533985	Streptomy	
1148	51.8	4469	6	AX578081	Sequence	1221	51.4	5.2	14999	3	AF218621S1	Nephila c	
1149	51.8	4469	9	AF056087	Homo sapi	1222	51.4	5.2	30000	6	AX250362	Sequence	
1150	51.8	4612	1	AF317284	Burkholde	cl223	51.4	5.2	35338	9	AL353799	Human DNA	
1151	51.8	5.2	10732	6	E32986	Gene encodi	1224	51.4	5.2	103450	1	AF440781	Streptomy
1152	51.8	5.2	11462	8	AF327876	Chlamydom	1225	51.4	5.2	110000	1	AY305378	Ralstonia
1153	51.8	5.2	15231	1	AY166598	Burkholde	cl226	51.4	5.2	110000	2	LMFLCHR15_0	Continuation (6 of
1154	51.8	5.2	34600	1	AY028431	Burkholde	cl227	51.4	5.2	110000	2	LMFLCHR15_6	Continuation (7 of
1155	51.8	5.2	40343	2	AC099831	Homo sapi	cl228	51.4	5.2	110000	2	LMFLCHR34_00	Continuation (7 of
1156	51.8	5.2	83123	2	AC148294	Zea mays	cl229	51.4	5.2	130273	8	OSUN000011	Continuation (7 of
1157	51.8	5.2	104190	8	AF004257	03	cl230	51.4	5.2	152828	8	AC133859	Continuation (7 of
1158	51.8	5.2	110000	2	BX255276	03	cl231	51.4	5.2	205054	10	AC098712	Continuation (7 of
1159	51.8	5.2	110000	1	LMFLCHR36_22	22	cl232	51.4	5.2	205054	10	AC098712	Continuation (7 of
1160	51.8	5.2	113193	1	AF357202	Streptomy	cl233	51.4	5.2	301332	1	AE016925	Streptomy
1161	51.8	5.2	113193	6	AX703543	Sequence	cl234	51.4	5.2	302300	1	AP005034	Streptomy
1162	51.8	5.2	123149	9	AC008655	Homo sapi	1235	51.4	5.2	343473	1	AX640451	Bordetell
1163	51.8	5.2	185539	2	AC018349	Homo sapi	1236	51.2	5.2	699	6	AX412281	Sequence
1164	51.8	5.2	190590	2	AC135045	Homo sapi	1237	51.2	5.2	699	6	AX412282	Sequence
1165	51.8	5.2	202050	1	AL646065	Ralstonia	1238	51.2	5.2	699	6	AX507044	Sequence
1166	51.8	5.2	203050	1	AL646071	Ralstonia	1239	51.2	5.2	699	6	AX651360	Sequence
1167	51.8	5.2	217514	2	AC145779	Sus scrofi	1240	51.2	5.2	993	6	BD179823	Highly th
1168	51.8	5.2	298300	1	AP005025	Streptomy	1241	51.2	5.2	1182	12	AY659409	Synthetic
1169	51.8	5.2	298450	1	SC0939107	Streptomy	1242	51.2	5.2	1220	6	MZETASSELS	Zeaa mays
1170	51.8	5.2	298550	1	AP005047	Streptomy	1243	51.2	5.2	1683	6	AX697979	Sequence
1171	51.8	5.2	298900	1	AP005937	Bradyrhiz	1244	51.2	5.2	2181	8	AK100401	Oryza sat
1172	51.8	5.2	295925	1	AP005042	Streptomy	1245	51.2	5.2	2277	6	AK004983	Sequence
1173	51.8	5.2	300550	1	AP005030	Streptomy	1246	51.2	5.2	2815	1	SLCUTRS	S.lividans
1174	51.8	5.2	301675	1	AP005027	Streptomy	cl247	51.2	5.2	3480	1	CFICEND	Cellulomona
1175	51.8	5.2	305520	1	AE016780	Pseudomon	1248	51.2	5.2	3993	8	AB017481	Heterosig
1176	51.8	5.2	349008	1	BX640444	Bordetell	1249	51.2	5.2	4467	6	E33370	NA+-ATPase
1177	51.8	5.2	349841	1	BX572606	Rhodopseu	1250	51.2	5.2	6125	1	PSPSTD	Pseudomonae
1178	51.6	5.2	486	1	AF071792	Micromono	1251	51.2	5.2	6125	1	AE004549	Pseudomon
1179	51.6	5.2	730	8	AF060180	Nicotiana	cl252	51.2	5.2	10375	1	AE004549	Pseudomon
1180	51.6	5.2	1584	6	BD180289	Highly th	1253	51.2	5.2	11334	1	AE004471	Pseudomon
1181	51.6	5.2	2595	6	BD179554	Highly th	cl254	51.2	5.2	12357	1	AE004471	Pseudomon
1182	51.6	5.2	2865	8	AF019296	Zeaa mays	1255	51.2	5.2	13802	1	STE579650	Streptomy
1183	51.6	5.2	4523	14	MNULGENES	X95710 Pseudorabie	1256	51.2	5.2	22437	1	AY027524	Frankia s
1184	51.6	5.2	4548	8	AY499410	Zeaa mays	1257	51.2	5.2	77457	1	AF210249	Streptomy
1185	51.6	5.2	29148	14	AY486470S04	Human her	1258	51.2	5.2	103458	8	AC108502	Oryza sat
1186	51.6	5.2	39576	3	AC008054	Leishmani	1259	51.2	5.2	118018	8	AP005675	Oryza sat
1187	51.6	5.2	93821	2	AC021596	Human her	cl260	51.2	5.2	137651	8	AC130600	Oryza sat
1188	51.6	5.2	93821	2	AC021596	Human her	cl260	51.2	5.2	165634	2	CR354375	Danio rer



1261	51.2	5.2	185437	8	AP005422	AP005422 Oryza sat	cl334	51	5.2	189050	1	AL646066	AL646066 Ralstonia
1262	51.2	5.2	189370	1	AF010496	AF010496 Rhodobact	cl335	51	5.2	232885	2	AC106163	AC106163 Rattus no
1263	51.2	5.2	267320	2	AC106562	AC106562 Rattus no	cl336	51	5.2	234888	2	AC102097	AC102097 Mus muscu
1264	51.2	5.2	298550	1	SC0939116	AL939116 Streptomy	cl337	51	5.2	248550	1	SC0939120	AL939120 Streptomy
1265	51.2	5.2	298550	1	AP005029	AP005029 Streptomy	1338	51	5.2	299800	1	AP005040	AP005040 Streptomy
1266	51.2	5.2	300425	1	AP005022	AP005022 Streptomy	1339	51	5.2	299850	1	AP005949	AP005949 Bradyrhiz
1267	51.2	5.2	301925	1	AP005046	AP005046 Streptomy	cl340	51	5.2	300029	8	AE017104	AE017104 Oryza sat
1268	51.2	5.2	313200	1	AP005214	AP005214 Corynebact	cl341	50.8	5.1	741	6	AX573720	AX573720 Sequence
1269	51.2	5.2	348997	1	BX640427	BX640427 Bordetell	1342	50.8	5.1	1155	6	AR169160	AR169160 Sequence
1270	51.2	5.2	349028	1	BX640413	BX640413 Bordetell	1343	50.8	5.1	1155	6	BD205825	BD205825 Compounds
1271	51.2	5.2	349028	1	BX640433	BX640433 Bordetell	1344	50.8	5.1	1155	6	CQ785411	CQ785411 Sequence
1272	51	5.2	473	1	AB066368	AB066368 Streptomy	1345	50.8	5.1	1155	6	AR182450	AR182450 Sequence
1273	51	5.2	473	1	AB066369	AB066369 Streptomy	1346	50.8	5.1	1155	6	AR194833	AR194833 Sequence
1274	51	5.2	591	12	AY658503	AY658503 Synthetic	1347	50.8	5.1	1155	6	AR233105	AR233105 Sequence
1275	51	5.2	846	6	BD179798	BD179798 Highly th	1348	50.8	5.1	1155	6	AR353310	AR353310 Sequence
1276	51	5.2	846	6	BD179798	BD179798 Highly th	1349	50.8	5.1	1155	6	AR353310	AR353310 Sequence
1277	51	5.2	959	8	AY513924	AY513924 Zea mays	1350	50.8	5.1	1155	6	AX429604	AX429604 Sequence
1278	51	5.2	1004	8	AY513936	AY513936 Zea mays	1351	50.8	5.1	1155	6	AX832589	AX832589 Sequence
1279	51	5.2	1007	8	AF377762	AF377762 Zea mays	1352	50.8	5.1	1155	6	BD006453	BD006453 Compounds
1280	51	5.2	1008	8	AF377752	AF377752 Zea mays	1353	50.8	5.1	1155	6	BD006453	BD006453 Compounds
1281	51	5.2	1008	8	AF377755	AF377755 Zea mays	1354	50.8	5.1	1173	6	AX653829	AX653829 Sequence
1282	51	5.2	1008	8	AF377763	AF377763 Zea mays	1355	50.8	5.1	1221	6	BD180290	BD180290 Highly th
1283	51	5.2	1012	8	AF377764	AF377764 Zea mays	1356	50.8	5.1	1479	6	AX654603	AX654603 Sequence
1284	51	5.2	1012	8	AF377764	AF377764 Zea mays	1357	50.8	5.1	1494	8	AK109381	AK109381 Oryza sat
1285	51	5.2	1012	8	AF377749	AF377749 Zea mays	1358	50.8	5.1	1502	8	AY187941	AY187941 Oryza sat
1286	51	5.2	1012	8	AF377756	AF377756 Zea mays	1359	50.8	5.1	1897	1	MPUPFMS14	MPUPFMS14 M. olive
1287	51	5.2	1012	8	AF377756	AF377756 Zea mays	1360	50.8	5.1	2018	8	AK106761	AK106761 Oryza sat
1288	51	5.2	1012	8	AF377766	AF377766 Zea mays	1361	50.8	5.1	2025	5	GGCYP1A4	GGCYP1A4 G. gallus
1289	51	5.2	1014	8	AF377746	AF377746 Zea mays	1362	50.8	5.1	2098	5	AK121052	AK121052 Oryza sat
1290	51	5.2	1015	8	AY513919	AY513919 Zea mays	1363	50.8	5.1	2356	8	AK121052	AK121052 Oryza sat
1291	51	5.2	1015	8	AY513926	AY513926 Zea mays	1364	50.8	5.1	2358	8	ABU40823	ABU40823 Azospirillu
1292	51	5.2	1018	8	AF377747	AF377747 Zea mays	1365	50.8	5.1	2445	8	AK072584	AK072584 Oryza sat
1293	51	5.2	1018	8	AF377750	AF377750 Zea mays	1366	50.8	5.1	2490	6	BD179835	BD179835 Highly th
1294	51	5.2	1018	8	AF377750	AF377750 Zea mays	cl367	50.8	5.1	4217	5	AF331669	AF331669 Dromaius
1295	51	5.2	1018	8	AF377757	AF377757 Zea mays	1368	50.8	5.1	5760	6	AX616761	AX616761 Sequence
1296	51	5.2	1018	8	AF377758	AF377758 Zea mays	1369	50.8	5.1	10970	1	AE001869	AE001869 Deinococc
1297	51	5.2	1019	8	AF377760	AF377760 Zea mays	1370	50.8	5.1	12885	1	AE012472	AE012472 Xanthomon
1298	51	5.2	1019	8	AY513915	AY513915 Zea luxur	1371	50.8	5.1	14789	1	AE004916	AE004916 Pseudomon
1299	51	5.2	1021	8	AY513925	AY513925 Zea mays	1372	50.8	5.1	21953	6	CQ792619	CQ792619 Sequence
1300	51	5.2	1021	8	AY513935	AY513935 Zea mays	cl373	50.8	5.1	32870	1	AF007101	AF007101 Streptomy
1301	51	5.2	1025	8	AY513922	AY513922 Zea mays	cl374	50.8	5.1	36270	1	SLLINC	X79146 S. lincolne
1302	51	5.2	1231	8	AF168778	AF168778 Eucalyptu	1375	50.8	5.1	37000	14	BHTIUL	Z78205 Bovine herp
1303	51	5.2	1231	8	AK108802	AK108802 Oryza sat	1376	50.8	5.1	53951	2	AC148879	AC148879 Chlamydom
1304	51	5.2	1236	1	AF162938	AF162938 Streptomy	1377	50.8	5.1	63082	2	AC022663	AC022663 Homo sapi
1305	51	5.2	2192	8	AK109617	AK109617 Oryza sat	1378	50.8	5.1	64259	2	AC136782	AC136782 Homo sapi
1306	51	5.2	2560	4	AY453841	AY453841 Oryctolag	cl379	50.8	5.1	85268	2	AC022648	AC022648 Homo sapi
1307	51	5.2	2561	6	AR409339	AR409339 Sequence	cl380	50.8	5.1	90348	1	AF497482	AF497482 Micromono
1308	51	5.2	2561	6	AX239605	AX239605 Sequence	1381	50.8	5.1	136687	8	AC136148	AC136148 Oryza sat
1309	51	5.2	2687	9	BC066775	BC066775 Homo sapi	cl382	50.8	5.1	143266	10	AC121997	AC121997 Mus muscu
1310	51	5.2	2710	6	AX540750	AX540750 Sequence	cl383	50.8	5.1	143266	10	AC121997	AC121997 Mus muscu
1311	51	5.2	2801	9	BC066124	BC066124 Homo sapi	cl384	50.8	5.1	149303	8	AC087412	AC087412 Oryza sat
1312	51	5.2	3570	1	STMAFSR	D90155 Streptomyce	1385	50.8	5.1	160922	2	AC104848	AC104848 Oryza sat
1313	51	5.2	3757	1	CFXNCGN	Z50866 C. fimi xync	1386	50.8	5.1	180705	9	AC022167	AC022167 Homo sapi
1314	51	5.2	5123	14	HEPVIE	X15120 Pseudorabie	1387	50.8	5.1	228492	10	AC132058	AC132058 Rattus no
1315	51	5.2	6281	14	AF352564	AF352564 Pseudorab	1388	50.8	5.1	300425	1	AP005022	AP005022 Streptomy
1316	51	5.2	8199	1	STMAFSK1	M57505 Pseudorabie	cl389	50.8	5.1	301146	1	AE017311	AE017311 Desulfovi
1317	51	5.2	8438	14	SHILLT	AE004454 Pseudorab	1390	50.8	5.1	301675	1	AP005027	AP005027 Pseudomon
1318	51	5.2	11127	1	AE004454	AE004454 Pseudorab	1391	50.8	5.1	301995	1	AE016779	AE016779 Bordetell
1319	51	5.2	11157	1	AE011938	AE011938 Xanthomon	1392	50.8	5.1	346274	1	BX640443	BX640443 Bordetell
1320	51	5.2	11702	1	AE001916	AE001916 Deinococc	1393	50.6	5.1	508	6	AK236701	AK236701 Sequence
1321	51	5.2	11763	1	AE005774	AE005774 Caulobact	cl394	50.6	5.1	1147	8	AK071797	AK071797 Oryza sat
1322	51	5.2	110000	1	AP003896	Continuation (31 o	1395	50.6	5.1	1326	8	AK104577	AK104577 Oryza sat
1323	51	5.2	135357	8	AP003896	AP003896 Oryza sat	1396	50.6	5.1	1359	8	AK071886	AK071886 Oryza sat
1324	51	5.2	137651	8	AC130600	AC130600 Oryza sat	1397	50.6	5.1	1712	8	AX121535	AX121535 Oryza sat
1325	51	5.2	144724	8	AC078948	AC078948 Oryza sat	1398	50.6	5.1	1931	3	AY061814	AY061814 Nephila c
1326	51	5.2	150283	8	OSJN00136	OSJN00136 Oryza sat	1399	50.6	5.1	3764	1	AB011291	AB011291 Thermus t
1327	51	5.2	151806	9	AP002093	AP002093 Oryza sat	cl401	50.6	5.1	4233	9	HUMCMHC	U75308 Human TBP-a
1328	51	5.2	160530	9	AC090330	AC090330 Homo sapi	1402	50.6	5.1	5820	9	HUMCMHC	D00943 Homo sapien
1329	51	5.2	162227	9	OSJN00192	OSJN00192 Oryza sat	1403	50.6	5.1	10165	1	AE001935	AE001935 Deinococc
1330	51	5.2	166618	9	AC10323	AC10323 Homo sapi	cl404	50.6	5.1	12095	1	AE005853	AE005853 Caulobact
1331	51	5.2	177374	8	AC135429	AC135429 Oryza sat	1405	50.6	5.1	12945	8	AP006165	AP006165 Oryza sat
1332	51	5.2	178757	10	AC122509	AC122509 Mus muscu	1406	50.6	5.1	66599	8	AP003707	AP003707 Oryza sat
1333	51	5.2	185495	8	AP005620	AP005620 Oryza sat							



1407	50.6	5.1	79677	8	AC090435	Chlamydom	AC090435	1480	50.4	5.1	131049	8	AP005391	AP005391	Oryza sat
1408	50.6	5.1	87817	9	AC079174	Chlamydom	AC079174	1481	50.4	5.1	155106	8	AC117988	AC117988	Oryza sat
1409	50.6	5.1	102653	9	AC090436	Chlamydom	AC090436	1482	50.4	5.1	157754	10	AC132313	AC132313	Mus muscu
1410	50.6	5.1	110000	1	AE016822_09	Continuation (23 o	AE016822_09	1483	50.4	5.1	162407	8	AP004121	AP004121	Oryza sat
1411	50.6	5.1	110000	1	AE016822_22	Continuation (13 o	AE016822_22	1484	50.4	5.1	166050	1	AL646085	AL646085	Ralstonia
1412	50.6	5.1	110000	2	LMFLCHR25_05	Continuation (6 of	LMFLCHR25_05	1485	50.4	5.1	169812	2	AC150169	AC150169	Gallus ga
1413	50.6	5.1	111313	8	AP003685	Oryza sat	AP003685	1486	50.4	5.1	230138	14	AF232689	AF232689	Rat cytom
1414	50.6	5.1	129506	2	AC136100	Rattus no	AC136100	1487	50.4	5.1	262048	2	AC109382	AC109382	Rattus no
1415	50.6	5.1	144644	8	AP002818	Oryza sat	AP002818	1488	50.4	5.1	262998	2	AC109723	AC109723	Rattus no
1416	50.6	5.1	144644	2	AP003505	Oryza sat	AP003505	1489	50.4	5.1	274676	1	AE017305	AE017305	Thermus t
1417	50.6	5.1	159593	2	AC026302	Homo sapi	AC026302	1490	50.4	5.1	300271	8	AE016901	AE016901	Eremothec
1418	50.6	5.1	162400	8	AP005637	Oryza sat	AP005637	1491	50.4	5.1	300263	1	AE016781	AE016781	Pseudomon
1419	50.6	5.1	164853	8	AC135498	Oryza sat	AC135498	1492	50.4	5.1	303450	1	SC0939130	SC0939130	Streptomy
1420	50.6	5.1	166005	8	AC120506	Oryza sat	AC120506	1493	50.4	5.1	308147	1	AE016915	AE016915	Chromobac
1421	50.6	5.1	179047	8	AP005838	Oryza sat	AP005838	1494	50.4	5.1	309135	1	AP005946	AP005946	Bradyrhiz
1422	50.6	5.1	183095	2	AP005186	Oryza sat	AP005186	1495	50.4	5.1	348014	1	BX640430	BX640430	Bordetell
1423	50.6	5.1	187336	2	AP005427	Oryza sat	AP005427	1496	50.4	5.1	349442	1	BX640447	BX640447	Bordetell
1424	50.6	5.1	190834	8	AP002863	Oryza sat	AP002863	1497	50.4	5.1	349606	1	BX842583	BX842583	Mycobacte
1425	50.6	5.1	290452	2	AC079167	Mus muscu	AC079167	1498	50.4	5.1	960	11	PM1204G	PM1204G	Penicilli
1426	50.6	5.1	292400	1	SC0939129	Streptomy	SC0939129	1499	50.2	5.1	981	8	AY513911	AY513911	Zea luxur
1427	50.6	5.1	300343	1	AE017310	Desulfovi	AE017310	1500	50.2	5.1	981	8	AY513921	AY513921	Zea may
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1431	50.6	5.1	309350	1	AP005215	Corynebac	AP005215								
1432	50.6	5.1	310550	1	SC0939113	Streptomy	SC0939113								
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1435	50.6	5.1	348171	1	BX640412	Bordetell	BX640412								
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1441	50.4	5.1	742	5	BX932382	Gallus ga	BX932382								
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1443	50.4	5.1	1034	8	AK104550	Oryza sat	AK104550								
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1449	50.4	5.1	1800	1	ANTRA	Homo sapi	ANTRA								
1450	50.4	5.1	1912	1	SRBPS	Streptomyce	SRBPS								
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1452	50.4	5.1	2550	12	AY181196	Synthetic	AY181196								
1453	50.4	5.1	2826	8	AK110150	Oryza sat	AK110150								
1454	50.4	5.1	2949	8	AK068849	Oryza sat	AK068849								
1455	50.4	5.1	3029	14	AF078728	Caprine h	AF078728								
1456	50.4	5.1	3225	1	SAU29446	Streptomyce	SAU29446								
1457	50.4	5.1	3267	1	TTALAS	T.thermophi	TTALAS								
1458	50.4	5.1	4406	1	AF124138	Streptomy	AF124138								
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1474	50.4	5.1	87688	1	AV365053	Wauteria	AV365053								
1475	50.4	5.1	88203	5	AC097628	Takifugu	AC097628								
1476	50.4	5.1	106057	8	AC119796	Oryza sat	AC119796								
1477	50.4	5.1	108603	8	AP004213	Oryza sat	AP004213								
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ALIGNMENTS

LOCUS	AX201342	989 bp	DNA	linear	PAT 30-AUG-2001
DEFINITION	Sequence 21 from Patent WO0153486.				
ACCESSION	AX201342				
VERSION	AX201342.1	GI:15391164			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V., Stone, D.M., Watanabe, C.K. and Wood, W.I.				
TITLE	Compositions and methods for the treatment of tumour				
JOURNAL	Patent: WO 0153486-A 21 26-JUL-2001;				
FEATURES	Genetech, Inc. (US)				
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	/db_xref="taxon:9606"				
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Best Local Similarity	100.0%	Pred. No. 7.5e-125;			
Matches 989;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	CGCGCGCGCGCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACGTGACCTGTCTCACTGCC	60		
Db	1	CGCGCGCGCGCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACGTGACCTGTCTCACTGCC	60		
Qy	61	TCCCGCGCGCTTCTGCTCCCGCGCATGACCCAGCGGTGCGCGCTTCTGCTGCGCGCGG	120		
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Qy	121	CGCTGGCGCTGGCTCAGCGCGCTTCCGCGCGCTTCCGCGCTTCTGCTGCGCGGGA	180		
Db	121	CGCTGGCGCTGGCTCAGCGCGCTTCCGCGCGCTTCCGCGCTTCTGCTGCGCGGGA	180		
Qy	181	GGCGGTGCGCGCGCGAGCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCTGCTGCGCGGGA	240		
Db	181	GGCGGTGCGCGCGCGAGCGCGCGCTTCCGCGCGCTTCCGCGCGCTTCTGCTGCGCGGGA	240		
Qy	241	CCCTGTGCGCTATCTTCTGAGCGCTTCCATGCGGAGCACCGCGCGTTCGGAACCTGA	300		
Db	241	CCCTGTGCGCTATCTTCTGAGCGCTTCCATGCGGAGCACCGCGCGTTCGGAACCTGA	300		



241 GCCTGTGCACTATCTTCTGAGCCGCTCCATGCGGAGACACCCGCGCTCGAAGCTGA 300  
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301 GCCTGTGCACTATCTTCTGAGCCGCTCCATGCGGAGACACCCGCGCTCGAAGCTGA 360  
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RESULT 2  
AX697237 989 bp DNA linear PAT 02-APR-2003  
LOCUS Sequence 305 from Patent WO0078961.  
DEFINITION AX697237  
ACCESSION AX697237  
VERSION AX697237.1 GI:29498404  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Ferrera, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.Q., Pan, J., Berstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0078961-A 305 28-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
Location/Qualifiers  
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 VERSION AV358476.1 GI:37182074  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 989)  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wisand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.  
 The Secretd Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
 PUBMED 12975309  
 REFERENCE 2 (bases 1 to 989)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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 ORIGIN  
 Query Match 100.0%; Score 989; DB 9; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-125;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 ACCESSION AV338454  
 VERSION AV338454.1 GI:18128893  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Meyers,R.A. and Williamson,M.  
 25692, a novel human o-methyltransferase family member and uses  
 TITLE



thereof:	
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Matches 987; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS	BC047774				
DEFINITION	Homo sapiens catechol-O-methyltransferase domain containing 1, mRNA (CDNA clone MGC:54273 IMAGE:5761696), complete cds.				
ACCESSION	BC047774				
VERSION	BC047774.1	GI:28839536			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1041)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fane, J., Helton, E., Kettman, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Jones, S.J., Smal, U., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBLISHED	12477932				
REFERENCE	2 (bases 1 to 1041)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs@mail.nih.gov">cgabs@mail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,				



R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 98 Row: g Column: 5  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

## FEATURES

source

Location/Qualifiers

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## ORIGIN

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DEFINITION Human signal peptide-containing protein.
ACCESSION BD222712
VERSION BD222712.1 GI:33032482
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,
Baughn, M.R., Akerman, I.E., Young, J.A., Yue, H., Patterson, C.,
Reddy, R., Hillman, J.L. and Bandman, O.
Human signal peptide-containing protein
Patent: JP 2002519030-A 58 02-JUL-2002;
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PN JP 2002519030-A/58
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762 31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686 11-DEC-1998 US 60/112129 PI PRETI
LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,
PI MARIAH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,
PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN
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Accession			
AK074421.1 GI:18677019			
Version			
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AUTHORS			
1 Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Taghio, H., Ota, T., Suzuki, Y., Obayashi, M., Nishi, I., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.			
NEDO human cDNA sequencing project			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
2 (bases 1 to 988)			
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.			
Direct Submission			
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan			
E-mail: flcdna@u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416			
COMMENT			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).			
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MGC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
```

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Aramini,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A.C., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 913)

Strausberg,R.

Direct Submission

Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Dec 19, 2003 this sequence version replaced gi:23959051.

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Iaric,P., Legaspi,R., Maduro,Q.I., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>

Series: IRAL Plate: 39 Row: j Column: 6

This clone was selected for full length sequencing because it passed the following selection criteria: GenomesScan gene prediction, Similarity but not identity to protein.

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Location/Qualifiers

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/note="Vector: pOTB7"

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gene

CDS



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Best Local Similarity 99.8%; Pred. No. 7.8e-114;
Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 259 TGAGCGCTCCATGCGGAGCACCGCGCTGCGAAGCTCTGAGGCTGTGACCTGGAGC 318
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Qy 499 CCCGAGCTGGGAGCGGCCCTGTGGAGGCGAGCGCGAGGACCAAGATCGACCTCC 558
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Qy 919 CCAGGAATTGACCCCTGAGTTTAAATTCGAAATAAAGTGGGGCTGGGACACAAAAA 978
Db 841 CCAGGAATTGACCCCTGAGTTTAAATTCGAAATAAAGTGGGGCTGGGACACAAAAA 900
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Qy 979 AAAAAAAAAA 989
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RESULT 9
LOCUS       CQ721501              789 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 7435 from Patent WO02068579.
ACCESSION   CQ721501
VERSION     CQ721501.1 GI:42282358
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 7435 06-SEP-2002;
            PE Corporation
  FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1e-97;
Matches 789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 ATGACCCAGCGGTGCGCGCTCTCCGTGCCCCCGCGCTGGCCCTGGGCTCAGCCGCA 143
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Qy 324 CAGGGGATTTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACTTGGCGGGCTC 383
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Db 301 ATCCAGGCCAAGAGGCGCTGGAACCTGGGACCTTTCAGGGGCTACTCCGCCCTGGCCCTG 360

Qy 444 GCCTTGGCGCTTGGCGCGGAGCGGGCGCTGTGTGACCTTGGAGGTGGAGCGCGAGCCCCCG 503
Db 361 GCCTTGGCGCTTGGCGCGGAGCGGGCGCTGTGTGACCTTGGAGGTGGAGCGCGAGCCCCCG 420

Qy 504 GAGCTGGAGCGGCCCTTGTGGAGCGAGCCGAGGCGGAGCAAGATCGACTCTCGGGCTG 563
Db 421 GAGCTGGAGCGGCCCTTGTGGAGCGAGCCGAGGCGGAGCAAGATCGACTCTCGGGCTG 480

Qy 564 AAGCCCGCTTTGGAGACCTTGGAGCTGTGTGGCGGGCGAGCGCGGACCTTTCGAC 623
Db 481 AAGCCCGCTTTGGAGACCTTGGAGCTGTGTGGCGGGCGAGCGCGGACCTTTCGAC 540

Qy 624 GTGGCGGTGTGGATGCGGACAAGAGAACTGTCTCGGCTTACTACGAGGCTCTCTGAC 683
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QY 744 CAACCTCCGAAGAGGAGGTGGCGCGGAGTGTGTGCGAACTTAAACGAACGATCCGG 803

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QY 864 AAGATCTAG 872

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RESULT 10

AX338456

LOCUS

DEFINITION

Sequence 3 from Patent WO0183719.

ACCESSION

AX338456

VERSION

AX338456.1 GI:18128895

KEYWORDS

ORGANISM

Homo sapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

MEYERS, R.A. and WILLIAMSON, M.

25692, a novel human o-methyltransferase family member and uses thereof

Patent: WO 0183719-A 3 08-NOV-2001;

Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers

1..789

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

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source

ORIGIN

Query Match 79.8%; Score 789; DB 6; Length 789;

Best Local Similarity 100.0%; Pred. No. 1e-97;

Matches 789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCGGCTGGCCCTGGGCTCAGCCGCA 143

Db 1 ATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCGGCTGGCCCTGGGCTCAGCCGCA 60

QY 144 CTGGGCGCGCTTCCGCACTGGCTCTTCTGGGAGCGGTGCGCCCATGGCGAGGC 203

Db 61 CTGGGCGCGCTTCCGCACTGGCTCTTCTGGGAGCGGTGCGCCCATGGCGAGGC 120

QY 204 CGCGAGAGCAGTGTCTGCTTCCCCCGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC 263

Db 121 CGCGAGAGCAGTGTCTGCTTCCCCCGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC 180

QY 264 CGCTCATGCGGAGCAGCCGCGGTGCGAGCTGTGAGGCTGTGACCTTGAGAGAGCG 323

Db 181 CGCTCATGCGGAGCAGCCGCGGTGCGAGCTGTGAGGCTGTGACCTTGAGAGAGCG 240

QY 324 CAGGGGATTTATGATGACCTGCGAGCGCCAGCTTTGGCCAACTGGCGGGCTC 383

Db 241 CAGGGGATTTATGATGACCTGCGAGCGCCAGCTTTGGCCAACTGGCGGGCTC 300

QY 384 ATCCAGGCCAAGAGCGCTGACCTGGGCACTTTACGGGCTACTCCGCGCTGSCCTG 443

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QY 444 GCGCTGGCGCTGCCCGGAGCGGGCGCTGTGTGACCTGCGAGGTGAGCGCGAGCCCGC 503

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QY 504 GAGCTGGGACCGGCGGCTGTGTGAGGAGGAGCCGAGGCGGAGCAAGATCGACCTCCGGCTG 563

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Db 601 CTGTGCGACCCGAGGAGCATCTCGCCTCTCAGAGTCTGTGTGGCGGAGGAGTGTG 660

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QY 864 AAGATCTAG 872

Db 781 AAGATCTAG 789

RESULT 11

BC049670

LOCUS

DEFINITION

Mus musculus catechol-O-methyltransferase domain containing 1, mRNA

ACCESSION

BC049670

VERSION

BC049670.1 GI:29612504

KEYWORDS

MGC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 946)

STRAUSBERG, R.L., FEINGOLD, E.A., GROUSE, L.H., DERGE, J.G.,

KLAUSNER, R.D., COLLINS, P.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D.,

ALTSCHUL, S.F., ZEEBERG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K.,

HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F.,

DIATCHENKO, L., MARUSINA, K., FARMER, A.A., RUBIN, G.M., HONG, L.,

STAPLETON, M., SOARES, M.B., BONALDO, M.F., CASAVANT, T.L.,

SCHETZ, T.E., BROWNSTEIN, M.J., USIDIN, T.B., TOSHIYUKI, S.,

CARNINCI, P., PRANGE, C., RAHA, S.S., LOQUELLANO, N.A., PETERS, G.J.,

ABRAMSON, R.D., MULLAHY, S.J., BOSAK, S.A., MCEWAN, P.J.,

McKERNAN, R.J., MALEK, J.A., GUNARATNE, P.H., RICHARDS, S.,

WORLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W.,

VILLALON, D.K., MUZYNY, D.M., SODERGREN, E.J., LU, X., GIBBS, R.A.,

FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., YOUNG, A.C., RODRIGUES, S.,

SANCHEZ, A., WHITING, M., MADAN, A., MADAN, A., RODRIGUES, S.,

BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D.,

DICKSON, M.C., RODRIGUEZ, A.C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M.,

BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALAK, U., SMALL, D.E.,

SCHNERCH, A., SCHEIN, J.E., JONES, S.J., AND MARRA, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

REFERENCE

2 (bases 1 to 946)

STRAUSBERG, R.

Direct Submission

Submitted (31-MAR-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA







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Best Local Similarity 99.7%; Pred. No. 5.8e-33;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 649 AGAAGTGTCTCGGCC-TACTACGAGCGCTGCTCGAGCTGCTGCGACCGGAGGATCTCTC 707
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QY 768 GCCGAGTGTGCGAAACCTTAACGACGATCCGCGCGGAGCTGAGGCTTACATCAGC 827
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RESULT 13
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LOCUS Rattus norvegicus clone CH230-34D17, WORKING DRAFT SEQUENCE, 2
DEFINITION
unordered pieces.
ACCESSION AC120475
VERSION AC120475.7 GI:25137871
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 237829)
Muzny, D.Marie, Metzker, M.Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, A.,
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Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, C., Hamilton, K.,
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuheva, L., Loulseghe, H., Lozada, R.J., Lu, X., Ma, J.,
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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
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Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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TITLE JOURNAL
REFERENCE
AUTHORS
TITLE JOURNAL
REFERENCE
AUTHORS
TITLE JOURNAL
COMMENT

Nwaokemeh, O., Okwuonu, G., Olarpunsgoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shivartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K.,
Valas, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 237829)
Worley, K.C.
Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237829)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23267656.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMLH
Center clone name: CH230-34D17
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 218320 bases at least Q40
Consensus quality: 222359 bases at least Q30
Consensus quality: 225092 bases at least Q20
Estimated insert size: 222440; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 236267: contig of 236267 bp in length
* 236268 236367: gap of unknown length

```



\* 236368 237829: contig of 1462 bp in length.

FEATURES

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clone\_end:Sp6"  
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7112..7990  
misc\_feature  
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site:  
end\_sequence: BH359353"  
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misc\_feature  
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end\_sequence: BH358581"

ORIGIN

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Best Local Similarity 69.6%; Pred. No. 2.6e-33;  
Matches 433; Conservative 0; Mismatches 188; Indels 1; Gaps 1;  
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Db 81826 TTACTGGTCCCAAGTCTGCTGCGGCTCTACTCCAGCAGACGTGACCTCTGCTTTGTAAC 81885  
QY 113 GCCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 172  
Db 81886 CGCACATGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 81945  
QY 173 CTTGGGAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 232  
Db 81946 CTTGGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 82005  
QY 233 GGACAGCGCTGCTGGGAGTATCTTCTGAGCGGCTCCATGCGGAGGAGGAGGAGGAGGAGG 292  
Db 82006 GGACAAATCCCTGCTGGGAGTATCTGCTGAGCTGCTCCATGAGGAGGAGGAGGAGGAGG 82065  
QY 293 AAGCTGAGGCTGCTGACCTGAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 352  
Db 82066 GAGCTTGCGACTGCTGACCTGAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 82125  
QY 353 GGCCGAGCTTTGGCCAACTGCGGCGGCTCATCCAGGCGCAAGAGGCGCTGGACCTGGG 412  
Db 82126 GSCCCAACTTCTGGTCAACTGGCGGCGGCTCATCAAGCAAGAAAGCTCTGGATCTGGG 82185  
QY 413 CACTTACGGGCTA-CTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 471  
Db 82186 TACTTTACGGGCTACTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 82245  
QY 472 TGGTCACTGCGAGGTGAGCGGCGGAGCCCGGAGCTGGAGCGGCGGCTGCTGGAGGCGAGG 531  
Db 82246 TGGTCACTGCGAGGTGAGCGGCGGAGCCCGGAGCTGGAGCGGCGGCTGCTGGAGGCGAG 82305  
QY 532 CCGAGCGGAGCACAAGATCGACCTCCGCGTGAAGCCCGGCTTGGAGACCTTGGACGAGC 591  
Db 82306 CAGAAGTGGAGCAGAAGATCGAACTTCGCTGCGCGCGGCTGCGGCTGCGGCTGCGGCTG 82365  
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QY 652 ACTGCTCGGCTTACTACGAGCG 673  
Db 82426 CTGCTGCACTCTTACGCGCG 82447

RESULT 14  
AL390034/c  
LOCUS  
DEFINITION  
Human DNA sequence from clone RP11-375G3 on chromosome 10, complete sequence.  
ACCESSION  
AL390034 -  
VERSION  
AL390034.23 GI:18041549  
KEYWORDS  
HTG.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 38679)  
Wray, P.  
Direct Submission  
Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Jan 2, 2002 this sequence version replaced gi:18032099.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/c\_elegans/wormpep/ This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr10  
RP11-375G3 is from the library RP11-11.2 constructed by the group of Peter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-375G3 It may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true left end of clone RP11-399K21 is at 36680 in this sequence. The true right end of clone RP11-487I5 is at 2000 in this sequence.  
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ORIGIN

Query Match 26.0%; Score 256.8; DB 9; Length 38679;  
Best Local Similarity 97.4%; Pred. No. 5.2e-26;  
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 704 CTTGCCCTCTCAGAGTCTGTGCGCGGAGAGGTGCTGCAACCTCCGAAGGGGAGCT 763  
Db 7761 CCGCGCCCTCCGCGAGTCTGTGCGCGGAGAGGTGCTGCAACCTCCGAAGGGGAGCT 7702



QY 764 GCGGCCGAGTGTGTGCGAAACCTAAACGAACGATCCGGCGGAGCTCAGGCTTACAT 823  
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 QY 824 CAGCCTCTCTGCCCCCTGGCGGATGAGTCACTTGGCTTCAAGATCTAGGCTGCGCCCT 883  
 Db 7641 CAGCCTCTCTGCCCCCTGGCGGATGAGTCACTTGGCTTCAAGATCTAGGCTGCGCCCT 7582  
 QY 884 AGTAGTGGCTCGAGGAGGTTCCCTGGGAACCCCAAGGATTAACCTGAGTTTAAA 943  
 Db 7581 AGTAGTGGCTCGAGGAGGTTCCCTGGGAACCCCAAGGATTAACCTGAGTTTAAA 7522  
 QY 944 TTCGAATAAAGTGGGCTGGACACA 971  
 Db 7521 TTCGAATAAAGTGGGCTGGACACA 7494

RESULT 15  
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 DEFINITION Homo sapiens chromosome 10 clone RP11-770D23 map 10, WORKING DRAFT  
 SEQUENCE, 28 unordered pieces.  
 ACCESSION AC027393  
 VERSION AC027393.3 GI:8076860  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 10, clone RP11-770D23  
 Unpublished  
 2 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,  
 Campopiano,A., Castie,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
 Levine,J., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vasiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Direct Submission  
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,  
 Campopiano,A., Castie,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
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 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
 Levine,J., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
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 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,  
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 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 25, 2000 this sequence version replaced gi:7652066.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997),  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L6572  
 Center clone name: 770 D 23

----- Summary Statistics  
 Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 155213 bases at least Q40  
 Consensus quality: 162022 bases at least Q30  
 Consensus quality: 164973 bases at least Q20  
 Insert size: 179000; agarose-bp  
 Insert size: 166912; sum-of-contigs  
 Quality coverage: 4.1 in Q20 bases; agarose-bp  
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1191: contig of 1191 bp in length  
 \* 1192: gap of 100 bp  
 \* 1292: contig of 1113 bp in length  
 \* 2405: gap of 100 bp  
 \* 2505: contig of 1201 bp in length  
 \* 3706: gap of 100 bp  
 \* 4735: contig of 929 bp in length  
 \* 4835: contig of 1736 bp in length  
 \* 6571: gap of 100 bp  
 \* 6671: contig of 1313 bp in length  
 \* 8584: gap of 100 bp  
 \* 10290: contig of 1607 bp in length  
 \* 10391: gap of 100 bp  
 \* 10391: contig of 1548 bp in length  
 \* 11939: gap of 100 bp  
 \* 12039: contig of 3801 bp in length  
 \* 15840: gap of 100 bp  
 \* 15940: contig of 3264 bp in length  
 \* 19204: gap of 100 bp  
 \* 19304: contig of 3278 bp in length  
 \* 22582: gap of 100 bp  
 \* 22682: contig of 2266 bp in length  
 \* 25048: gap of 100 bp  
 \* 28167: contig of 3120 bp in length  
 \* 28168: gap of 100 bp  
 \* 32083: contig of 3816 bp in length  
 \* 32183: gap of 100 bp  
 \* 32184: contig of 3350 bp in length  
 \* 35534: gap of 100 bp  
 \* 41517: contig of 5884 bp in length



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* 41518 41617: gap of 100 bp
* 41618 47143: contig of 5526 bp in length
* 47144 47243: gap of 100 bp
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* 51694 51794: gap of 100 bp
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* 57570 57671: gap of 100 bp
* 57671 63190: contig of 5520 bp in length
* 63190 63291: gap of 100 bp
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* 70708 70808: gap of 100 bp
* 70808 79088: contig of 8180 bp in length
* 79088 86527: contig of 7439 bp in length
* 86527 86628: gap of 100 bp
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* 99114 99215: gap of 100 bp
* 99215 110221: contig of 11007 bp in length
* 110221 110321: gap of 100 bp
* 110321 123287: contig of 12966 bp in length
* 123287 123388: gap of 100 bp
* 123388 147877: contig of 24490 bp in length
* 147877 147978: gap of 100 bp
* 147978 169612: contig of 21635 bp in length.
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Query Match      26.0%; Score 256.8; DB 2; Length 169612;
Best Local Similarity 97.4%; Pred. No. 3.6e-26;
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 704 CCTCGCGTCTCTAGAGTCCTGTGGCGGGGAAGTGTGCAACCTCCGAAAGGGGACGT 763
Db 140411 CCGCGCCCTCCCGCAGGTCTGTGGCGGGGAAGTGTGCAACCTCCGAAAGGGGACGT 140352

QY 764 GCGCGCCGAGTGTGTGGGAAACCTAAACGAACGATCCGGCGGGACGTCAGGGTCTACAT 823
Db 140351 GCGCGCCGAGTGTGTGGGAAACCTAAACGAACGATCCGGCGGGACGTCAGGGTCTACAT 140292

QY 824 CAGCCTCTCTGCCCTCTGGCGGATGGACTCACCTTGGCCCTTCAAGATCTAGGGCTGCCCT 883
Db 140291 CAGCCTCTCTGCCCTCTGGCGGATGGACTCACCTTGGCCCTTCAAGATCTAGGGCTGCCCT 140232

QY 884 AGTGAGTGGGCTCGAGGGAGGGTTGCCCTGGGAAACCCAGGAAATTGACCTGAGTTTAAA 943
Db 140231 AGTGAGTGGGCTCGAGGGAGGGTTGCCCTGGGAAACCCAGGAAATTGACCTGAGTTTAAA 140172

QY 944 TTCGAAATAAAGTGGGCTGGGACACA 971
Db 140171 TTCGAAATAAAGTGGGCTGGGACACA 140144

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Search completed: January 12, 2005, 21:28:41  
Job time : 4280 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 12:52:52 ; Search time 3040 Seconds  
(without alignments)  
11854.900 Million cell updates/sec

Title: US-10-017-407A-305  
Perfect score: 989  
Sequence: 1 gcgggcccggagtcgcgaga.....caaaaaaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_g881.\*
- 9: gb\_g882.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797.4	80.6	889	4	RM451059 AGENCOURT
2	762.6	77.1	771	6	CB852030
3	743	75.1	814	4	BM051236
4	736	74.4	756	6	CA777547
5	721	72.9	1006	2	BF663323
6	716	72.4	921	2	BF664198
7	707.2	71.5	921	5	BM976177
8	699.8	70.8	750	6	CB852718
9	684.4	69.2	772	2	BE796570
10	669.8	67.7	779	2	BF663695
11	666.4	67.4	934	5	BQ931589
12	630	63.7	1065	5	BQ072503
13	625	63.2	625	4	BM768764
14	621	62.8	912	4	BG339399
15	609.2	61.6	2243	3	AK054334
16	607.6	61.4	919	3	AK007659
17	603.4	61.0	606	2	AW157329
18	587.8	59.4	910	6	BY707694
19	585.8	59.2	589	1	AI692198
20	585.6	59.2	1122	4	BG339315
21	580	58.6	580	4	BM769685
22	579	58.5	998	5	BQ918468
23	578.4	58.5	581	1	AI923359
24	578.4	58.5	691	2	BE279279

25	574.6	58.1	904	6	CB194568
26	574.2	58.1	826	5	BP433057
27	564.4	57.1	582	2	AW157252
28	562.8	56.9	886	6	CB181160
29	560.2	56.6	753	5	BP463671
30	557.2	56.3	977	5	BU841828
31	549.2	55.5	578	1	AW003514
32	548.6	55.5	620	1	AA584408
33	545.4	55.1	1308	3	CR602194
34	542.8	54.9	909	6	CB194405
35	542	54.8	572	1	AI765658
36	540.2	54.6	639	4	BG910899
37	538.4	54.4	566	2	AW163525
38	538.4	54.4	999	3	BC019467
39	535	54.1	564	2	AW163385
40	533.4	53.9	790	4	BI411825
41	526.2	53.2	688	7	CK464189
42	522.6	52.8	546	2	AW157459
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46	519	52.5	725	7	CN159458
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48	511.8	51.7	516	4	BG285119
49	509.8	51.5	710	5	BQ746381
50	487.4	49.3	676	2	BB666437
51	482.4	48.8	710	7	CK771494
52	471.8	47.7	638	1	AI924025
53	470.2	47.5	1321	3	CR625911
54	466.4	47.2	666	7	CK463833
55	465.2	47.0	614	7	CK622065
56	460.8	46.6	682	7	CN166896
57	460	46.5	675	7	CN161942
58	460	46.5	675	7	CN163323
59	460	46.5	685	7	CN157439
60	460	46.5	685	7	CN159383
61	456.8	46.2	681	7	CK838500
62	456	46.1	456	5	BQ083301
63	450.2	45.5	622	6	CD674768
64	447.4	45.2	449	2	AW163255
65	446.2	45.1	573	4	BI340505
66	446	45.1	446	4	BM825668
67	445.6	45.1	453	1	AI963924
68	441.4	44.6	459	1	AI929284
69	439.6	44.4	629	1	AI989669
70	439	44.4	1110	4	BI198020
71	438.8	44.4	454	5	BU500439
72	438.4	44.3	487	7	CK819654
73	438.4	44.3	507	4	BM129438
74	438.4	44.3	519	4	BM141699
75	437.6	44.2	556	2	BE665755
76	437.2	44.2	538	1	AI659582
77	434	43.9	434	4	BM826016
78	427.8	43.3	605	2	BG895491
79	427.4	43.2	549	2	BE014998
80	427.2	43.2	546	2	BE237447
81	426.2	43.1	543	2	BE665750
82	425.6	43.0	550	2	BE684896
83	422.6	42.7	525	4	BM129725
84	419.8	42.4	579	4	BI341406
85	417.4	42.2	460	1	AI340993
86	417	42.2	599	4	BQ498801
87	416.2	42.1	970	5	BX422891
88	415.4	42.0	448	1	AI349083
89	413	41.8	413	5	BQ082692
90	411.4	41.6	421	2	AW299522
91	410.8	41.5	422	2	BF593185
92	410.6	41.5	513	2	BF193231
93	406.4	41.1	580	4	BI680796
94	406	41.1	415	2	AW299513
95	404.8	40.9	695	4	BG081244
96	398.2	40.3	1162	2	AI340991
97	397.8	40.2	1162	2	BE797685

CB194568	AGENCOURT
BP433057	BP433057
AW157252	au3e01.x
CB181160	AGENCOURT
BP463671	BP463671
BU841828	AGENCOURT
AW003514	wq6g10.x
AA584408	nm8103.s
CR602194	full-leng
CB194405	AGENCOURT
AI765658	w182g12.x
BG910899	602812540
AW163525	au9sh04.y
BC019467	Mus muscu
AW163385	au94f01.y
BI411825	602966437
CK464189	935151 MA
AW157459	au95h04.x
BM339546	BM339546
BF341318	602013260
CN157520	946232 MA
CN159458	948536 MA
AI810740	tu04a11.x
BG285119	602409396
CK771494	959788 MA
AI924025	wn73e06.x
CR625911	full-leng
CK463833	934767 MA
CK622065	ml32b11.y
CN166896	998978 MA
CN161942	951279 MA
CN163323	952815 MA
CN157439	946147 MA
CN159383	948451 MA
CK838500	UI-R-AFI-
BQ083301	K-EST0145
CD674768	fa15a05.y
AW163255	au93e01.y
BI340505	365795 MA
BM825668	K-EST0097
AI963924	wq77f05.x
AI929284	au59e03.x
AI989669	wb35a05.x
BI198020	602762169
BU500439	AGENCOURT
CK819654	if22d02.x
BM129438	if22d02.x
BM141699	if24h03.x
BE665755	154904 MA
AI659582	tt87c02.x
BM826016	K-EST0097
BG895491	358968 MA
BE014998	126934 MA
BE237447	146741 MA
BE665750	154898 MA
BE684896	186649 MA
BM129725	if22d02.y
BI341406	368809 MA
AI340993	q082909.x
BQ498801	602544450
BX422891	EX422891
AI349083	q083909.x
BQ082692	K-EST0144
AW299522	x840h01.x
BF593185	7050a03.x
BF193231	244743 MA
BI680796	459974 MA
AW299513	x840g01.x
BG081244	H3062H08-
AI340991	q082907.x
BE797685	601584583



98	397.6	40.2	524	6	CB720369	AMGNNUC:N	171	253	25.6	1292	3	CR681700	Tetraodon
99	397.2	40.2	584	7	CF360100	821402.WA	172	252.8	25.6	1208	3	CR700159	Tetraodon
100	396	40.0	405	1	AI912836	t286c05.x	173	251.4	25.4	1178	3	CR660388	Tetraodon
101	390.2	39.5	516	6	CB716330	AMGNNUC:C	174	251.4	25.4	1201	3	CR633873	Tetraodon
102	387	39.1	411	4	BN768965	K-EST0052	175	251.4	25.4	1205	3	CR692309	Tetraodon
103	385.2	38.9	502	7	CK819655	K-EST0052	176	251.4	25.4	1220	3	CR682032	Tetraodon
104	375.2	37.9	565	4	BN753400	K-EST0030	177	251.4	25.4	1224	3	CR698208	Tetraodon
105	373.8	37.8	517	9	CG651631	OST413096	178	251.4	25.4	1228	3	CR731482	Tetraodon
106	373.2	37.7	474	4	BN141962	BM141962	179	251.4	25.4	1229	3	CR701700	Tetraodon
107	370	37.4	506	4	BI340371	BI340371	180	250.8	25.4	1215	3	CR676419	Tetraodon
108	365.2	36.9	370	1	AI341293	AI341293	181	249.8	25.3	1161	3	CR682009	Tetraodon
109	364	36.8	485	5	BS524890	BS524890	182	249.8	25.3	1226	3	CR695099	Tetraodon
110	361.2	36.5	977	4	BI198073	BI198073	183	249.8	25.3	1238	3	CR682588	Tetraodon
111	358.2	35.7	732	2	BE287985	BE287985	184	249.8	25.3	1244	3	CR732330	Tetraodon
112	346.2	35.0	362	2	BF509580	BF509580	185	249.8	25.3	1247	3	CR727683	Tetraodon
113	345.8	35.0	365	6	CB050636	NISC_GJ118	186	249.8	25.3	1290	3	CR647544	Tetraodon
114	345.6	34.9	553	2	BE286087	601095931	187	249.8	25.3	1572	3	CR693937	Tetraodon
115	344.2	34.8	365	6	CB050637	NISC_GJ118	188	249.2	25.2	1218	3	CR727337	Tetraodon
116	343	34.7	1056	5	BX339545	BX339545	189	249	25.2	1216	3	CR732881	Tetraodon
117	342.6	34.6	515	6	CF181537	CF181537	190	248.8	25.2	1218	3	CR687075	Tetraodon
118	339.4	34.3	505	1	AA016453	mh40c05.r	191	248.6	25.1	1224	3	CR662508	Tetraodon
119	335	33.9	458	4	BG689814	BG689814	192	248.2	25.1	1198	3	CR695082	Tetraodon
120	332.2	33.6	539	2	BB769048	BB769048	193	248.2	25.1	1231	3	CR687110	Tetraodon
121	329	33.3	442	7	CK457735	922062.WA	194	248.2	25.1	1243	3	CR638609	Tetraodon
122	329	33.3	442	7	CK458804	923214.WA	195	247.6	25.0	360	5	BY057583	BY057583
123	328.4	33.2	341	1	AI650609	AI650609	196	247.6	25.0	1186	3	BY057583	BY057583
124	326.4	33.0	470	6	CA777819	CA777819	197	246.8	25.0	423	2	AW52701	UI-R-BJO-
125	315.4	31.9	499	4	BG995780	BG995780	198	246.6	24.9	1222	3	CR696179	Tetraodon
126	313.4	31.7	528	1	AI548694	AI548694	199	244.6	24.7	1150	3	CR684437	Tetraodon
127	312	31.5	326	2	BE233897	BE233897	200	244.6	24.7	375	5	BY04191	BY04191
128	311.8	31.5	426	2	AI325680	mm60d11.y	201	244.4	24.6	1143	3	CR685515	Tetraodon
129	306.6	31.0	414	1	AI892364	mm60d11.y	202	243	24.6	1143	3	BI832844	BI832844
130	303.4	30.7	402	6	CB769191	AMGNNUC:N	203	243	24.5	1211	3	CR698267	Tetraodon
131	301.2	30.5	414	1	AI892364	mm60d11.y	204	242.4	24.5	401	6	CB698999	AMGNNUC:N
132	300.2	30.4	458	6	CB739243	AMGNNUC:N	205	242.2	24.5	372	5	BY042000	BY042000
133	296	29.9	413	5	BY094423	BY094423	206	241	24.4	1188	3	CR690884	Tetraodon
134	292.2	29.5	398	1	AA132529	AA132529	207	241	24.4	1263	3	CR727342	Tetraodon
135	292	29.5	382	4	EM856156	K-EST0139	208	240.6	24.3	503	3	BG669239	BG669239
136	291.8	29.5	971	4	BG680071	602628219	209	238.4	24.1	413	2	AW52346	UI-R-BJO-
137	291.6	29.5	428	5	BY041621	BY041621	210	238	24.1	411	2	AW52346	UI-R-BJO-
138	291.6	29.5	479	2	BF522579	BF522579	211	237.8	24.0	1188	3	CR698292	Tetraodon
139	288.8	29.2	379	6	CA480947	CA480947	212	237.2	24.0	1200	3	CR690706	Tetraodon
140	288.2	29.1	1074	6	CA480947	AGENCOURT	213	237.2	24.0	1200	3	CR690806	Tetraodon
141	283.2	28.6	754	5	BE653217	BE653217	214	236.8	23.9	740	5	BX074246	BX074246
142	279	28.2	375	2	BF181707	BF181707	215	235.2	23.8	240	1	AI420833	AI420833
143	274.8	27.8	664	2	BU615801	BU615801	216	234.4	23.7	439	5	BY447416	BY447416
144	274.2	27.7	400	5	BY050241	BY050241	217	234.4	23.7	937	6	CA458592	CA458592
145	270	27.3	683	5	BU615801	BU615801	218	234.4	23.7	1215	3	CR726092	CR726092
146	262.8	26.6	434	2	BB787832	BB787832	219	234	23.7	273	1	AI307481	AI307481
147	262	26.5	384	1	AA068794	mm60d11.r	220	232.8	23.5	913	3	CR638711	CR638711
148	262	26.5	421	1	AA068794	mm60d11.r	221	232.6	23.5	344	5	BY057551	BY057551
149	262	26.5	473	6	CA395926	CA395926	222	232.4	23.5	583	9	CS567423	CS567423
150	261.8	26.5	1235	6	BI304044	BI304044	223	232.4	23.5	325	3	AW52346	UI-R-BJO-
151	261.4	26.4	722	5	CR721460	CR721460	224	231	23.4	871	3	CR653669	CR653669
152	261.2	26.3	1171	3	CR731130	CR731130	225	231	23.4	362	5	BY045218	BY045218
153	260.2	26.3	1275	3	CR686979	CR686979	226	230.8	23.3	419	7	CN542838	CN542838
154	260.2	26.3	1194	3	CR725106	CR725106	227	230	23.3	878	3	CR654482	Tetraodon
155	258.6	26.1	1207	3	CR646763	Tetraodon	228	229.4	23.2	1181	3	CR692840	Tetraodon
156	258	26.1	1232	3	CR722216	CR722216	229	229.2	23.2	769	6	CA346219	CA346219
157	258	26.1	1211	3	CR722184	CR722184	230	229.2	23.2	336	5	BY048400	BY048400
158	257	25.9	436	2	AW521225	AW521225	231	229	23.2	885	3	CR633632	CR633632
159	256.6	25.9	296	4	BI711000	BI711000	232	228.4	23.1	360	1	AA279903	AA279903
160	255.8	25.8	1133	3	CR640078	CR640078	233	228	23.1	862	3	CR650550	Tetraodon
161	255.4	25.8	1183	3	CR696993	CR696993	234	225.4	22.8	876	3	CR649975	Tetraodon
162	255	25.7	1156	3	CR685973	CR685973	235	225.2	22.8	406	4	BI288752	BI288752
163	254.6	25.7	371	5	BY048974	BY048974	236	225.2	22.7	881	3	CR656653	CR656653
164	253.8	25.7	374	5	BY037587	BY037587	237	224.8	22.6	874	3	CR651698	Tetraodon
165	253.8	25.7	1144	3	CR700317	CR700317	238	223.8	22.6	884	3	CR653782	Tetraodon
166	253.8	25.7	1216	3	CR685301	CR685301	239	223.8	22.6	904	3	CR639009	Tetraodon
167	253.8	25.6	298	2	AW664650	hi84b01.x	240	223.8	22.6	924	3	CR655129	Tetraodon
168	253.2	25.6	169	2	CR683289	Tetraodon	241	223.8	22.5	858	3	CR641707	Tetraodon
169	253	25.6	1162	3	CR683190	Tetraodon	242	223	22.5	873	3	CR733986	Tetraodon
170	253	25.6	1245	3	CR683190	Tetraodon	243	222.8	22.5				



244	222.4	22.5	449	1	AA132590	AA132590	zo20d02.r	317	184.6	18.7	638	4	BJ711589	BJ711589	BJ711589	BJ711589
245	222.4	22.5	860	3	CR656656	CR656656	Tetraodon	318	184	18.6	670	6	CA355616	CA355616	CA355616	227543 NC
246	222.2	22.5	910	3	CR637704	CR637704	Tetraodon	319	184	18.6	678	7	CN974704	CN974704	CN974704	23486 125
247	221	22.3	863	3	CR644752	CR644752	Tetraodon	320	184	18.6	869	7	CN985211	CN985211	CN985211	57529 127
248	220	22.2	863	3	CR637158	CR637158	Tetraodon	321	183.2	18.5	691	4	BJ708514	BJ708514	BJ708514	BJ708514
249	219.4	22.2	746	6	CA374473	CA374473	648906 NC	322	182.2	18.4	527	5	BQ615750	BQ615750	BQ615750	fab14b01.
250	219.4	22.2	860	3	CR655148	CR655148	Tetraodon	323	182.2	18.4	336	5	BY398227	BY398227	BY398227	BY398227
251	219.4	22.2	861	3	CR634105	CR634105	Tetraodon	324	180.8	18.3	539	6	CA333551	CA333551	CA333551	haa85c09.
252	219.4	22.2	864	3	CR653465	CR653465	Tetraodon	325	177.6	18.0	677	7	CR647326	CR647326	CR647326	Tetraodon
253	219	22.1	910	3	CR637674	CR637674	Tetraodon	326	177	17.9	177	7	F36952	F36952	F36952	HSPD34933 H
254	217.8	22.0	526	5	BY468703	BY468703	BY468703	327	175.6	17.8	505	4	BG835402	BG835402	BG835402	354522 MA
255	217.8	22.0	862	3	CR645383	CR645383	Tetraodon	328	173.2	17.5	598	7	CR895107	CR895107	CR895107	SGP154357
256	217.6	22.0	388	5	BY405666	BY405666	BY405666	329	172.6	17.5	1100	7	CK161647	CK161647	CK161647	FGAS01451
257	217.2	22.0	724	6	CA382012	CA382012	661717 NC	330	172.2	17.4	593	7	CR895655	CR895655	CR895655	SGP158175
258	217	21.9	386	5	BY394806	BY394806	BY394806	331	171	17.3	967	7	CK409756	CK409756	CK409756	AUF lph0k
259	215.8	21.8	747	6	CA388383	CA388383	670627 NC	332	170.2	17.2	873	7	CN978664	CN978664	CN978664	29757 125
260	215	21.7	715	7	F36954	F36954	HSPD34939 H	333	169	17.1	653	4	BM426804	BM426804	BM426804	pgf2n-ph0
261	215	21.7	351	5	BY085557	BY085557	BY085557	334	169	17.1	907	2	BE412589	BE412589	BE412589	MCG002.C1
262	214.8	21.7	370	5	BY398556	BY398556	BY398556	335	168.6	17.0	749	2	BF626523	BF626523	BF626523	HVSMEa001
263	213.4	21.6	678	6	CA353706	CA353706	625267 NC	336	168.6	17.0	864	7	CK195971	CK195971	CK195971	FGAS00441
264	212.4	21.5	582	4	BM574123	BM574123	fx59d04.Y	337	168.4	17.0	587	7	CK896420	CK896420	CK896420	SGP158963
265	212.2	21.5	596	4	BM574082	BM574082	fx59h01.Y	338	168	17.0	673	5	BO752785	BO752785	BO752785	WHE4119 B
266	212	21.4	790	4	BJ719956	BJ719956	BJ719956	339	168	17.0	682	1	AJ612197	AJ612197	AJ612197	AJ612197
267	211.8	21.4	854	3	CR651108	CR651108	Tetraodon	340	168	17.0	704	2	BF228537	BF228537	BF228537	EST00248
268	211.4	21.4	1189	3	CR734171	CR734171	Tetraodon	341	167.6	16.9	469	4	BJ010311	BJ010311	BJ010311	BJ010311
269	210.2	21.3	264	2	AW477994	AW477994	18030 MAR	342	167.4	16.9	819	7	CK193277	CK193277	CK193277	FGAS00169
270	209.8	21.2	337	2	AW356352	AW356352	38646 WAR	343	167.2	16.9	881	6	CF250863	CF250863	CF250863	esa018 a1
271	209.4	21.2	213	7	F29823	F29823	HSPD19935 H	344	167	16.9	692	6	CD866963	CD866963	CD866963	AZO2.1040
272	209	21.1	1206	3	CR641100	CR641100	Tetraodon	345	167	16.9	794	7	CK193235	CK193235	CK193235	FGAS00164
273	208.6	21.1	576	4	BM529070	BM529070	fx61f11.Y	346	166.4	16.8	499	1	AL919863	AL919863	AL919863	AL919863
274	208.2	21.1	765	6	CA341770	CA341770	671433 NC	347	166.2	16.8	836	7	CK195388	CK195388	CK195388	FX22a08.Y
275	207.6	21.0	582	5	BQ615284	BQ615284	fab24d05.	348	166	16.8	208	2	BE853865	BE853865	BE853865	uax02a08.Y
276	207.2	21.0	371	5	BY404587	BY404587	BY404587	349	165.8	16.8	713	6	CD869948	CD869948	CD869948	AZO2.113A
277	206.6	20.9	581	5	BQ450896	BQ450896	fab12d03.	350	165.6	16.7	566	7	CK885643	CK885643	CK885643	SGP166021
278	206.6	20.9	720	6	CA360096	CA360096	633318 NC	351	165.6	16.7	816	2	BF064997	BF064997	BF064997	HV CEB002
279	206.4	20.9	569	5	BQ480163	BQ480163	fab86g07.	352	165.4	16.7	630	4	BY960166	BY960166	BY960166	HVSMEa000
280	205.4	20.8	1002	2	BE785237	BE785237	601474760	353	165.2	16.7	1148	7	CN988270	CN988270	CN988270	64067 125
281	205.2	20.7	756	4	BJ739050	BJ739050	BJ739050	354	165	16.7	694	2	BE214450	BE214450	BE214450	HV CEB000
282	205.2	20.7	764	4	BJ716953	BJ716953	BJ716953	355	165	16.7	705	2	BE216491	BE216491	BE216491	HV CEB001
283	205	20.7	581	5	BQ783563	BQ783563	fab31c01.	356	165	16.7	697	2	BE216491	BE216491	BE216491	AL503249
284	204.6	20.7	1000	5	BX422892	BX422892	HSPD34927 H	357	165	16.7	700	1	AL503249	AL503249	AL503249	AL503249
285	204	20.6	205	7	F36948	F36948	HSPD34927 H	358	165	16.7	705	2	BE519617	BE519617	BE519617	HV CEB001
286	203.8	20.6	796	7	CF931709	CF931709	EST0141 A	359	165	16.7	714	2	BE519891	BE519891	BE519891	HV CEB002
287	203.4	20.6	357	5	BY406134	BY406134	BY406134	360	165	16.7	737	2	BE559087	BE559087	BE559087	HV CEB002
288	203	20.5	363	5	BY400948	BY400948	BY400948	361	165	16.7	780	5	BO752940	BO752940	BO752940	WHE4120 H
289	202.8	20.5	1205	5	CR652934	CR652934	Tetraodon	362	164.6	16.6	673	4	BM370604	BM370604	BM370604	EBR008 SQ
290	201.2	20.3	688	6	CA350955	CA350955	621897 NC	363	164.6	16.6	804	2	BF624054	BF624054	BF624054	HVSMEa000
291	201	20.3	263	2	AW370022	AW370022	QV4-BT023	364	163.6	16.5	551	7	CK896911	CK896911	CK896911	SGP159468
292	200.8	20.3	204	1	AA618529	AA618529	np30d12.s	365	163	16.5	667	6	CA196132	CA196132	CA196132	SCSBAD108
293	200.6	20.3	364	2	AW252050	AW252050	UI-R-BJ70-	366	163	16.5	649	2	BE216025	BE216025	BE216025	HV CEB000
294	200.4	20.3	555	4	BM154433	BM154433	fv85a10.Y	367	163	16.5	1038	7	CK213384	CK213384	CK213384	FGA502529
295	200.4	20.3	561	4	BM186124	BM186124	fv98c04.Y	368	162.8	16.5	543	6	C23048	C23048	C23048	C23048
296	199.8	20.2	614	1	AL180003	AL180003	AL180003	369	162.6	16.4	600	6	C23352	C23352	C23352	Japa
297	199.4	20.2	553	4	BM186049	BM186049	fv97a10.Y	370	162.2	16.4	715	6	CD883740	CD883740	CD883740	FI.114E16
298	198.2	20.0	643	6	CB512007	CB512007	ssalrpb53	371	161.8	16.4	711	6	CD873066	CD873066	CD873066	AZO2.122E
299	198.2	20.0	644	6	CA333572	CA333572	haa85h10.	372	161.4	16.3	699	1	AJ615461	AJ615461	AJ615461	AJ615461
300	196.6	19.9	407	5	BY395434	BY395434	BY395434	373	161.4	16.3	706	2	BF625981	BF625981	BF625981	HVSMEa001
301	196.6	19.9	407	5	BY395434	BY395434	BY395434	374	161.4	16.3	714	6	CD864630	CD864630	CD864630	AZO2.001G
302	196.4	19.9	635	8	AZ958898	AZ958898	2M022D022	375	161.4	16.3	1121	7	CK162943	CK162943	CK162943	FGAS01555
303	196.4	19.9	365	5	BY079881	BY079881	BY079881	376	160.8	16.3	648	4	BY959235	BY959235	BY959235	HVSMEa001
304	196.4	19.9	537	4	BM534699	BM534699	fx70d07.Y	377	160.6	16.2	709	5	BO752659	BO752659	BO752659	WHE4119 B
305	195.6	19.8	645	4	BJ705610	BJ705610	BJ705610	378	160.6	16.2	795	5	BO752791	BO752791	BO752791	WHE4119 B
306	194	19.6	660	4	BJ727162	BJ727162	BJ727162	379	160.6	16.2	807	2	BF065240	BF065240	BF065240	HV CEB002
307	193.4	19.6	352	1	AL172475	AL172475	UI-R-AFL-	380	160.6	16.2	810	7	CK197247	CK197247	CK197247	FGA500571
308	192.8	19.5	837	6	C23373	C23373	CU3373 Japa	381	160.6	16.2	930	4	BI956791	BI956791	BI956791	HVSMEa000
309	192.6	19.5	302	2	BF605771	BF605771	272357 MA	382	160.4	16.2	802	6	CA158127	CA158127	CA158127	SCEZRZ305
310	192.4	19.5	429	5	BY412806	BY412806	BY412806	383	160.4	16.2	869	7	CK409595	CK409595	CK409595	AUF lflvr
311	191.8	19.4	629	1	AU179577	AU179577	AU179577	384	160.4	16.2	1052	7	CK210051	CK210051	CK210051	FGA502184
312	191.8	19.4	1211	3	CR683715	CR683715	Tetraodon	385	160	16.2	642	1	A1477552	A1477552	A1477552	fb58g04.Y
313	189.6	19.2	439	5	BY599654	BY599654	BY599654	386	160	16.2	666	1	AL504625	AL504625	AL504625	AL504625
314	189.2	19.1	731	4	BU722907	BU722907	BU722907	387	159.8	16.2	652	4	BI960399	BI960399	BI960399	HVSMEa002
315	188.8	19.1	855	7	CN985363	CN985363	58335 126	388	159.8	16.2	655	5	BQ838311	BQ838311	BQ838311	WHE2909 A
316	185.4	18.7	513	5	BO783421	BO783421	fab29f02.	389	159.8	16.2	66					



390	159.8	16.2	694	6	CD937240	OV.106G10	463	150.4	15.2	621	5	BQ743179	BQ743179	WHE4101_C
391	159.8	16.2	729	6	CD885596	G118.0010	464	150.4	15.2	726	5	BQ838107	BQ838107	WHE2906_F
392	159.8	16.2	731	6	CD885623	G118.001P	465	150.4	15.2	733	5	BQ838231	BQ838231	WHE2908_A
393	159.8	16.2	732	6	CD939542	OV.11302A	466	150.4	15.2	776	5	BQ618942	BQ618942	RNOSEQ1F0
394	159.8	16.2	813	7	CD939542	OV.11302A	467	150.2	15.2	596	2	BQ403578	BQ403578	WHE0434_C
395	159.8	16.2	814	7	CD939542	OV.11302A	468	150.2	15.2	631	2	BQ473218	BQ473218	WHE0922_H
396	159.6	16.1	747	1	AJ614420	FGAS00897	469	150.2	15.2	874	7	CD169125	CD169125	AGENCOURT
397	159.6	16.1	1121	6	CA131093	SCBFR106	470	150.2	15.2	693	6	CA153085	CA153085	SCSRBZ202
398	159.4	16.1	661	4	BT468189	EST00596	471	150.2	15.2	789	7	CD108171	CD108171	WHE3876_E
399	159.4	16.1	868	7	CD405866	AUF_Iflvtr	472	149.8	15.1	588	2	BE493850	BE493850	WHE1276_H
400	159.4	16.1	943	7	CD409493	AUF_Iflvtr	473	149.6	15.1	655	2	CF626673	CF626673	Zmrw05_0
401	159.2	16.1	683	6	CD930335	GR45.110P	474	149.6	15.1	658	4	BM072891	BM072891	WHE55-D0
402	159.2	16.1	866	6	CD930335	GR45.110P	475	149.6	15.1	668	4	BM072891	BM072891	WHE55-D0
403	158.8	16.1	653	4	CD930335	GR45.110P	476	149.6	15.1	708	6	CD878344	CD878344	AZOA.102I
404	158.6	16.0	646	6	CD930335	GR45.110P	477	149.6	15.1	654	4	BI950057	BI950057	HVSMEN001
405	158.6	16.0	722	5	CD930335	GR45.110P	478	149.2	15.1	880	4	BI950057	BI950057	HVSMEN001
406	158.4	16.0	866	6	CD930335	GR45.110P	479	149.2	15.1	881	7	CK196097	CK196097	FGAS00454
407	158.2	16.0	647	4	CD930335	GR45.110P	480	149.2	15.1	1072	3	AY108449	AY108449	Zea maye
408	157.6	15.9	721	5	CD930335	GR45.110P	481	148.8	15.0	363	2	AM658108	AM658108	93873 MAR
409	157.4	15.9	639	6	CD930335	GR45.110P	482	148.8	15.0	398	4	BM573972	BM573972	FX57d11_Y
410	157.4	15.9	649	6	CD930335	GR45.110P	483	148.4	15.0	640	5	BQ743388	BQ743388	WHE4103_D
411	157.2	15.9	731	5	CD930335	GR45.110P	484	148.4	15.0	665	8	BZ641948	BZ641948	OGAMK72TM
412	157.2	15.9	1064	7	CD930335	GR45.110P	485	148.4	15.0	899	9	CG397599	CG397599	OG1A080TV
413	157.2	15.9	1064	7	CD930335	GR45.110P	486	148.4	15.0	902	7	CK406893	CK406893	AUF_Iflvtr
414	156.6	15.8	1142	7	CD930335	GR45.110P	487	148.4	15.0	934	7	CK406893	CK406893	AUF_Iflvtr
415	156.2	15.8	921	7	CD930335	GR45.110P	488	148.4	15.0	956	7	CK406893	CK406893	AUF_Iflvtr
416	156.2	15.8	756	6	CD930335	GR45.110P	489	148.4	15.0	681	4	BI959659	BI959659	HVSMEN002
417	156.2	15.8	799	7	CD930335	GR45.110P	490	148.4	15.0	681	4	BI959659	BI959659	HVSMEN002
418	155.8	15.8	1126	7	CD930335	GR45.110P	491	148.4	15.0	807	2	BF259949	BF259949	HVSMEN002
419	155.6	15.7	918	7	CD930335	GR45.110P	492	148.4	15.0	1146	3	AY104406	AY104406	Zea maye
420	155.6	15.7	1080	7	CD930335	GR45.110P	493	147.6	14.9	505	7	CK895885	CK895885	SGP158415
421	155.2	15.7	752	7	CD930335	GR45.110P	494	147.6	14.9	505	7	CK895885	CK895885	SGP158415
422	155.2	15.7	764	5	CD930335	GR45.110P	495	147.6	14.9	659	1	AJ615423	AJ615423	AJ615423
423	155.2	15.7	1138	7	CD930335	GR45.110P	496	147.6	14.9	746	7	CO520722	CO520722	3530_1-13
424	155.2	15.7	797	7	CD930335	GR45.110P	497	147.6	14.9	780	7	CO528134	CO528134	3530_1-18
425	155.2	15.7	846	7	CD930335	GR45.110P	498	147.6	14.9	465	4	BJ498661	BJ498661	BJ498661
426	154.8	15.7	880	4	CD930335	GR45.110P	499	147.4	14.9	499	4	BJ527812	BJ527812	BJ527812
427	154.8	15.7	817	7	CD930335	GR45.110P	500	147.4	14.9	515	4	BJ490344	BJ490344	BJ490344
428	154.6	15.6	905	4	CD930335	GR45.110P	501	147.4	14.9	562	4	BJ496988	BJ496988	BJ496988
429	154.6	15.6	1054	7	CD930335	GR45.110P	502	146.8	14.8	610	7	CK896728	CK896728	SGP159280
430	154.4	15.6	557	5	CD930335	GR45.110P	503	146.8	14.8	615	6	CA246946	CA246946	SGSGFV5C0
431	154.4	15.6	624	5	CD930335	GR45.110P	504	146.8	14.8	737	2	AW012934	AW012934	Ldt.-0102
432	154.4	15.6	624	5	CD930335	GR45.110P	505	146.8	14.8	739	7	CK896728	CK896728	SGP159280
433	154.4	15.6	627	5	CD930335	GR45.110P	506	146.8	14.8	692	6	CD868552	CD868552	AZ02.109E
434	154.4	15.6	628	5	CD930335	GR45.110P	507	146.6	14.8	877	6	CA755835	CA755835	BR0300290
435	154.4	15.6	646	5	CD930335	GR45.110P	508	146.6	14.8	649	6	CD904272	CD904272	G356.112P
436	154.4	15.6	646	5	CD930335	GR45.110P	509	146.4	14.8	670	6	CA151503	CA151503	SCJFR2201
437	153.8	15.6	416	5	CD930335	GR45.110P	510	146.4	14.8	896	7	CK407472	CK407472	AUF_Iflvtr
438	153.6	15.5	629	4	CD930335	GR45.110P	511	146.4	14.8	664	5	BP184560	BP184560	BP184560
439	153.6	15.5	643	5	CD930335	GR45.110P	512	146.2	14.8	923	7	CK407551	CK407551	AUF_Iflvtr
440	153.6	15.5	823	2	CD930335	GR45.110P	513	146.2	14.8	613	7	CK896516	CK896516	SGP159062
441	153.4	15.5	550	6	CD930335	GR45.110P	514	146.2	14.8	654	6	CA131555	CA131555	SCBGR104
442	153.4	15.5	617	2	CD930335	GR45.110P	515	146.2	14.8	684	2	BF256079	BF256079	HVSMEN000
443	153.4	15.5	630	7	CD930335	GR45.110P	516	146.2	14.8	853	2	BF256079	BF256079	HVSMEN000
444	153.4	15.5	636	6	CD930335	GR45.110P	517	146.2	14.8	746	7	CK201455	CK201455	FGAS00997
445	153.2	15.5	686	5	CD930335	GR45.110P	518	145.8	14.7	851	7	CK201455	CK201455	FGAS00997
446	152.8	15.4	756	2	CD930335	GR45.110P	519	145.6	14.7	915	6	CK215205	CK215205	FGAS02715
447	152.8	15.4	638	4	CD930335	GR45.110P	520	145.6	14.7	671	5	CK215205	CK215205	FGAS02715
448	152.6	15.4	672	2	CD930335	GR45.110P	521	145.6	14.7	627	5	CK215205	CK215205	FGAS02715
449	152.4	15.4	798	7	CD930335	GR45.110P	522	145.2	14.7	915	6	CK215205	CK215205	FGAS02715
450	152.4	15.4	817	7	CD930335	GR45.110P	523	144.8	14.6	637	5	CK215205	CK215205	FGAS02715
451	152.4	15.4	817	7	CD930335	GR45.110P	524	144.6	14.6	774	6	CA065807	CA065807	SCBGR104
452	151.8	15.3	610	5	CD930335	GR45.110P	525	144.4	14.6	616	4	BJ259369	BJ259369	BJ259369
453	151.8	15.3	624	6	CD930335	GR45.110P	526	144.4	14.6	635	6	CK2181	CK2181	C23181 Japa
454	151.6	15.3	666	6	CD930335	GR45.110P	527	144.4	14.6	649	6	CB870888	CB870888	HC15J04W
455	151.2	15.3	684	1	CD930335	GR45.110P	528	144.4	14.6	803	4	BJ247474	BJ247474	BJ247474
456	151.2	15.3	1141	7	CD930335	GR45.110P	529	144.4	14.6	856	7	CK202105	CK202105	FGAS01062
457	151.2	15.3	1106	7	CD930335	GR45.110P	530	144.4	14.6	774	9	CK202105	CK202105	FGAS01062
458	150.8	15.2	412	4	CD930335	GR45.110P	531	144.2	14.6	598	4	CK895980	CK895980	SGP158514
459	150.8	15.2	546	1	CD930335	GR45.110P	532	144.2	14.6	648	4	BJ024113	BJ024113	SGP158514
460	150.8	15.2	667	4	CD930335	GR45.110P	533	143.8	14.5	317	1	AI853323	AI853323	UI-M-BHO-
461	150.8	15.2	720	5	CD930335	GR45.110P	534	143.8	14.5	520	1	AU164541	AU164541	AU164541
462	150.4	15.2	472	5	CD930335	GR45.110P	535	143.8	14.5					



536	143.8	14.5	668	4	BI959395	HVSMEN001	BI959395	HVSMEN001	609	137.8	13.9	759	6	CD879592	AZ04.105M
537	143.8	14.5	831	7	CK201781	FGAS01030	CK201781	FGAS01030	610	137.6	13.9	469	6	CA497305	WHE3225_F
538	143.8	14.5	881	7	CK202172	FGAS01069	CK202172	FGAS01069	611	137.6	13.9	661	6	CA107862	SCSHR105
539	143.4	14.5	812	7	CO804908	AGENCOURT	CO804908	AGENCOURT	612	137.4	13.9	532	2	BE361185	DGL 70 D1
540	143.4	14.5	817	7	CK193931	FGAS00235	CK193931	FGAS00235	613	137.4	13.9	537	2	BE490625	WHE0370 D
541	143.4	14.5	996	4	BG837909	Zm10_09q1	BG837909	Zm10_09q1	614	137.4	13.9	590	4	BI779395	EBR001_SQ
542	143.2	14.5	419	2	BF483204	WHE1787_B	BF483204	WHE1787_B	615	137.4	13.9	628	6	CD909626	G468.113C
543	143.2	14.5	660	4	BI957746	HVSMEN001	BI957746	HVSMEN001	616	137.4	13.9	660	6	CD899633	GI74.113A
544	143.2	14.5	718	6	CD938268	OV_109123	CD938268	OV_109123	617	137.2	13.9	690	6	CD918343	G608.109A
545	143.2	14.5	718	6	CD938289	OV_109K04	CD938289	OV_109K04	618	137.2	13.9	905	7	CK407588	AUF IF1Lvr
546	142.8	14.4	506	2	CK138077	WHE2305_A	CK138077	WHE2305_A	619	137	13.9	496	5	BQ247189	TaE15028C
547	142.8	14.4	836	7	CK200685	FGAS00920	CK200685	FGAS00920	620	136.6	13.8	709	6	CA146291	SCVPR207
548	142.8	14.4	803	7	CK189143	EST1778458	CK189143	EST1778458	621	136.6	13.8	816	8	BZ541105	OGAST43TC
549	142.8	14.4	867	7	CF636603	Zmrw00_0	CF636603	Zmrw00_0	622	136.6	13.8	823	2	BF256995	HVSMEN001
550	142.8	14.4	873	7	CK189144	EST1778459	CK189144	EST1778459	623	136.6	13.8	889	6	CA159865	SCVPR23C0
551	142.6	14.4	518	4	BG300054	HVSMEN001	BG300054	HVSMEN001	624	136.2	13.8	588	1	AL822798	AL822798
552	142.6	14.4	595	1	AI857214	603008D06	AI857214	603008D06	625	136.2	13.8	605	6	CA733178	w1p1c_Pk0
553	142.6	14.4	606	6	CD895487	GI74.001P	CD895487	GI74.001P	626	136	13.8	589	6	CA018785	HV09K09r
554	142.6	14.4	664	1	AL820289	AL820289	AL820289	AL820289	627	136	13.8	649	6	CA290596	SCUTSD102
555	142.4	14.4	684	6	CA142702	SCMCR210	CA142702	SCMCR210	628	136	13.8	675	6	CA209393	SCCST3C1
556	142.4	14.4	684	6	CA142702	SCMCR210	CA142702	SCMCR210	629	136	13.8	756	7	CK215844	FGAS02781
557	142.4	14.4	808	7	CK977279	27484_125	CK977279	27484_125	630	135.8	13.7	454	4	BM136098	WHE2602_F
558	142.2	14.4	626	2	BE423372	WHE0065_D	BE423372	WHE0065_D	631	135.8	13.7	540	4	BI779178	EBR001_SQ
559	142.2	14.4	636	4	BJ259464	BJ259464	BJ259464	BJ259464	632	135.8	13.7	551	1	AL828595	AL828595
560	142.2	14.4	677	4	BQ905724	TaE1141H	BQ905724	TaE1141H	633	135.8	13.7	605	4	BM660519	952039C01
561	142.2	14.4	797	6	CD868553	AL820289	CD868553	AL820289	634	135.8	13.7	613	6	CD911360	G550.110P
562	142	14.4	611	4	BI957501	HVSMEN000	BI957501	HVSMEN000	635	135.8	13.7	743	4	BJ252414	BJ252414
563	142	14.4	622	1	AI637136	603001A11	AI637136	603001A11	636	135.2	13.7	540	4	BG842718	BG842718
564	142	14.4	624	5	BP184421	BP184421	BP184421	BP184421	637	135.2	13.7	590	4	BM660518	BM660518
565	142	14.4	646	4	BJ466490	BJ466490	BJ466490	BJ466490	638	135.2	13.7	645	8	BZ628759	ih62b02.9
566	141.8	14.3	178	1	AL962519	wq53a08.x	AL962519	wq53a08.x	639	135.2	13.7	786	6	CA137489	CA137489
567	141.6	14.3	354	7	CK847633	970292_MA	CK847633	970292_MA	640	134.6	13.6	663	6	CA280962	CA280962
568	141.6	14.3	1086	7	CK213734	FGAS02564	CK213734	FGAS02564	641	134.4	13.6	503	6	C23213	C23213
569	141.4	14.3	406	6	CD080702	LcA04J05C	CD080702	LcA04J05C	642	134.4	13.6	540	6	C23049	C23049
570	141.4	14.3	526	6	CF059783	OC516904	CF059783	OC516904	643	134.4	13.6	605	6	CA155532	SCACR2310
571	141.4	14.3	629	6	CA146427	SCVPR208	CA146427	SCVPR208	644	134.4	13.6	673	4	BM371957	BM371957
572	141.4	14.3	660	5	BQ806305	WHE3577_C	BQ806305	WHE3577_C	645	134.2	13.6	409	5	BQ471953	BQ471953
573	141.4	14.3	736	2	BF630555	HVSMEN001	BF630555	HVSMEN001	646	134	13.5	683	4	BG370011	HVSMEN002
574	141.2	14.3	627	4	BG293937	HVSMEN001	BG293937	HVSMEN001	647	134	13.5	756	6	CB680447	OSJNEF05C
575	141.2	14.3	660	6	CA123437	SCMCL101	CA123437	SCMCL101	648	133.8	13.5	476	6	CA117774	SCBGLR104
576	141.2	14.3	814	7	CK201094	FGAS00961	CK201094	FGAS00961	649	133.8	13.5	507	6	CD9711462	QAD9b02.8
577	141	14.3	588	1	AL808354	AL808354	AL808354	AL808354	650	133.8	13.5	694	4	BZ61281	BZ61281
578	141	14.3	616	5	BQ788665	WHE4152_E	BQ788665	WHE4152_E	651	133.6	13.5	847	7	CA175403	AGENCOURT
579	140.8	14.2	509	4	BJ549094	BJ549094	BJ549094	BJ549094	652	133.6	13.5	486	3	CR640865	Tetraodon
580	140.8	14.2	562	2	BF484304	WHE2321_F	BF484304	WHE2321_F	653	133.4	13.5	622	4	BI679740	949078E04
581	140.8	14.2	578	4	BM068669	WHE3461_D	BM068669	WHE3461_D	654	133.4	13.5	666	5	BQ468365	BM01A23T
582	140.8	14.2	687	6	CA192398	SCCST3C0	CA192398	SCCST3C0	655	133.4	13.5	719	7	CA145340	WOUND1_39
583	140.8	14.2	759	2	BF259495	HVSMEN001	BF259495	HVSMEN001	656	133.4	13.5	805	8	BZ533265	OGAST43TC
584	140.6	14.2	893	4	BI952091	HVSMEN000	BI952091	HVSMEN000	657	133.2	13.5	580	4	BM100502	BM100502
585	140.4	14.2	408	2	BE361254	DGL 70 D1	BE361254	DGL 70 D1	658	133.2	13.5	670	5	BU998750	H112A22r
586	140.4	14.2	723	6	CB653598	OSJNEC04M	CB653598	OSJNEC04M	659	133.2	13.5	781	5	BU296625	BU296625
587	140.2	14.2	454	6	CA006913	HU06B07r	CA006913	HU06B07r	660	133	13.4	712	5	BU672830	BU672830
588	140	14.2	650	6	CA191213	SCCCT2C0	CA191213	SCCCT2C0	661	133	13.4	802	9	CG615544	OGM0T23TV
589	140	14.2	664	5	BQ762267	EBR001_SQ	BQ762267	EBR001_SQ	662	132.8	13.4	592	4	BI478930	949071A06
590	140	14.2	691	1	AJ613139	AJ613139	AJ613139	AJ613139	663	132.8	13.4	637	4	BI960118	HVSMEN002
591	139.8	14.1	720	6	CA172879	SCUTSB103	CA172879	SCUTSB103	664	132.6	13.4	593	7	CK888688	SGP160680
592	139.4	14.1	740	7	CN011226	WHE3881_F	CN011226	WHE3881_F	665	132.4	13.4	289	1	AV075054	AV075054
593	139.4	14.1	802	2	BF261040	HVSMEN002	BF261040	HVSMEN002	666	132.4	13.4	448	6	CA190352	SCCCT1C0
594	139.4	14.1	814	7	CK202356	FGAS01088	CK202356	FGAS01088	667	132.2	13.4	581	6	CB878369	HP08E22T
595	139.2	14.1	540	6	CD878426	AZ04.102L	CD878426	AZ04.102L	668	132	13.3	370	2	BE406401	BE406401
596	139.2	14.1	741	5	BX074245	BX074245	BX074245	BX074245	669	132	13.3	673	6	CA234708	SCJUSB106
597	139.2	14.1	836	9	CG323590	OGWIE5TV	CG323590	OGWIE5TV	670	132	13.3	756	7	BF065160	BF065160
598	139	14.1	618	7	CN010871	WHE3877_C	CN010871	WHE3877_C	671	131.6	13.3	573	2	CP065160	HV_CEB002
599	139	14.1	623	8	BZ641943	OGAMK72TC	BZ641943	OGAMK72TC	672	131.6	13.3	634	6	CA136726	SCQSR103
600	139	14.1	750	6	CD898674	GI74.109L	CD898674	GI74.109L	673	131.6	13.3	692	6	CA142664	SCMCR210
601	138.6	14.0	411	1	AA943314	EST198813	AA943314	EST198813	674	131.6	13.3	808	7	CA142664	SCMCR210
602	138.6	14.0	716	4	BI960085	HVSMEN002	BI960085	HVSMEN002	675	131.2	13.3	573	6	CD877325	AZ04.100B
603	138.6	14.0	743	6	CA180815	SCACST316	CA180815	SCACST316	676	131.2	13.3	655	4	BI960535	HVSMEN002
604	138.4	14.0	636	6	CD934106	GR45_123A	CD934106	GR45_123A	677	131.2	13.3	691	5	BQ840928	WHE4205_B
605	138.4	14.0	678	6	CA071322	SCACAM107	CA071322	SCACAM107	678	131	13.2	679	6	CA253440	SCJLFLA10
606	138.4	14.0	765	2	BE705618	SC01_0351	BE705618	SC01_0351	679	130.8	13.2	501	2	BE586643	WHE0508_C
607	138.2	14.0	511	4	BG262486	WHE0936_E	BG262486	WHE0936_E	680	130.8	13.2	799	7	CF635242	Zmrw00_0
608	137.8	13.9	561	1	AL819807	AL819807	AL819807	AL819807	681	130.6	13.2	507	6	CA181402	SCBFST313



682	130.6	13.2	650	1	AJ432275	AJ432275	AJ432275	755	125	12.6	647	6	CA285613	SCR2SD107
683	130.6	13.2	654	6	CA175542	SCJLST101	CA175542	756	125	12.6	694	4	B265176	BJ265176
684	130.6	13.2	857	7	CN172476	AGCUSTOCT	CN172476	c 757	125	12.6	1049	7	CK163799	FGAS01643
685	130.4	13.2	286	1	AV070774	AV070774	AV070774	758	124.8	12.6	554	6	CA686379	wlm96.pk0
686	130.4	13.2	679	6	CA141617	SCJLRT205	CA141617	759	124.8	12.6	652	4	BI957644	HVSMEN001
687	130.4	13.2	691	6	CA182059	SCBGST310	CA182059	c 760	124.8	12.6	695	6	CA090038	SCSGAM207
688	130.4	13.2	819	7	CN127149	RHOHI_21	CN127149	761	124.6	12.6	448	1	AU182287	AU182287
689	130.4	13.2	850	7	CK204382	FGAS01291	CK204382	762	124.6	12.6	696	6	CA280310	SCVPLB2C0
690	130.2	13.2	436	7	CK896903	SGP159460	CK896903	763	124.6	12.6	720	7	CN989253	65281_125
691	130.2	13.2	685	5	BUL03556	SCCCHRI00	BUL03556	764	124.2	12.6	577	5	BP184433	BP184433
692	130.2	13.2	685	6	CA102750	SCCCHRI00	CA102750	765	124.2	12.6	670	7	CF433879	NIT1_30_C
693	130.2	13.2	813	4	BG321263	ZM04_0350	BG321263	766	124.2	12.6	713	6	CA221136	SCB2FLA04
694	130	13.1	319	2	AW670333	114312_MA	AW670333	767	124	12.5	493	4	BG263195	WHB2339_B
c 695	130	13.1	553	5	BQ036499	SL5_0018	BQ036499	768	123.8	12.5	538	5	BQ468035	BQ468035
696	130	13.1	720	6	CA221618	SCSGFLA03	CA221618	769	123.8	12.5	737	6	CA216695	SCCST3C1
697	130	13.1	973	6	CA136643	SCQGRIT04	CA136643	770	123.6	12.5	464	2	BE125749	DGI_55_H1
698	129.2	13.1	626	4	EM895773	BM955773	EM895773	771	123.6	12.5	622	6	CA137725	SCCORT200
699	129	13.0	578	6	CB870318	HC13P20W	CB870318	772	123.6	12.5	702	7	CN123933	RHOHI_1_D
c 700	129	13.0	624	4	BU543510	BU543510	BU543510	773	123.2	12.5	659	6	CA089962	SCSGAM207
c 701	129	13.0	1090	7	CK216386	FGAS02837	CK216386	774	123.2	12.5	1088	4	BG338516	BG338516
702	128.8	13.0	812	6	CA183398	SCQGST312	CA183398	775	123.2	12.5	514	6	CA023538	HZA311B
703	128.6	13.0	193	2	BE863248	UI-M-BHO-	BE863248	776	123	12.4	514	6	CA023184	HZA5H18r
704	128.6	13.0	580	7	CK889037	SGP161045	CK889037	777	123	12.4	676	4	BI958752	HVSMEN001
705	128.6	13.0	582	7	CK889567	SGP161594	CK889567	778	122.8	12.4	587	6	CA208078	SCWCSB11
706	128.4	13.0	528	7	CK889538	SGP164404	CK889538	779	122.8	12.4	631	4	BI960531	HVSMEN002
707	128.4	13.0	669	6	CA187131	SCUTST308	CA187131	780	122.8	12.4	632	5	BU977317	HA11D12r
708	128.4	13.0	679	6	CA262688	SCPLTB202	CA262688	781	122.8	12.4	635	6	CA025276	HZ51K20r
c 709	128.2	13.0	327	7	CF368954	853716_MA	CF368954	c 782	122.8	12.4	647	6	CD988525	G174_109E
710	128.2	13.0	630	6	CA131650	SCBGRIT04	CA131650	783	122.8	12.4	803	4	BG837569	Zm10_02f1
711	128.2	13.0	685	6	CA121225	SCBGRIT09	CA121225	784	122.8	12.4	639	6	CA244742	SCSPFLA08
712	128.2	13.0	696	6	CA085150	SCBZAM206	CA085150	785	122.6	12.4	490	2	BF202447	WHEI764_G
713	128.2	13.0	727	6	CA219139	SCRFAD111	CA219139	786	122.4	12.4	274	1	AV074448	AV074448
c 714	128	12.9	597	4	BU505563	BU505563	BU505563	c 787	122.2	12.4	630	6	CA191567	SCCORT2C0
715	128	12.9	621	6	CA222622	SCR2FLA04	CA222622	788	122.2	12.4	274	1	BF092010	RC0-TN007
716	128	12.9	626	1	AU615113	AJ615113	AJ615113	c 789	122	12.3	163	2	AL826716	AL826716
717	128	12.9	673	6	CA220527	SCRFLA402	CA220527	790	122	12.3	525	1	BF092010	RC0-TN007
c 718	128	12.9	711	6	BU253542	BU253542	BU253542	c 791	122	12.3	623	6	CA223020	SCR2FLA03
719	127.8	12.9	441	4	BI342114	369789_MA	BI342114	792	122	12.3	648	6	CD936749	OV_105A20
720	127.8	12.9	489	2	BE500470	WHE0987-0	BE500470	793	122	12.3	904	2	BF972265	60240747
721	127.8	12.9	582	6	CD869339	AZ02_111G	CD869339	794	121.4	12.3	809	2	CA180913	SCACST316
722	127.6	12.9	569	5	BQ839243	WHE4163_H	BQ839243	795	121.2	12.3	509	2	BE050599	za67f09_g
723	127.6	12.9	641	1	AL827928	AL827928	AL827928	796	121.2	12.3	531	6	CA018264	HV08B21r
724	127.4	12.9	976	6	CA168547	SCBGRIT01	CA168547	797	121	12.2	635	7	CR292476	CR292476
725	127.2	12.9	446	6	CA190347	SCCORT1C0	CA190347	c 798	121	12.2	654	7	CF575000	MCSA142A0
726	127.2	12.9	561	6	CA019093	HV10M04r	CA019093	c 799	121	12.2	705	4	BJ467041	BJ467041
727	127.2	12.9	567	6	CA187040	SCUTST308	CA187040	c 800	120.8	12.2	641	6	CB651300	OSUNEB16D
728	127.2	12.9	734	9	CG327759	OGXFO38TH	CG327759	c 801	120.8	12.2	681	4	BM267355	MEST365-F
729	127	12.8	672	6	CA166266	SCUTRZ310	CA166266	c 802	120.8	12.2	774	4	CB651301	OSUNEB16D
730	126.6	12.8	425	6	CD969646	QAC5911_8	CD969646	c 803	120.6	12.2	978	7	CR286455	CR286455
731	126.4	12.8	567	6	CD879591	AZ04_105M	CD879591	c 804	120.2	12.2	1078	4	BG338728	602436489
732	126.4	12.8	636	6	CA183982	SCQST311	CA183982	805	120	12.1	442	7	CN967135	14632_100
733	126.4	12.8	641	6	CA145799	SCVPR207	CA145799	806	119.8	12.1	917	7	CK406909	AUF_ILVr
734	126.4	12.8	726	6	CA158055	SCBGRIT01	CA158055	c 807	119.8	12.1	295	2	BB020942	BB020942
735	126.2	12.8	742	6	CA146092	SCVPR207	CA146092	c 808	119.8	12.1	309	1	AV054462	AV054462
736	126	12.7	287	7	F26420	HSPD13893_H	F26420	c 809	119.8	12.1	508	2	BF624013	BF624013
737	126	12.7	318	1	AV212581	AV212581	AV212581	c 810	119.6	12.1	552	6	CA017209	CA017209
738	126	12.7	498	2	BF293046	WHE2159_G	BF293046	c 811	119.6	12.1	587	6	CD899632	G174_113A
739	126	12.7	546	7	CK896580	SGP159129	CK896580	c 812	119.4	12.1	360	2	AW070082	AW070082
740	126	12.7	558	7	CK896580	SGP159129	CK896580	c 813	119.2	12.1	468	7	CK895492	CK895492
741	126	12.7	666	3	AV104670	Zea maye	AV104670	814	119	12.0	649	4	BI958809	HVSMEN001
742	126	12.7	976	3	CL561927	OB_Ba002	CL561927	815	118.8	12.0	744	6	CD430220	ETH1_17_C
743	125.8	12.7	643	9	CA168805	SCBGRIT01	CA168805	816	118.6	12.0	309	1	AV101516	AV101516
744	125.8	12.7	692	4	BG935676	SL1-1037	BG935676	817	118.6	12.0	311	1	AU246119	AU246119
c 745	125.6	12.7	637	6	CD904273	G356_112P	CD904273	818	118.6	12.0	571	1	AU246119	AU246119
c 746	125.6	12.7	637	6	BF629072	HVSMEN000	BF629072	819	118.6	12.0	609	6	CA139015	CA139015
747	125.6	12.7	765	2	BE215821	HV_CEB000	BE215821	820	118.4	12.0	807	7	CK201722	CK201722
748	125.4	12.7	519	6	BE215821	HV_CEB000	BE215821	821	118.4	12.0	881	7	CK204040	CK204040
749	125.4	12.7	599	6	CD898673	G174_109L	CD898673	822	118.2	12.0	599	2	BF619963	HVSMEN000
750	125.4	12.7	622	6	CA182599	SCCST314	CA182599	823	118.2	12.0	649	6	CA120549	CA120549
751	125.2	12.7	584	2	BF065582	HV_CEB001	BF065582	824	118	11.9	150	7	T24436	EST011_Huma
c 752	125.2	12.7	847	4	BJ264257	BJ264257	BJ264257	825	117.8	11.9	316	2	BB138190	BB138190
753	125.2	12.7	650	2	BF260414	HVSMEN002	BF260414	826	117.8	11.9	544	6	CA143610	CA143610
754	125	12.6	470	2	BF484312	WHE2321_G	BF484312	827	117.6	11.9	316	2	BB312938	BB312938



828	117.6	11.9	502	1	AL825598	AL825598	901	108.8	11.0	634	4	BG415448	BG415448	HVSMEK000
829	117.4	11.9	141	5	BQ084098	K-EST0147	902	108.6	11.0	629	7	C0523183	C0523183	3530_1_15
830	117.4	11.9	681		CD430207	ETH1_17_H	903	108.4	11.0	488	6	CD737778	CD737778	4023355_1
831	117.2	11.9	300	2	BF393514	601310205	c 904	108.2	10.9	583	5	BQ167390	BQ167390	WHE00665_D
832	117.2	11.9	326	7	CF367618	842380_MA	c 905	108.2	10.9	683	2	BB594747	BB594747	BB594747
833	117.2	11.9	636	6	CA133289	SCBORT103	c 906	108.2	10.9	2171	3	AK046931	AK046931	MUB_muscu
834	117	11.8	487	2	BE215905	HV_CEB000	907	108	10.9	471	7	CK879029	CK879029	SGP143200
835	117	11.8	500	6	CA017659	HV05N12r	c 908	108	10.9	456	2	BE050598	BE050598	za67f09_D
836	116.6	11.8	259	5	BY044444	BY044444	c 909	107.8	10.9	700	7	CK570273	CK570273	HO15P22W
837	116.2	11.7	688	7	CR292950	CR292950	910	107.6	10.9	512	6	CD925726	CD925726	G750_118G
838	116.2	11.7	769	6	CA157738	SCBORT201	911	107.4	10.9	524	6	CA144242	CA144242	WHE2638_E
839	116	11.7	646	7	C0529747	3530_1_19	912	107.2	10.8	481	7	CN008201	CN008201	SCBRT104
c 840	116	11.7	946	6	CA270677	SCBRT206	913	107.2	10.8	487	1	AL819087	AL819087	AL819087
841	115.8	11.7	350	2	BE495474	BE495474	914	107.2	10.8	493	7	CN008123	CN008123	WHE2637_F
842	115.6	11.7	543	6	CA630673	wlein.pk0	915	107.2	10.8	597	4	BI955535	BI955535	HVSMEM002
843	115.6	11.7	654	6	CA069091	SCSBAD105	916	107.2	10.8	471	6	CA131726	CA131726	SCBRT104
844	115.6	11.7	702	6	CA179873	SCCST200	917	106.8	10.8	674	4	BJ464618	BJ464618	BJ464618
845	115.4	11.7	570	6	CA279207	SCBFLB209	918	106.8	10.8	480	5	BQ468043	BQ468043	HR01M03r
846	115.2	11.6	570	5	B0537567	STEM2_5_B	919	106.8	10.8	536	6	CA186007	CA186007	SCSFT308
847	115	11.6	515	5	BP184761	BP184761	c 920	106.6	10.8	499	4	BJ515365	BJ515365	BJ515365
848	115	11.6	638	6	CA208994	SCBZAD1C0	c 921	106.2	10.7	600	9	CR180853	CR180853	Forward_B
849	114.8	11.6	521	2	BE490745	BE490745	c 922	106.2	10.7	640	4	BJ255752	BJ255752	BJ255752
850	114.8	11.6	522	6	CF243853	3530_1_24	923	106.2	10.7	713	7	CN146262	CN146262	WGN01_39
851	114.8	11.6	592	4	BM660366	BM660366	924	106.2	10.7	810	6	CF213611	CF213611	CGF100079
852	114.6	11.6	573	2	AW257987	687065002	c 925	106.2	10.7	819	7	CF517012	CF517012	CAP0004_I
853	114.6	11.6	635	7	CN984292	CN984292	926	106.2	10.7	942	7	CF516928	CF516928	CAP0004_I
854	114.4	11.6	509	4	BG314500	WHE2495_E	927	105.8	10.7	662	4	BI954845	BI954845	HVSMEM002
855	113.8	11.5	312	6	CD080971	CD080971	c 928	105.4	10.7	595	6	CB616815	CB616815	3529_1_65
856	113.8	11.5	656	4	BG836117	Zm06_08f1	929	105.4	10.7	599	4	BG836020	BG836020	Zm06_10b0
857	113.6	11.5	486	4	BM443304	EBem09_SQ	930	105.4	10.7	653	6	CD229208	CD229208	CCCI_13_F
858	113.6	11.5	504	1	AL822404	AL822404	931	105.4	10.7	842	7	CK201404	CK201404	FGAS00992
859	113.6	11.5	869	6	CA130757	SCBRT106	932	105.2	10.6	483	1	AL829858	AL829858	AL829858
860	113.4	11.5	599	1	AI981881	pat.pk006	c 933	105.2	10.6	832	6	CF215096	CF215096	CAS0001
861	113.2	11.4	516	4	BM402624	SLA006D04	934	105.2	10.6	833	6	CF215293	CF215293	CAS0001
862	113.2	11.4	577	6	CD933864	GR45_122E	935	105	10.6	260	1	AV062880	AV062880	AV062880
863	113.2	11.4	614	6	CA137607	SCAGRT204	936	104.6	10.6	658	1	AJ805285	AJ805285	AJ805285
864	113.2	11.4	738	6	CA146644	SCVPT208	937	104.6	10.6	762	1	AJ792459	AJ792459	AJ792459
c 865	113	11.4	116	1	AI915440	tr28b04_x	938	104.4	10.6	471	2	B6330339	B6330339	946018DD08
c 866	113	11.4	718	6	CD888511	G111.108E	939	104.4	10.6	505	1	AV438086	AV438086	AV438086
c 867	112.8	11.4	622	6	CA170058	SCQGSB108	940	104.2	10.6	507	6	CA719362	CA719362	wkm2n.pk0
868	112.8	11.4	316	2	BA906887	BA906887	941	104.2	10.5	568	6	CA615505	CA615505	wr1.pk172
869	112.6	11.4	829	4	BG323539	602422001	942	104.2	10.5	604	6	CD429608	CD429608	ETH1_14_C
870	112.6	11.4	829	4	BG323539	602422001	943	104.2	10.5	629	6	CA139894	CA139894	SCBRT201
871	112.6	11.4	596	6	CA077827	SCRFAM102	944	104.2	10.5	631	7	CF432712	CF432712	NIT1_18_A
c 872	112.4	11.4	636	6	CD932185	GR45_117C	945	104.2	10.5	593	6	CA727938	CA727938	wdi1c.pk0
873	112.4	11.4	634	4	BI959396	HVSMEM001	946	104	10.5	593	6	CA727938	CA727938	wdi1c.pk0
874	112.2	11.3	649	6	CA180857	SCACST316	c 947	104	10.5	616	4	BI9563207	BI9563207	HVSMEM000
875	112	11.3	649	6	CA180857	SCACST316	c 948	104	10.5	648	6	CD878345	CD878345	AZ04_102I
876	111.8	11.3	489	7	CF931812	EST0244_A	c 949	104	10.5	789	8	BH022213	BH022213	GH_WB000
877	111.6	11.3	387	1	AU179319	AU179319	950	103.8	10.5	501	6	CB605514	CB605514	3529_1_67
878	111.6	11.3	517	4	BG935465	SL1_0818	c 951	103.8	10.5	603	7	CF432761	CF432761	NIT1_18_G
879	111.4	11.3	442	7	CN966263	13760_100	c 952	103.6	10.5	343	1	AA899498	AA899498	UI-R-E0-d
880	111.2	11.2	402	7	D22878	RICCI705A_R	953	103.6	10.5	896	6	CF215012	CF215012	CAS0001
881	111.2	11.2	650	6	CA120618	SCCCLR107	954	103.6	10.5	1041	6	CA207625	CA207625	SCBRT106
c 882	111.2	11.2	785	4	BG320047	Zm03_01c0	c 955	103.2	10.4	510	4	BM895774	BM895774	952065C05
c 883	111	11.2	543	5	BQ660910	HM01A23w	956	103.2	10.4	658	6	CA172349	CA172349	SCSGB100
884	111	11.2	638	6	CA070754	SCUTAD103	957	103	10.4	405	3	CR653216	CR653216	Tetraodon
885	110.8	11.2	259	1	AV261882	AV261882	958	103	10.4	583	1	AL504534	AL504534	AL504534
886	110.8	11.2	670	6	CA298654	SCSFLA04	c 959	103	10.4	584	5	CD898524	CD898524	G174_109E
887	110.6	11.2	489	4	BM444060	EBem09_SQ	c 960	102.8	10.4	645	5	BQ752825	BQ752825	WHE4119_E
888	110.6	11.2	613	6	CA276256	SCBFLB200	961	102.6	10.4	593	4	BI140992	BI140992	IP1_41_G1
889	110.4	11.2	488	6	CB095964	le98b07_b	962	102.6	10.4	595	4	BI141003	BI141003	IP1_41_H1
890	110.4	11.2	496	4	BJ246686	BJ246686	963	102.6	10.4	600	7	CF427278	CF427278	PH1_4_H04
891	110	11.1	516	5	BP184412	BP184412	c 964	102.2	10.3	551	6	CA039685	CA039685	ssalnw01
c 892	109.6	11.1	668	6	CD939543	OV_113024	965	102.2	10.3	552	6	CA193113	CA193113	SCRLAD104
893	109.4	11.1	500	1	AL505702	AL505702	966	102.2	10.3	680	6	CA130734	CA130734	SCBRT106
894	109.4	11.1	516	7	C0531897	C0531897	967	102	10.3	617	6	CA270275	CA270275	SCQSLB205
895	109.4	11.1	598	6	CD884471	FI_116L20	c 968	101.8	10.3	441	6	CA007423	CA007423	HU07017r
c 896	109.2	11.0	477	4	BI468157	EST00564	969	101.8	10.3	1068	7	CK162448	CK162448	FGAS01504
897	109.2	11.0	648	5	BQ743293	WHE4102_D	c 970	101.4	10.3	455	4	BI956370	BI956370	HVSMEM000
898	109	11.0	533	2	BE637000	WHE1808_A	971	101.4	10.3	467	4	BI957989	BI957989	HVSMEM001
899	108.8	11.0	486	2	BE215236	HV_CEB000	972	101.4	10.3	508	5	BQ239349	BQ239349	TaE0503249
900	108.8	11.0	491	2	BF6233901	HVSMEM000	973	101.4	10.3	684	6	CB091578	CB091578	he94a09_g



974	101	10.2	632	6	CA157288	SCFRZ309	1047	94.6	9.6	636	6	CB090660	CB090660
975	100.8	10.2	338	4	BU259370	BU259370	1048	94.6	9.6	709	7	CA0165605	CA0165605
976	100.6	10.2	634	6	CA124374	SCQGLR108	1049	94.4	9.5	466	6	CA704504	CA704504
c 977	100.2	10.1	261	9	CB5675240	tigr-988-	1050	94.4	9.5	516	2	BF429250	BF429250
978	100.2	10.1	553	7	CA135765	OX1 38 G0	1051	94.2	9.5	353	5	BY401495	BY401495
979	100.2	10.1	651	7	CF479933	PO11 62 E	1052	94.2	9.5	501	1	CO524755	CO524755
980	100.2	10.1	689	7	CA991252	67764 125	1053	94.2	9.5	737	7	CF397756	CF397756
981	100	10.1	900	7	CO488021	QQ255.B3	1054	94.2	9.5	762	7	CF472622	CF472622
c 982	99.8	10.1	227	1	AI614596	mm33C06.Y	1055	94	9.5	658	7	CK240496	CK240496
c 983	99.6	10.1	504	4	BU531649	BU531649	1056	93.8	9.5	614	1	AU101479	AU101479
c 984	99.4	10.1	500	4	BU511906	BU511906	c1057	93.6	9.5	417	1	AI477667	AI477667
c 985	98.4	10.1	592	6	CA020122	HV14G11r	1058	93.6	9.5	766	7	AI477667	AI477667
986	99.2	10.0	520	5	BU436475	BU436475	c1059	93.4	9.4	547	6	CD933865	CD933865
987	98.2	10.0	530	6	CA068263	SCRUAD106	1060	93.2	9.4	462	1	AJ434313	AJ434313
c 988	99	10.0	526	6	CA151587	CA151587	1061	93.2	9.4	648	7	CA192437	CA192437
c 989	98.8	10.0	736	6	CA151587	CA151587	1062	93.2	9.4	658	7	CA192437	CA192437
990	98.6	10.0	801	2	BF254803	BF254803	1063	93.2	9.4	708	7	CA192437	CA192437
991	98.4	9.9	542	6	CA112745	SCOLB106	1064	93.2	9.4	745	7	CA192437	CA192437
992	98.2	9.9	452	6	CA093002	CA093002	1065	93.2	9.4	812	7	CA192437	CA192437
993	98.2	9.9	538	6	CA207983	CA207983	1066	93.2	9.4	880	7	CA192437	CA192437
994	98.2	9.9	609	6	CA093108	CA093108	1067	93.2	9.4	856	7	CA192437	CA192437
995	98.2	9.9	679	6	CA191740	CA191740	1068	93.2	9.4	880	7	CA192437	CA192437
996	98	9.9	583	2	BE360219	DG1 62 C1	1069	93.2	9.4	236	1	AV141679	AV141679
997	97.6	9.9	586	6	CA254903	CA254903	1070	93	9.4	447	4	BG842772	BG842772
998	97.6	9.9	610	6	CA0836411	CA0836411	c1072	93	9.4	579	6	CB090738	CB090738
999	97.6	9.9	708	6	CA082691	CA082691	1073	93	9.4	591	5	AJ611537	AJ611537
1000	97.6	9.9	735	6	CA082691	CA082691	1074	93	9.4	695	5	BE252395	BE252395
1001	97.6	9.9	735	6	CA082691	CA082691	1075	93	9.4	843	7	CA082691	CA082691
1002	97.4	9.8	564	6	CD867866	CD867866	1076	92.6	9.4	592	6	CA082691	CA082691
1003	97.4	9.8	643	7	CF518411	CF518411	1077	92.6	9.4	436	6	CB091612	CB091612
1004	97	9.8	582	6	CA734194	CA734194	1078	92.4	9.3	660	6	BE498018	BE498018
1005	96.8	9.8	264	1	AV232544	AV232544	1079	92.4	9.3	666	6	CB092484	CB092484
1006	96.8	9.8	666	6	CB091902	CB091902	1080	92.2	9.3	666	6	CB092484	CB092484
1007	96.8	9.8	685	5	BE253301	BE253301	1081	92	9.3	731	1	AJ803420	AJ803420
1008	96.8	9.8	692	6	CB653599	CB653599	1082	92	9.3	521	2	BE493244	BE493244
1009	96.8	9.8	724	4	BI960633	BI960633	1083	91.8	9.3	701	7	CA0975504	CA0975504
1010	96.6	9.8	635	6	CA221355	CA221355	1084	91.8	9.3	798	7	CR288023	CR288023
1011	96.6	9.8	744	7	CF478537	CF478537	1085	91.6	9.3	551	4	BJ257751	BJ257751
c1012	96.6	9.8	794	7	CO174177	CO174177	1086	91.6	9.3	656	7	CF987647	CF987647
1013	96.4	9.7	809	7	CO165036	CO165036	1087	91.6	9.3	675	7	CF987647	CF987647
c1014	96.2	9.7	569	4	BU463542	BU463542	1088	91.6	9.3	833	7	CA082691	CA082691
c1015	96.2	9.7	589	6	CA453183	CA453183	1089	91.6	9.3	595	6	CA082691	CA082691
1016	96.2	9.7	612	5	BO699842	BO699842	1090	91.4	9.2	625	6	CA082691	CA082691
1017	96.2	9.7	745	7	CF470308	CF470308	1091	91.4	9.2	283	1	AV325538	AV325538
1018	96.2	9.7	782	7	CF669736	CF669736	1092	91.2	9.2	393	9	CG085800	CG085800
1019	96.2	9.7	792	7	CO363528	CO363528	1093	91.2	9.2	559	6	CD864258	CD864258
c1020	96.2	9.7	815	7	CO363528	CO363528	1094	91.2	9.2	565	4	BU252030	BU252030
c1021	96.2	9.7	822	7	CO364711	CO364711	1095	91.2	9.2	584	6	CD454107	CD454107
c1022	96.2	9.7	854	1	AA079945	AA079945	c1096	91.2	9.2	625	4	BI953755	BI953755
1023	96.2	9.7	219	7	CR464258	CR464258	c1097	91.2	9.2	584	6	CD454107	CD454107
c1024	96	9.7	349	7	CR464258	CR464258	c1098	91	9.2	625	4	BI953755	BI953755
c1025	96	9.7	212	5	BE632080	BE632080	c1100	90.8	9.2	519	4	BU263171	BU263171
c1026	95.8	9.7	520	1	AL450922	AL450922	1101	90.8	9.2	674	6	CA165465	CA165465
1027	95.6	9.7	520	1	AL450922	AL450922	1102	90.8	9.2	818	6	CF203341	CF203341
1028	95.6	9.7	671	4	BI954074	BI954074	1103	90.6	9.2	522	4	BE604615	BE604615
1029	95.6	9.7	747	7	CF396117	CF396117	c1104	90.6	9.2	600	7	CA080603	CA080603
1030	95.4	9.6	555	4	CA133810	CA133810	1105	90.4	9.1	635	1	AJ560090	AJ560090
1031	95.2	9.6	582	4	BU551247	BU551247	1106	90.4	9.1	638	7	CA080603	CA080603
1032	95.2	9.6	673	6	CB082763	CB082763	1107	90.4	9.1	580	5	BU977318	BU977318
1033	95.2	9.6	712	7	CF389766	CF389766	c1108	90.2	9.1	632	4	BM079242	BM079242
1034	95.2	9.6	712	7	CF473897	CF473897	c1109	90.2	9.1	689	5	BA250520	BA250520
1035	95.2	9.6	718	8	BE635220	BE635220	1110	90.2	9.1	728	7	CF418067	CF418067
1036	95.2	9.6	729	7	CF478998	CF478998	1111	90.2	9.1	550	4	BE605452	BE605452
c1037	95.2	9.6	752	7	CO172079	CO172079	1112	90	9.1	652	7	CF836276	CF836276
c1038	95.2	9.6	777	9	CC626240	CC626240	1113	90	9.1	726	7	CA190771	CA190771
c1039	95.2	9.6	787	9	CG367905	CG367905	1114	90	9.1	739	7	CK932928	CK932928
c1040	95.2	9.6	841	9	CG320079	CG320079	1115	90	9.1	848	7	CA191778	CA191778
c1041	95.2	9.6	852	9	CG367832	CG367832	c1116	90	9.1	860	7	CK933305	CK933305
c1042	95.2	9.6	880	9	CG329531	CG329531	1117	90	9.1	242	1	AV341874	AV341874
1043	95.2	9.6	919	4	CG235840	CG235840	1118	89.8	9.1				
1044	95.2	9.6	453	4	BI956521	BI956521	1119						
1045	94.6	9.6	590	6	CA080520	CA080520							



1120	89.8	9.1	537	6	CA215379	SCRLAD113	1193	86	8.7	751	6	CD821098	BN25.040N
1121	89.8	9.1	599	6	CA242898	SCSFFL309	1194	86	8.7	776	7	CN987035	62721.125
1122	89.8	9.1	660	7	CF418675	USDA-PP.1	1195	86	8.7	854	2	BF260683	HVSMF002
1123	89.8	9.1	674	5	BX251216	BX251216	1196	86	8.7	882	7	CK605765	gmtrRWw6-
1124	89.6	9.1	417	5	BQ539085	MEST611-B	1197	86	8.7	986	4	BG383133	Gc01.06d0
1125	89.4	9.0	439	2	BF145727	WHE1840.A	1198	85.8	8.7	788	4	BF1971175	GM830012B
1126	89.4	9.0	518	6	CA271127	SCRULB206	1199	85.8	8.7	789	2	BF860393	963016801
1127	89.4	9.0	848	2	AN982228	HVSMF000	1200	85.6	8.7	484	4	BJ246483	BJ246483
1128	89.2	9.0	627	6	CB910128	WVD174D02	1201	85.6	8.7	498	1	AL824727	AL824727
1129	89	9.0	564	8	BZ628758	ih62b02.b	1202	85.6	8.7	506	1	AL808335	AL808335
1130	89	9.0	644	2	BG635220	BG635220	1203	85.6	8.7	635	5	BU044203	PP.L6A001
1131	89	9.0	707	7	CN988152	CN988152	1204	85.6	8.7	677	7	CF806867	psH8016Xm
1132	89	9.0	3835	3	AK079754	Mus.muscu	1205	85.6	8.7	689	4	BG544230	E2031.Chi
1133	88.8	9.0	507	7	CF972935	PSU.2blon	1206	85.6	8.7	760	4	BG934808	SL1.-0074
1134	88.8	9.0	673	7	CF389114	RTDR2.13	1207	85.6	8.7	960	2	BE213939	HV.CEB000
1135	88.8	9.0	747	7	CF474427	CF474427	1208	85.4	8.6	404	1	BF221093	NXCI.163
1136	88.8	9.0	750	7	CO198619	CO198619	1209	85.4	8.6	714	1	AJ778942	AJ778942
1137	88.8	9.0	775	7	CF390634	CF390634	1210	85.4	8.6	840	7	CN191650	UCRCS06.0
1138	88.8	9.0	817	7	CF831643	CF831643	1211	85.2	8.6	501	1	AL818819	AL818819
1139	88.8	9.0	864	6	CB822986	CB822986	1212	85.2	8.6	742	5	BQ634193	NXRVO64.H
1140	88.4	8.9	637	7	CN189395	UCRCS06.0	1213	85	8.6	266	6	CF075267	EST00106
1141	88.4	8.9	775	6	CD576142	CD576142	1214	84.8	8.6	693	2	BQ623195	USDA-PP.0
1142	88.2	8.9	414	4	BJ281814	BJ281814	1215	84.8	8.6	704	6	CD817128	BN20.040N
1143	88.2	8.9	549	6	CD429497	ETH1.4.H0	1216	84.8	8.6	730	7	CF833321	UCRCS02.0
1144	88.2	8.9	608	7	CK750439	pan01-6ms	1217	84.8	8.6	715	7	CK939864	CGF100474
1145	88.2	8.9	671	6	CA160341	CA160341	1218	84.8	8.6	721	7	CF833360	UCRCS02.0
1146	88.2	8.9	829	2	BF260105	BF260105	1219	84.8	8.6	730	7	CF833321	UCRCS02.0
1147	88	8.9	454	7	CK887520	CK887520	1220	84.8	8.6	731	7	CN190617	UCRCS06.0
1148	88	8.9	769	6	CA784719	sat88a11.	1221	84.8	8.6	742	7	CF833684	UCRCS02.0
1149	87.8	8.9	534	6	CA701924	CA701924	1222	84.8	8.6	752	7	CN128863	RHOH1.32
1150	87.8	8.9	750	7	CF921444	CF921444	1223	84.8	8.6	826	7	CN128942	RHOH1.32
1151	87.6	8.9	785	6	CB346952	CB346952	1224	84.8	8.6	830	7	CF838016	UCRCS03.0
1152	87.6	8.9	1105	8	BZ549226	BZ549226	1225	84.8	8.6	394	2	BE969608	BE969608
1153	87.4	8.8	250	1	AV080674	AV080674	1226	84.6	8.6	486	6	CA688073	wlm96.pk0
1154	87.4	8.8	404	7	CF573768	CF573768	1227	84.6	8.6	534	6	CA630115	wlm96.pk0
1155	87.4	8.8	449	4	BG559195	BG559195	1228	84.6	8.6	544	4	BM527684	sal64f09.
1156	87.4	8.8	470	1	AV923789	AV923789	1229	84.6	8.6	550	6	CA178809	SCSFST106
1157	87.2	8.8	452	6	CB863482	CB863482	1230	84.6	8.6	510	7	CF971448	AUB.IFhrt
1158	87.2	8.8	484	1	AL809451	AL809451	1231	84.4	8.5	534	6	CD932184	G045.117F
1159	87.2	8.8	628	6	CB914191	CB914191	1232	84.4	8.5	684	5	BU875316	V005C03.P
1160	87.2	8.8	724	7	CF921036	CF921036	1233	84.4	8.5	694	5	BU877332	V032G08.P
1161	87	8.8	580	1	AL691472	AL691472	1234	84.4	8.5	696	6	CD832570	BN40.063N
1162	87	8.8	598	4	BJ321639	BJ321639	1235	84.4	8.5	716	5	BU874994	V001B12.P
1163	87	8.8	610	4	BJ726276	BJ726276	1236	84.4	8.5	808	6	CD827397	BN25.067F
1164	86.8	8.8	661	7	CK987646	CK987646	1237	84.4	8.5	492	6	CA686271	wlm96.pk0
1165	86.8	8.8	696	6	CA113262	SP7-B5(P1	1238	84.2	8.5	629	4	BI958431	HVSMF001
1166	86.8	8.8	757	2	CF395287	CF395287	1239	84.2	8.5	469	7	CN580794	Mdfw2030f
1167	86.6	8.8	487	2	BE356694	BE356694	1240	84	8.5	548	4	BM527768	sal65f09.
1168	86.6	8.8	550	6	CD462624	CD462624	1241	84	8.5	559	2	AM102353	sd86f04.Y
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## ALIGNMENTS

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VERSION BM451059.1 GI:18500099
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12121 row: d column: 08
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Technologies."
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## FEATURES

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Location/Qualifiers
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Technologies."
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## ORIGIN

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Query Match 80.6%; Score 797.4; DB 4; Length 889;
Best Local Similarity 95.5%; Pred. No. 2.5e-150;
Matches 821; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
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Qy	252	TATCTTCTGAGCCGCTCCATCGGAGACACCGCGGCTGTGAAGCCTGAGCTGTGACC	311
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Qy	372	CTGGCGCGGCTCATCAGGCCAAGAAGCGCTGTGAACCTTGGGCACTTTCAGGGGTACTCC	431
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Qy	492	GGCGAGCCCGGAGCTGGAGCGGCCCTGTGGAGCGAGCGGCGGAGGACCAAGATC	551
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Qy	672	CGCTGCTGAGCTGTGGACCCGCGAGGATCCTTGGCGCTCTCAGAGTCTGTGGGCG	731
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Db	721	GAACGATCCGCGGAGCTCAGGCTTACATCAGGCTCTTGGCCCTTGGGCGATGACTC	780
Qy	852	ACCTT-GGCTTCAAGATCTAGGGCT--GGCCCTTGTAGTGGG 893	
Db	781	ACCTTGGGCTTCAAGATCTAGGGGTTGGGCTTGTAGTGGG 825	
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DEFINITION	UI-CF-FNO-aes-j-02-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone		
ACCESSION	CB852030		
VERSION	CB852030.1 GI:30046884		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 771)		
TITLE	Normalizaton and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	9704477		
PUBMED	8889548		
COMMENT	Contact: McCray, PB McCray Lab University of Iowa		

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA			
Tel: 319 356 4866			
Fax: 319 356 7171			
Email: paul-mccray@uiowa.edu			
Tissue Procurement: Dr. M. J. Welsh, University of Iowa			
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).			
Seq primer: M13 FORWARD			
POLYA=Yes.			
Location/Qualifiers			
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/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized human lung epithelial cell libraries (EN1 and DU1). The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu			
TAG_SEQ=None found"			
FEATURES			
source			
ORIGIN			
Query Match 77.1%; Score 762.6; DB 6; Length 771;			
Best Local Similarity 99.5%; Pred. No. 2.6e-143;			
Matches 765; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
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Qy	341	GACTTGGAGAGCCGAGCTTGTGGCAACCTCTGGCGGCTCATCCAGGCCAAGAGGC	400
Db	651	GACTTGGAGAGCCGAGCTTGTGGCAACCTCTGGCGGCTCATCCAGGCCAAGAGGC	592
Qy	401	GCTGGACCTGGGCACCTTTCAGGGCTACTCTCGCCCTTGGCCCTTGGCGCTGCCGC	460
Db	591	GCTGGACCTGGGCACCTTTCAGGGCTACTCTCGCCCTTGGCCCTTGGCGCTGCCGC	532
Qy	461	GGAGGGCGCTGTGTGACCTTGGAGGTGGAGCGCGAGCCCGCGAGCTGGAGCGCCCT	520
Db	531	GGAGGGCGCTGTGTGACCTTGGAGGTGGAGCGCGAGCCCGCGAGCTGGAGCGCCCT	472
Qy	521	GTGGAGGCGAGCCGCGAGGCGGAGCAAGATCGAAGCTCTCGGCTGAAGCCCGCTTGGAG	580
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Qy	581	CCTGGACGAGCTGTGTGGCGGCGGAGCGCGGCACTTTCAGCTGGCCGCTGGTGTGTC	640
Db	411	CCTGGACGAGCTGTGTGGCGGCGGAGCGCGGCACTTTCAGCTGGCCGCTGGTGTGTC	352
Qy	641	GGAGAGGAGAACTGCTCGGCTTACTAGAGCGCTCTGCGAGCTGTGCGACCCCGGAGG	700
Db	351	GGAGAGGAGAACTGCTCGGCTTACTAGAGCGCTGTGCGAGCTGTGCGACCCCGGAGG	292
Qy	701	CATCTCTGCGCTCTCAGAGTCTTGTGGCGGCGGAGGTTGTGCAACTCTCGAAGGGGA	760
Db	291	CATCTCTGCGCTCTCAGAGTCTTGTGGCGGCGGAGGTTGTGCAACTCTCGAAGGGGA	232
Qy	761	CCTGGCGCGGAGGTGTGTGCGGAAACCTTAAACGCACTCCGCGGCGGAGCTCAGGGTCTA	820



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231 CTTGGGCGCGAGTGTGGCGAAACCTAAACGACGATCCGCGGACGTCAGGGTCTA 172
821 CATCAGCCTCTCTGCCCTCGGCGATGGACTCACCTTGGCTTCAAGATCTAGGGCTGGCC 880
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881 CCTAGTAGTGGCTCGAGGGAGGGTTCCTGGGAAACCCAGGAATGACCCCTGAGTTT 940
111 CCTAGTAGTGGCTCGAGGGAGGGTTCCTGGGAAACCCAGGAATGACCCCTGAGTTT 52
941 AAATTCGAAATATAAGTGGGCTGGGACACAAAAAAGAAAAA 989
51 AAATTCGAAATATAAGTGGGCTGGGACACAAAAAAGAAAAA 3

RESULT 3
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LOCUS 603634191F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5424766 5',
DEFINITION mRNA sequence.
ACCESSION BM051236
VERSION BM051236.1 GI:16780503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 814)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16M1886 row: e column: 23
High quality sequence stop: 811.
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/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

Query Match 75.1%; Score 743; DB 4; Length 814;
Best Local Similarity 98.6%; Pred. No. 2,3e-139;
Matches 802; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

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2 CCCAGCCGGTCCCGGCTCTCCGCGCGCGCTGGCCCTCAGCCGCACTGG 61
148 GCGCGCCTTCGCACTGGCTCTCTCCGCGCGCGCTGGCCCTCAGCCGCGC 207
62 GCGCGCCTTCGCACTGGCTCTCTCCGCGCGCGCTGGCCCTCAGCCGCGC 121

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208 GAGAGCAGTGTGCTTCTCCCGCGAGGACAGCCGCTGTGGCAGTATCTTGTGACCGCT 267
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268 CCATGCGGGAGCACCCGCGCTGCGAGGCTGAGGCTGCTGACCTGCGAGGAGCCGCGAG 327
182 CCATGCGGGAGCACCCGCGCTGCGAGGCTGAGGCTGCTGACCTGCGAGGAGCCGCGAG 241
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242 GGGATTCTATGATGACCTTGGCAGGAGCCAGCTCTTGGCCAAACCTGCGCGGCTCATCC 301
388 AGGCCAAGAGGCGCTGGACCTTGGGCACCTTCAAGGCTACTTCCGCCCTTGGCCCTTGGCCC 447
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448 TGGCGCTGCCCGCGAGCGGCGCTGGTGACCTTGGAGGTGAGCGCGAGGCGCCCGGAGC 507
362 TGGCGCTGCCCGCGAGCGGCGCTGGTGACCTTGGAGGTGAGCGCGAGGCGCCCGGAGC 421
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422 TGGACGCGCCCTTGGAGGCGAGCGCGAGGCGGAGCACAAAGATCGACCTCGGGCTGAAGC 481
568 CCGCTTGGAGACCTTGGACGAGCTGTGTGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGG 625
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626 GCGCGTGGTGAGTGGGACAGGAGACTGCTCGCGCTTACTACGAGCGCTGCTGCGCGG 584
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## RESULT 4

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LOCUS CA777547.1  
DEFINITION ip21907.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5217933 3', similar to TR:085769 085769 HYPOTHETICAL 24.8 KD PROTEIN. ;, mRNA sequence.

## ACCESSION

CA777547  
VERSION CA777547.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 756)  
MELTON, D., BROWN, J., KENTY, G., PERMUTT, A., LEE, C., KAESTNER, K., LEMISHKA, I., SCARCE, M., BRESTELLI, J., GRADWOL, G., CLIFTON, S., HILLIER, L., MARRA, M., PAPE, D., WYLIE, T., MARTIN, J., BLISFAIN, A., SCHMITT, A., THEISING, B., RITTER, E., RONKO, I., BENNETT, J., CARDENAS, M., GIBBONS, M., MCCANN, R., COLE, R., TEAGAREISHVILI, R., WILLIAMS, T., JACKSON, Y. and BOWERS, Y.

## AUTHORS

Endocrine Pancreas Consortium  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

## TITLE

Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

## JOURNAL

Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

## COMMENT

Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue



Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmeitton@biohp.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 462.  
Location/Qualifiers  
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/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permut Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

FEATURES  
source

RESULT 5  
BF663323  
LOCUS  
DEFINITION  
BF663323  
ACCSSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

ORIGIN

Query Match 74.4%; Score 736; DB 6; Length 756;  
Best Local Similarity 99.2%; Pred. No. 5.9e-138;  
Matches 750; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
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QY 582 CTGGACAGAGCTGTGCGCGCGGCGAGCCGCGCACTTCAAGCTGGCGCTGTGGATGCG 641  
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QY 762 GTGGCGCGCGAGTGTGTGCGAAACCTAAACGAAACCATCCGCGGAGCGTCAAGGCTTAC 821  
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mRNA sequence.

BF663323 1 GI:11937218  
BF663323

ACCSSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgs.nci.nih.gov/

1 (bases 1 to 1006)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1CML152 row: m column: 16

High quality sequence stop: 745.

Location/Qualifiers

1. .1006

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/tissue\_type="Primary B-cells from tonsils (cell line)"

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/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

Query Match 72.9%; Score 721; DB 2; Length 1006;

Best Local Similarity 90.9%; Pred. No. 6.3e-135; Indels 9; Gaps 6;

Matches 835; Conservative 0; Mismatches 75; Indels 9; Gaps 6;

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Db 302 GGCTCATCCAGGCCCAAGAGCGCTTGACCTTGGGCACCTTTCACGGGCTACTCCGCGCTGG 361  
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Db 362 CCCTGGCCCTGGCGTGCCTGGCGGAGCGGGCGGTGGTACCTTGGAGTGAGCGGCGAGC 421  
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VERSION BF664198.1 GI:11938093  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 921)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
Plate: LICM182 row: h column: 03  
High quality sequence stop: 726.  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="IMAGE:4309298"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
Site:2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

FEATURES  
source

ORIGIN

Query Match 72.4%; Score 716; DB 2; Length 921;  
Best Local Similarity 97.4%; Pred No. 6.3e-134;  
Matches 781; Conservative 0; Mismatches 15; Indels 6; Gaps 5;  
Qy 79 GCGCATGACCCAGCGGTGCGCGCTCTCCGTGCGCGCGCGCTGGCGCTGAGCTCAG 138  
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Qy 139 CCGCACTGGGCGCGCTTGGCACTGGCTCTTCTTGGGAGGCGGTGCCCCCATGGC 198  
Db 62 CCGCACTGGGCGCGCTTGGCACTGGCTCTTCTTGGGAGGCGGTGCCCCCATGGC 121  
Qy 199 GAGCGCGGAGAGAGTGTCTTCCCGGAGGAGAGCGCGCTGTGGCAGTATCTTC 258  
Db 122 GAGCGCGGAGAGAGTGTCTTCCCGGAGGAGAGCGCGCTGTGGCAGTATCTTC 181  
Qy 259 TGAGCGCTCCATGCGGAGAGCACCGCGGCTGCGAAGCTGAGGCTGTGACCTGGAGC 318  
Db 182 TGAGCGCTCCATGCGGAGAGCACCGCGGCTGCGAAGCTGAGGCTGTGACCTGGAGC 241  
Qy 319 AGCGCGAGGCGATTCATGATGACCTGCGAGAGCGCGCAGCTTGGGCCAACTTGGCGC 378  
Db 242 AGCGCGAGGCGATTCATGATGACCTGCGAGAGCGCGCAGCTTGGGCCAACTTGGCGC 301  
Qy 379 GGCTCATCCAGGCCCAAGAGCGCTGAGCTTGGGACCTTTCACGGGCTACTCCGCGCTGG 438  
Db 302 GGCTCATCCAGGCCCAAGAGCGCTTGGACCTTGGGACCTTTCACGGGCTACTCCGCGCTGG 361  
Qy 439 CCCTGGCGCTTGGCGCTGCCCGCGAGCGGGCGGTGGTACCTTGGAGTGAGCGGCGAGC 498  
Db 362 CCCTGGCGCTTGGCGCTGCCCGCGAGCGGGCGGTGGTACCTTGGAGTGAGCGGCGAGC 420  
Qy 499 CCCGAGAGCTGGGACGCGCCCTGTGGAGGAGCGGCGGAGGCGGAGCACAAAGATCGACCTCC 558  
Db 421 CCCGAGAGCTGGGACGCGCCCTGTGGAGGAGCGGCGGAGGCGGAGCACAAAGATCGACCTCC 480  
Qy 559 GGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTGCTGGCGGCGGCGGAGCGCGCACCT 618  
Db 481 GGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTGCTGGCGGCGGCGGAGCGCGCACCT 540



QY 619 TCGACGCTGCTGCGACGAGGAACTGCTCGCGCTACTACGAGCGTGC 678  
DB 541 TCGACGCTGCTGCGACGAGGAACTGCTCGCGCTACTACGAGCGTGC 599  
QY 679 TCGACGCTGCTGCGACGAGGAACTGCTCGCGCTACTACGAGCGTGC 738  
DB 600 TCGACGCTGCTGCGACGAGGAACTGCTCGCGCTACTACGAGCGTGC 659  
QY 739 TCGTCAACCTCCGAAAGGAGGAGTGGCGCGCGAGTGTGCGAACTTAAACGAAAGCA 798  
DB 660 TCGTCAACCTCCGAAAGGAGGAGTGGCGCGCGAGTGTGCGAACTTAAACGAAAGCA 718  
QY 799 TCGCGCGGAGCTCAGGCTTACATCAGCTCTTCCCTCGCGGAGTGTGCGAACTTAAACGAAAGCA 858  
DB 719 TCGCGCGGAGCTCAGGCTTACATCAGCTCTTCCCTCGCGGAGTGTGCGAACTTAAACGAAAGCA 775  
QY 859 CTTTCAAGATCTAGGCTGGCC 880  
DB 776 GCCTCAGGATCTAGGCGCTGCC 797

RESULT 7  
BM976177/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

714 bp mRNA linear EST 21-FEB-2003  
UI-CF-EN1-acy-e-23-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
UI-CF-EN1-acy-e-23-0-UI 3', mRNA sequence.  
BM976177.1 GI:19593768  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 714)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul.mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA-Yes.  
Location/Qualifiers  
1..714  
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/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-EN1 is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into p773-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGGT.  
TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG\_LTB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 71.5%; Score 707.2; DB 5; Length 714;  
Best Local Similarity 99.6%; Pred. No. 3.7e-132;  
Matches 709; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 278 GCACCCGGCGCTGCGAAGCTGAGGCTGTGACCTCTTGGCAACCTTGGCGCGCTCATCCAGGCCAAGAA 337  
DB 714 GCACCCGGCGCTGCGAAGCTGAGGCTGTGACCTCTTGGCAACCTTGGCGCGCTCATCCAGGCCAAGAA 655  
QY 338 GATGACCTGGGAGCAGCCGCTTGGCAACCTTGGCGCGCTCATCCAGGCCAAGAA 397  
DB 654 GATGACCTGGGAGCAGCCGCTTGGCAACCTTGGCGCGCTCATCCAGGCCAAGAA 595  
QY 398 GGCGCTGGACCTGGGCAACCTTACCGGCTTACCTCCGCTTGGCGCGCTTGGCGCGCTTGGCGCGCT 457  
DB 594 GGCGCTGGACCTGGGCAACCTTACCGGCTTACCTCCGCTTGGCGCGCTTGGCGCGCTTGGCGCGCT 535  
QY 458 CGCGACCGGCGCTGTGACCTGCGAGGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 517  
DB 534 CGCGACCGGCGCTGTGACCTGCGAGGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 475  
QY 518 CCTGTGAGGAGCG 577  
DB 474 CCTGTGAGGAGCG 415  
QY 578 GACCTCTGGACGAGCTGTGCG 637  
DB 414 GACCTCTGGACGAGCTGTGCG 355  
QY 638 TCGGACGAGGAGGAGCTGCTCCGCTTACTAGAGCGCTGCTGCGCTGCTGCGACCGCG 697  
DB 354 TCGGACGAGGAGGAGCTGCTCCGCTTACTAGAGCGCTGCTGCGCTGCTGCGACCGCG 295  
QY 698 AGGCATCTCTCGCGCTCTCAGAGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 757  
DB 294 AGGCATCTCTCGCGCTCTCAGAGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 235  
QY 758 GGACGTGGCGCGCGAGTGTGCGAACCCTAAACGAGCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 817  
DB 234 GGACGTGGCGCGCGAGTGTGCGAACCCTAAACGAGCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 175  
QY 818 CTACATCAGCTCTCTCGCGCTGCGAGTGTGCACTCACTTGGCGCTTCAAGATCTAGGCGCTG 877  
DB 174 CTACATCAGCTCTCTCGCGCTGCGAGTGTGCACTCACTTGGCGCTTCAAGATCTAGGCGCTG 115  
QY 878 GCCCTCTAGTGTGGCTTCGAGGAGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 937  
DB 114 GCCCTCTAGTGTGGCTTCGAGGAGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 55  
QY 938 TTTAAATTCGAAATTAAGTGGGCTGGGACACACAAAAA 989  
DB 54 TTTAAATTCGAAATTAAGTGGGCTGGGACACACAAAAA 3

RESULT 8  
CB852718  
LOCUS  
DEFINITION

750 bp mRNA linear EST 22-APR-2003  
UI-CF-FNO-afl-p-08-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
UI-CF-FNO-afl-p-08-0-UI 3', mRNA sequence.



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ACCESSION      CB852718
VERSION        CB852718.1  GI:30047716
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 750)
AUTHORS        Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE          Normalization and subtraction: two approaches to facilitate gene
               discovery
JOURNAL        Genome Res. 6 (9), 791-806 (1996)
MEDLINE        9704477
PubMed        8889548
COMMENT        Contact: McCray, PB
               University of Iowa
               2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
               Tel: 319 356 4866
               Fax: 319 356 7171
               Email: paul-mccray@uiowa.edu
               Tissue Procurement: Dr. M. J. Welsh, University of Iowa
               cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
               cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
               DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
               Clone Distribution: Researchers may obtain clones from Research
               Genetics (www.resgen.com) or from Open Biosystems
               (www.openbiosystems.com).
               Seq primer: M13 FORWARD
POLYA=No.      Location/Qualifiers
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               /mol_type="mRNA"
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               /clone="UI-CF-FNO-af1-p-08-0-UI"
               /tissue_type="Human Lung Epithelial cells"
               /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
               /clone_libs="UI-CF-FNO"
               /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
               modified polylinker; Site 1: EcoR I; Site 2: Not I;
               UI-CF-FNO is a subtracted cDNA library derived from two
               normalized Human lung epithelial cell libraries (EN1 and
               DU1) The library was subtracted according to according to
               Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
               1996. For additional information, contact:
               bento-soares@uiowa.edu
               TAG_SEQ=None found"

FEATURES             source
   LOCUS          BE796570 772 bp mRNA linear EST 20-SEP-2000
   DEFINITION      601592247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946546 5',
   ACCESSION       BE796570
   VERSION         BE796570.1  GI:10217768
   KEYWORDS        EST.
   SOURCE          Homo sapiens (human)
   ORGANISM        Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   REFERENCE       1 (bases 1 to 772)
   AUTHORS         NIH-MGC http://mgs.nci.nih.gov/.
   TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
   JOURNAL         Unpublished (1999)
   COMMENT         Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-re@mail.nih.gov
               Tissue Procurement: DCTD/DTF
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
               Plate: L1CM806 row: m column: 11
               High quality sequence stop: 766.
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               /cell_line="MGC3"
               /lab_host="DH10B (phage-resistant)"
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               /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
               EcoRI; cDNA made by oligo-dr priming. Directionally
               cloned into EcoRI/XhoI sites using the following 5'

QY      TGGCGCTCCCGCGGACCGGCGCGTGTGTGACCTGTGGAGGTGGAACGCGCAGACCCCGGAGC 507
|       |||||
Db      TGGCGCTCCCGCGGACCGGCGCGTGTGTGACCTGTGGAGGTGGAACGCGCAGACCCCGGAGC 360
|       |||||
QY      TGGGACGCGCCCTGTGGAGGCGAGCGCGGAGGCGGAGCACAAGATCGACCTCCGGCTGGAAGC 567
|       |||||
Db      TGGGACGCGCCCTGTGGAGGCGAGCGCGGAGGCGGAGCACAAGATCGACCTCCGGCTGGAAGC 420
|       |||||
QY      CCGCTTTGGAGACCTGTGACGAGCTGTCTGGCGGGCGGAGCGCGGACCTTCGACGTGG 627
|       |||||
Db      CCGCTTTGGAGACCTGTGACGAGCTGTCTGGCGGGCGGAGCGCGGACCTTCGACGTGG 480
|       |||||
QY      CCGTGTGGATGCGGACCAAGGAGAACTCTCTCGGCTTACTAGAGCGCTGCTTGCAGCTGC 687
|       |||||
Db      CCGTGTGGATGCGGACCAAGGAGAACTCTCTCGGCTTACTAGAGCGCTGCTTGCAGCTGC 540
|       |||||
QY      TGGGACCGGAGGCGATCTCTCGGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 747
|       |||||
Db      TGGGACCGGAGGCGATCTCTCGGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 600
|       |||||
QY      CTCCGAAAGGGGACGTCGCGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 807
|       |||||
Db      CTCCGAAAGGGGACGTCGCGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 660
|       |||||
QY      ACGTGAGGCTTACATCAGCCTCTCTGCGCCCTGGGCGATGGAATCACTTGGCTTTCAAGA 867
|       |||||
Db      ACGTGAGGCTTACATCAGCCTCTCTGCGCCCTGGGCGATGGAATCACTTGG-CTTCAAGA 719
|       |||||
QY      TCTAGGGCTGCGCCCTAGTGAGTGGCTCGAG 899
|       |||||
Db      TCTAGGGCTGG-CCCTAGTGAGTGGCTCGAG 750

RESULT 9
BE796570
LOCUS          BE796570 772 bp mRNA linear EST 20-SEP-2000
DEFINITION      601592247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946546 5',
ACCESSION       BE796570
VERSION         BE796570.1  GI:10217768
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 772)
AUTHORS         NIH-MGC http://mgs.nci.nih.gov/.
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-re@mail.nih.gov
               Tissue Procurement: DCTD/DTF
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
               Plate: L1CM806 row: m column: 11
               High quality sequence stop: 766.
               Location/Qualifiers
               1..772
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:3946546"
               /tissue_type="small cell carcinoma"
               /cell_line="MGC3"
               /lab_host="DH10B (phage-resistant)"
               /clone_lib="NIH_MGC_7"
               /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
               EcoRI; cDNA made by oligo-dr priming. Directionally
               cloned into EcoRI/XhoI sites using the following 5'

QY      TGGCGCTCCCGCGGACCGGCGCGTGTGTGACCTGTGGAGGTGGAACGCGCAGACCCCGGAGC 507
|       |||||
Db      TGGCGCTCCCGCGGACCGGCGCGTGTGTGACCTGTGGAGGTGGAACGCGCAGACCCCGGAGC 360
|       |||||
QY      TGGGACGCGCCCTGTGGAGGCGAGCGCGGAGGCGGAGCACAAGATCGACCTCCGGCTGGAAGC 567
|       |||||
Db      TGGGACGCGCCCTGTGGAGGCGAGCGCGGAGGCGGAGCACAAGATCGACCTCCGGCTGGAAGC 420
|       |||||
QY      CCGCTTTGGAGACCTGTGACGAGCTGTCTGGCGGGCGGAGCGCGGACCTTCGACGTGG 627
|       |||||
Db      CCGCTTTGGAGACCTGTGACGAGCTGTCTGGCGGGCGGAGCGCGGACCTTCGACGTGG 480
|       |||||
QY      CCGTGTGGATGCGGACCAAGGAGAACTCTCTCGGCTTACTAGAGCGCTGCTTGCAGCTGC 687
|       |||||
Db      CCGTGTGGATGCGGACCAAGGAGAACTCTCTCGGCTTACTAGAGCGCTGCTTGCAGCTGC 540
|       |||||
QY      TGGGACCGGAGGCGATCTCTCGGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 747
|       |||||
Db      TGGGACCGGAGGCGATCTCTCGGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 600
|       |||||
QY      CTCCGAAAGGGGACGTCGCGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 807
|       |||||
Db      CTCCGAAAGGGGACGTCGCGCGCGGAGTGTGCGAAACCTAAACGAAACGCAATCCGCGGG 660
|       |||||
QY      ACGTGAGGCTTACATCAGCCTCTCTGCGCCCTGGGCGATGGAATCACTTGGCTTTCAAGA 867
|       |||||
Db      ACGTGAGGCTTACATCAGCCTCTCTGCGCCCTGGGCGATGGAATCACTTGG-CTTCAAGA 719
|       |||||
QY      TCTAGGGCTGCGCCCTAGTGAGTGGCTCGAG 899
|       |||||
Db      TCTAGGGCTGG-CCCTAGTGAGTGGCTCGAG 750

QUERY MATCH
Query Match    70.8%; Score 699.8; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 1.1e-130;
Matches 732; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY      148 GCGCGCGCTTCCGCACTGGCTCTTCTTCGCGGAGCGGTGCGCCCGCATATGGCGAGCGCGC 207
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Db      1 GCGGCGCGCTCCACACACCTCTCTCCCGTCAGGAGGCGGTGCGCCCGCATATGGCGAGCGCGC 60
|       |||||
QY      208 GAGGACGTGCTGCTTCCCGCGGAGGACGCGCGTGTGGCAGTATCTTCTGAGCGCT 267
|       |||||
Db      61 GAGGACGTGCTGCTTCCCGCGGAGGACGCGCGTGTGGCAGTATCTTCTGAGCGCT 120
|       |||||
QY      268 CCATGCGGAGCACCGCGCGCTGCGAAGCTGTGAGGCTGTGACCTGAGCAGCGCGAGG 327
|       |||||
Db      121 CCATGCGGAGGACACCGCGCGTGTGCGAAGCTGTGAGGCTGTGACCTGAGCAGCGCGAGG 180
|       |||||
QY      328 GGGATTCTATGATGACCTCGAGCAGGCGCCAGCTTTCGCCAACCTGCGCGGCTCATCC 387
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Db      181 GGGATTCTATGATGACCTCGAGCAGGCGCCAGCTTTCGCCAACCTGCGCGGCTCATCC 240
|       |||||
QY      388 AGGCCAAGAGCGCTGACCTGGGACCTTTCAGCGGCTATCTCGCCCTGCGCTGGCC 447
|       |||||
Db      241 AGGCCAAGAGCGCTGACCTGGGACCTTTCAGCGGCTATCTCGCGCTGCGCTGGCC 300

```



adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

ORIGIN

Query Match 69.2%; Score 684.4; DB 2; Length 772;  
Best Local Similarity 97.4%; Pred. No. 1.5e-127;  
Matches 760; Conservative 0; Mismatches 11; Indels 9; Gaps 6;  
QY 83 CATGACCCAGCGGTGCCCGGCTCTCCGTCCCGCGCGCTGACCTTGGGCTCAGCGC 142  
Db 1 CATGACCCAGCGGTGCCCGGCTCTCCGTCCCGCGCGCTGACCTTGGGCTCAGCGC 60  
QY 143 ACTGGCGCGGCTTGGCAGCTGGCTTCTTCTGGGAGGGGCTGCCCTCATGGCGAGG 202  
Db 61 ACTGGCGCGGCTTGGCAGCTGGCTTCTTCTGGGAGGGGCTGCCCTCATGGCGAGG 120  
QY 203 CCGCGAGAGAGTGCCTTCTTCCCGCGAGAGAGCGCGCTGTGGCAGTATCTTCTGAG 262  
Db 121 CCGCGAGAGAGTGCCTTCTTCCCGCGAGAGAGCGCGCTGTGGCAGTATCTTCTGAG 180  
QY 263 CGCTTCCATGCGGGAGCACCGCGGCTCCGAAGCTGAGGCTGTGACCTTGGAGCAGCC 322  
Db 181 CGCTTCCATGCGGGAGCACCGCGGCTCCGAAGCTGAGGCTGTGACCTTGGAGCAGCC 240  
QY 323 CGAGGGGATTTATGATGACTGCGAGAGCGCCAGCTTCTTGGCCACCTTGGCGGCT 382  
Db 241 CGAGGGGATTTATGATGACTGCGAGAGCGCCAGCTTCTTGGCCACCTTGGCGGCT 300  
QY 383 CATTCAGGCGAAGAGGCGCTGGACCTTGGGACCTTTCACGGGCTACTCGGCCCT 442  
Db 301 CATTCAGGCGAAGAGGCGCTGGACCTTGGGACCTTTCACGGGCTACTCGGCCCT 360  
QY 443 GGCCTTGGCGTCCCGCGGAGCGGCGGTGTGACCTTGGAGGTGGAGCGGCGGCT 502  
Db 361 GGCCTTGGCGTCCCGCGGAGCGGCGGTGTGACCTTGGAGGTGGAGCGGCGGCT 420  
QY 503 GGAGTGGAGCGGCGGCTTGGAGCGGCGGCGGAGCGGAGCGGAGTGCCTCGGCT 562  
Db 421 GGAGTGGAGCGGCGGCTTGGAGCGGCGGCGGAGCGGAGCGGAGTGCCTCGGCT 480  
QY 563 GAAGCGCGCTTGGAGACCTTGGAGCGGCGGCGGCGGAGCGGCGGCGGCTTGA 622  
Db 481 GAAGCGCGCTTGGAGACCTTGGAGCGGCGGCGGAGCGGCGGCGGAGGCTTGA 538  
QY 623 CGTGGCGGTGGTGGATGCGGAGCAAGGAGAACTGCTCCGCTTACTACGAGCGCTGCTGA 682  
Db 539 CGTGGCGGTGGTGGATGCGGAGCAAGGAGAACTGCTCCGCTTACTACGAGCGCTGCTGA 598  
QY 683 GCTGCTGCGACCGGAGGCGATCTCGCGCTCTCAGAGTCTTGGCGGGAAGTGT 742  
Db 599 GCTGCTGCGACCGGAGGCGATCTCGCGCTCTCAGAGTCTTGGCGGGAAGTGT 658  
QY 743 GC-AACTCCGAAGAGGAGCTGGCGGCGGAGTGTGTGGAACCTTAAACGAGCATCC 801  
Db 659 GC-AACTCCGAAGAGGAGCTGGCGGCGGAGTGTGTGGAACCTTAAACGAGCAT-C 715  
QY 802 GCGGAGCTGAGGTCTTACATGAGCTCTCGGCCCTGGGCGATGAGTCACTTGGCT 861  
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RESULT 10

BF663695 779 bp mRNA linear EST 21-DEC-2000  
LOCUS 602145414F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309010 5',  
DEFINITION mRNA sequence.  
ACCESSION BF663695  
VERSION BF663695.1 GI:11937590  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 779)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LMC181 row: 1 column: 03

High quality sequence stop: 761.

Location/Qualifiers

FEATURES

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1..779

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4309010"

/tissue\_type="primary B-cells from consils (cell line)"

/lab\_host="DH10B (phage-resistant)"

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/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 67.7%; Score 669.8; DB 2; Length 779;  
Best Local Similarity 98.1%; Pred. No. 1.3e-124;  
Matches 762; Conservative 0; Mismatches 7; Indels 8; Gaps 8;  
QY 79 GCGCAGTACCCAGCGGTGCCCGGCTCTCCGTCCCGCGCGCTGCGGCTGGGCTCAG 138  
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QY 139 CCGCACTGGGCGCGGCTTTCGCCACTGCGCTCTTCTTGGGAGCGGTGCCCCCATGGC 198  
Db 62 CCGCACTGGGCGCGGCTTTCGCCACTGCGCTCTTCTTGGGAGCGGTGCCCCCATGGC 121  
QY 199 GAGCGCGGCGAGAGAGTGCCTGCTTCCCCCGGAGGACAGCGGCTGTGGCAGTATCTTC 258  
Db 122 GAGCGCGGCGAGAGAGTGCCTGCTTCCCCCGGAGGACAGCGGCTGTGGCAGTATCTTC 181  
QY 259 TGAGCGGCTCCATGCGGAGCACCCGCGCTGCGAAGCTGAGGCTGTGACCTTGGAGC 318  
Db 182 TGAGCGGCTCCATGCGGAGCACCCGCGCTGCGAAGCTGAGGCTGTGACCTTGGAGC 241  
QY 319 AGCCCGAGGGGATTTCTATGATGACCTTCGAGCA-GGCCAGCTTGGCCAACTGGC- 376  
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QY 495 CAGGCGCGGAGCTGGGAGCGGCGCTGTGGAGGAGGCGGCGGAGGAGGAGGAGGAG 554  
Db 422 CAGGCGCGGAGCTGGGAGCGGCGCTGTGGAGGAGGCGGCGGAGGAGGAGGAGGAG 481



QY 555 CTCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTCTGCGCGCGCGCGCGCGCG 614  
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 QY 615 ACCTTCGAGCTGGCGCTGGT-CGATCGCGACCAAGGAGAACTCTCGCTACTACGAGCG 673  
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 QY 674 CTGCTCGAGCTGCTGCGACCGCGGAGCA-TCTCGCGCTCTCAGAGTCTGTGGCGCG 732  
 DB 602 CTGCTCGAGCTGCTGCGACCGCGGAGCACTCTCGCGCTCTCAGAGTCTGTGGCGCG 661  
 QY 733 GGAAGTGTCTCAACTCTCGAAAGGAGAC-GTGGCGCGCGAGTGTGTGCGAAACCTAAAC 791  
 DB 662 GGAAGTGTCTCAACTCTCGAAAGGAGACGCTGGCGCGCGAGTGTGTGCGAAACCTAAAC 721  
 QY 792 GAACGATCTCGCGCGGGA-CGTGAGGTCTACATCAGCTTCTGCGCGCTTGGCGGATGG 847  
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RESULT 11  
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 LOCUS  
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 AGENCOURT\_8795361 NIH\_MGC\_101 Homo sapiens cDNA clone IMAGE:6427775  
 5', mRNA sequence.  
 ACCESSION BQ931589  
 VERSION BQ931589.1 GI:22346620  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 934)  
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLM2613 row: e column: 24  
 High quality sequence stop: 532.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:6427775"  
 /tissue="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
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 /note="Organ: lung; Vector: pOTB7; Site:1: EcoRI; Site:2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## FEATURES

source  
 Query Match 67.4%; Score 666.4; DB 5; Length 934;  
 Best Local Similarity 95.8%; Pred. No. 6.2e-124;  
 Matches 751; Conservative 0; Mismatches 21; Indels 12; Gaps 6;  
 QY 87 ACCGAGCCGGTCCCGGCTCTCCGTGCCCGCGCGCTGGCCCTGAGCGCACTG 146

## ORIGIN

Query Match 67.4%; Score 666.4; DB 5; Length 934;  
 Best Local Similarity 95.8%; Pred. No. 6.2e-124;  
 Matches 751; Conservative 0; Mismatches 21; Indels 12; Gaps 6;  
 QY 87 ACCGAGCCGGTCCCGGCTCTCCGTGCCCGCGCGCTGGCCCTGAGCGCACTG 146

DB 1 ACCGAGCCGGTCCCGGCTCTCCGTGCCCGCGCGCTGGCCCTGAGCGCACTG 60  
 QY 147 GCGCGCGCTTTCGCCACTTGGCTCTTCTTGGGAGGCGTGGCCCTTGGGCTGAGCGCGG 206  
 DB 61 GCGCGCGCTTTCGCCACTTGGCTCTTCTTGGGAGGCGTGGCCCTTGGGCTGAGCGCGG 120  
 QY 207 CGAGAGCAGTGCCTGCTTTCGCCCTCGAGCAGCCCTGTGGCAGTATCTTCTGAGCGCG 266  
 DB 121 CGAGAGCAGTGCCTGCTTTCGCCCTCGAGCAGCCCTGTGGCAGTATCTTCTGAGCGCG 180  
 QY 267 TCCATGCGGAGCAGCCCGCGCTGCGAGCCTGAGGCTGCTGAGCCTGGAGCAGCGGAG 326  
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 DB 237 GGGGATTTCTATGATGACCTTGGAGCAGCCCTTGGGCAACCTTGGCGGCTCATC 296  
 QY 387 CAGGCCAAGAGGCGCTGGACTTGGGCACTTACCGGCTACTCCGCTCTGGCCCTTGGCC 446  
 DB 297 CAGGCCAAGAGGCGCTGGACTTGGGCACTTACCGGCTACTCCGCTCTGGCCCTTGGCC 356  
 QY 447 CTGGCGCTTTCGCCCTGCGGAGCGGCGCTGCTGACCTGCGAGGTGGAGCGGAGCCCGGAG 506  
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 QY 567 CCGCGCTTGGAGACCTTGGAGAGCTGCTGGCGGCGGAGCGGCGGAGCCTTTCGACGCTG 626  
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 QY 627 GCGGTGTGGATGCGGACAGGAGAACTGCTCCGCTACTACGAGCGTCCCTGAGCTG 686  
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 QY 687 CTGGACCGCGGAGGCACTCTCGCTCTCAGAGTCTGTCGCGGCGGAGAGTGTGTCAA 746  
 DB 597 CTGGACCGCGGAGGCACTCTCGCTCTCAGAGTCTGTCGCGGCGGAGAGTGTGTCAA 656  
 QY 747 CTTCCAAAGGGAGCGT--GGCGGCGGAGTGTGTG--CGAAACCTTAAACGAGCG--ATCC 801  
 DB 657 CTTCCAAAGGGAGCGT--GGCGGCGGAGTGTGTG--CGAAACCTTAAACGAGCGCGCATCCG 716  
 QY 802 GCGGAGCGTCA-GGGTCTATACGCTCTCTG--CCCTTGGCGGAGTGTGACTCAGCTTGG 858  
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 DB 777 CCTT 780

RESULT 12  
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 LOCUS  
 DEFINITION BQ072503 1065 bp mRNA linear EST 02-APR-2002  
 AGENCOURT\_6838941 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5761696  
 5', mRNA sequence.  
 ACCESSION BQ072503  
 VERSION BQ072503.1 GI:19901549  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1065)  
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.



ch	63.7%;	Score 630;	DB 5;	Length 1065;
1	Similarity 96.7%;	Pred. No. 1.3e-116;		
6/5;	Conservative 0;	Mismatches 20;	Indels 3;	Gaps 3;
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61	TCCGCGCGCTCTCTGCCGCGCCATGACCCAGCGGTGCCCGGCTCTCCGTGCCCGCGG	120		
61	TCCGCGCGCTCTCTGCCGCGCCATGACCCAGCGGTGCCCGGCTCTCCGTGCCCGCGG	120		
21	CGTGGCGCTGGGCTCAGCGCAGCTGGCGCGCGCTTCGCGCACCTGGGCTCTTCTCTGGGGA	180		
21	CGTGGCGCTGGGCTCAGCGCAGCTGGCGCGCGCTTCGCGCACCTGGGCTCTTCTCTGGGGA	180		
81	GGCGGTGCCCCCATGCGGAGCGCGCGAGAGCATGTGCTGTCTCCGCCGAGAGCAGCC	240		
81	GGCGGTGCCCCCATGCGGAGCGCGCGAGAGCATGTGCTGTCTCCGCCGAGAGCAGCC	240		
941	GCCTGTGGCAGTATCTTCTGAGCGCTTCATGCGGAGACACCGCGCGTTCGAGACCTCTGA	300		
941	GCCTGTGGCAGTATCTTCTGAGCGCTTCATGCGGAGACACCGCGCGTTCGAGACCTCTGA	300		
01	GGCTGCTGACCTCGAGCAGCGCGAGGGGGATTCTATGATGACCTTCGAGCAGGCGCCAGC	360		
01	GGCTGCTGACCTCGAGCAGCGCGAGGGGGATTCTATGATGACCTTCGAGCAGGCGCCAGC	360		
961	TCTTTGGCCAACTGCGCGGCTCATCAGGCGCAAGAGCGGTGAGACTGGGCACTTCA	420		
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21	CGGGCTACTCGCCCTTGGCCCTGGCCCTGGCGCTGCCCGCAGCGGGCGCTGTGTGACCT	480		
21	CGGGCTACTCGCCCTTGGCCCTGGCCCTGGCGCTGCCCGCAGCGGGCGCTGTGTGACCT	480		
481	CGCAGGTGGAACGCGCAGCGCCCCCGAGCTGGGACGGCCCTGTGTGGAGGCAAGGCCGCGG	540		
481	CGCAGGTGGAACGCGCAGCGCCCCCGAGCTGGGACGGCCCTGTGTGGAGGCAAGGCCGCGG	540		
541	AGCAACAAGATGCACTTCGGCTGAGACCCGCTTGGAGA-CCCTGGACGAGCTGTCTGGCG	599		
541	AGCAACAAGATGCACTTCGGCTGAGACCCGCTTGGAGA-CCCTGGACGAGCTGTCTGGCG	599		

	ORIGIN
Query Match	63.2%; Score 625; DB 4; Length 625;
Best Local Similarity	100.0%; Pred. No. 1.3e-115;
Matches 625; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	65 GCAGCTCTGCGCGGCATCACCAGCCGGTCCCGCGCTCTCGTGCCCGCCGCCGT 124                   
D8	1 GCAGCTCTGCGCGGCATCACCAGCCGGTCCCGCGCTCTCGTGCCCGCCGCCGT 60                   
QY	125 GGCCCTGGGCTCAGCCGCAC TGCGGCGCCGCTTCGCACATGGCGCTTCTCTGGGGAGGCG 184                   



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Db 61 GGCCTTGGCTCAGCGGCTGGGCGCCCTTGGCCACTGGCCCTTCTCTGGGAGGG 120
QY 185 GTGCCCCCATGCGGAGGCGCGGAGAGAGTGCCTTCTTCCCGGAGGAGCAGCCGCT 244
Db 121 GTGCCCCCATGCGGAGGCGCGGAGAGAGTGCCTTCTTCCCGGAGGAGCAGCCGCT 180
QY 245 GTGCGAGTATCTTCTGAGCGCTTCATGCGGAGAGCAGCCGCGCTGCGAGGCTGAGGCT 304
Db 181 GTGCGAGTATCTTCTGAGCGCTTCATGCGGAGAGCAGCCGCGCTGCGAGGCTGAGGCT 240
QY 305 GCTGACCTTGGAGAGCGCGAGGGGATTTCTATGATGACCTGCGAGCAGGCGCCAGCTCTT 364
Db 241 GCTGACCTTGGAGAGCGCGAGGGGATTTCTATGATGACCTGCGAGCAGGCGCCAGCTCTT 300
QY 365 GCGCAACCTTGGCGCGGCTCATCCAGGCCAAGAGCGCTTGGACCTTGGGACACCTTCACGGG 424
Db 301 GCGCAACCTTGGCGCGGCTCATCCAGGCCAAGAGCGCTTGGACCTTGGGACACCTTCACGGG 360
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Db 361 CTACTCGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 420
QY 485 GGTGACGCGCAGCGCCCGGAGCTGGAGCGGCGCTTGGAGCGGCGGCGGCGGAGGCA 544
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QY 545 CAAGATCGACCTTCCGCTTGAAGCGCGCTTGGAGCGGCGCTTGGAGCGGCGGCGGCGG 604
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DEFINITION 602437508F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4555609 5',
mRNA sequence.
ACCESSION BG339399
VERSION BG339399.1 GI:13145837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 912)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1256 row: o column: 02
High quality sequence stop: 719.
Location/Qualifiers
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FEATURES  
source

RESULT 15  
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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## ORIGIN

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Query Match 62.8%; Score 621; DB 4; Length 912;
Best Local Similarity 96.5%; Pred. No. 8.6e-115;
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QY 133 GCTCAGCGCACTGGGCGCGCTTTCGCACTTGGCTCTTCTCTGGGAGGCGGTCGCC 192
Db 62 GCTCAGCGCACTGGGCGCGCTTTCGCACTTGGCTCTTCTCTGGGAGGCGGTCGCC 121
QY 193 CATGCCAGGCGCGGAGAGAGTGCCTTCTTCCCGGAGGAGCAGCGGCTTGGCAGT 252
Db 122 CATGCCAGGCGCGGAGAGAGTGCCTTCTTCCCGGAGGAGCAGCGGCTTGGCAGT 181
QY 253 ATCTTCTGAGCGCTTCATGCGGAGCACCCTGGGCTTCCGAGCTGAGGCTTGGACCC 312
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QY 313 TGGAGCAGCGCGGAGGATTTCTATGATGATGATGATGATGATGATGATGATGATG 372
Db 242 TGGAGCAGCGCGGAGGATTTCTATGATGATGATGATGATGATGATGATGATGATG 301
QY 373 TGGCGCGGCTCATCCAGGCCAAGAGCGCTTGGACCTTGGGACCTTTCAGGGCTACTCG 432
Db 302 TGGCGCGGCTCATCCAGGCCAAGAGCGCTTGGACCTTGGGACCTTTCAGGGCTACTCG 361
QY 433 CCCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGG 492
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QY 493 CGCAGCGCGCGAGCTGGGAGCGGCGCTTGGAGCGGCGGCGGCGGCGGCGGCGGCGG 552
Db 421 CGCAGCGCGCGAGCTGGGAGCGGCGCTTGGAGCGGCGGCGGCGGCGGCGGCGGCGG 479
QY 553 ACCTCCGCGCTGAAGCGCGCTTGGAGCGGCTTGGAGCGGCTTGGAGCGGCGGCGGCGG 612
Db 480 ACCTCCGCGCTGAAGCGCGCTTGGAGCGGCTTGGAGCGGCTTGGAGCGGCGGCGGCGG 539
QY 613 GCACCTTTCAGCTGGCGCTTGGATGCGGAGCAAGGAGAACTGCTTCCGCTTACTACGAGC 672
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QY 673 GCTGCTGCGAGCTTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732
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LOCUS AK054334 2243 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330016L21 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.

ACCESSION AK054334 GI:26344156  
VERSION AK054334.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL 20493374  
MEDLINE 11042159  
PUBMED 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED 11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

6 (bases 1 to 2243)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, K., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/

FEATURES  
Location/Qualifiers  
1..2243  
/organism="Mus musculus"  
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polyA\_site  
2243  
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19 CCGCGCTGTCTAACTGACACATGCTCAGCCCGCTCTGCTATCTATCCAGCGCA 78  
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79 CTGGCGCTGGGCTGGCGCGCTGGCGCGCTTCGCTACTGCTGCTCTTCTCTGGGAAA 138  
183 CGGTGCCCCCATGCGGAGCGCGGAGAGCAGTGCCTGCTTCCCGCGGAGAGCAGCGCG 242  
139 CGGTGGCTCTCATGGGGTCCAGGCGGCGGCGCTGCTGCCACCTGAGGCAATCC 198  
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319 CTGGCCACCTGCGCGCGCTCATTAAGCGCCAGAAAGCTCTGGATCTGGTACTTTCAG 378  
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379 GGCTACTCGCGCTGCGCGCTGCGCGCTGCGCGCGGAGCGCGCTGCGCGCTGCGCG 438  
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Scoring table: IDENTITY_NUC
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Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database : N Geneseq_23Sep04:*
Listing first 1500 summaries
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
No. Score Match Length DB ID Description
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ID AA337107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
FN WO200012708-A2.
PD 09-MAR-2000.
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RESULT 2
ID AAF54419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
FN WO200078961-A1.
PD 28-DEC-2000.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
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ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
FN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 4
ID AC68458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
FN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 5
ID ACH04560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
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ID AC68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
FN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 7
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
FN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 8
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 9
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 10
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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RESULT 11
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FN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
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RESULT 12
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FN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 13
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 14
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FN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;

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RESULT 15
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 16
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
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PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 18
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 20
ID ADF5994 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 22
ID ADJ37302 standard; cDNA; 989 BP.
DE Human tumour therapy associated PRO1558 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 23
ID ADE96678 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 24
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 25
ID ADF24988 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 26
ID ADF29624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 27
ID ADE97155 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 28
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 29
ID ADH04147 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 30
ID ADH03670 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 31
ID ADG68226 standard; cDNA; 989 BP.
DE Human PRO polypeptide cDNA #11.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 32
ID ADH04624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 989; DB 12; Length 989;
  Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 33
ID ADH61625 standard; cDNA; 989 BP.
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
 PN US2004014130-A1.  
 PD 22-JAN-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-156;  
 RESULT 34  
 ID ADL94824 standard; cDNA; 989 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
 PN US2004073015-A1.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-156;  
 RESULT 35  
 ID ADO42276 standard; cDNA; 989 BP.  
 DE Human NOVX polynucleotide #63.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 PA (AGEE) AGEE M L.  
 PA (ALSO) ALSOBROOK J P.  
 PA (ANDE) ANDERSON D W.  
 PA (BERG) BERGHS C.  
 PA (BOLD) BOLDOG F L.  
 PA (BURG) BURGESS C E.  
 PA (CATT) CATTERTON E.  
 PA (DIPI) DIPIPPO V A.  
 PA (EDIN) EDINGER S R.  
 PA (EISE) EISEN A.  
 PA (ELLE) ELLERMAN K.  
 PA (GANG) GANGOLLI E A.  
 PA (GERL) GERLACH V.  
 PA (GORM) GORMAN L.  
 PA (ROTH) ROTHBERG B G.  
 PA (GUOX) GUO X S.  
 PA (HERR) HERRMANN J L.  
 PA (HALV) HALVORSEN Y.  
 PA (JIWV) JI W.  
 PA (KEKU) KEKUDA R.  
 PA (KHRA) KHRAMTSOV N V.  
 PA (LARO) LAROCHELLE W J.  
 PA (LEPL) LEFLEY D M.  
 PA (LILL) LI L.  
 PA (MACD) MACDOUGALL J R.  
 PA (MILL) MILLER C E.  
 PA (ORTT) ORT T.  
 PA (PADI) PADIGARU M.  
 PA (PATT) PATURAJAN M.  
 PA (PENA) PENA C E A.  
 PA (PEYM) PEYMAN J A.  
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 PA (ROTH) ROTHENBERG M E.  
 PA (SHEN) SHENOY S G.  
 PA (SMIT) SMITHSON G.  
 PA (SPAD) SPADERNA S K.  
 PA (SPYT) SPYTEK K A.  
 PA (STON) STONE D J.  
 PA (TAUP) TAUPIER R J.  
 PA (VERN) VERNET C A M.  
 PA (VOSS) VOSS E Z.  
 PA (ZHON) ZHONG M.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-156;  
 RESULT 36  
 ID ABA05419 standard; cDNA; 1037 BP.  
 DE Human O-methyltransferase family member 25692 encoding cDNA.  
 PN WO200183719-A2.  
 PD 08-NOV-2001.  
 PA (MILL) MILLENNIUM PHARM INC.  
 Query Match 99.7%; Score 985.8; DB 6; Length 1037;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-155;  
 RESULT 37  
 ID AA298166 standard; cDNA; 985 BP.

DE Human signal peptide containing protein HSPP-58 cDNA SEQ ID NO:192.  
 PN WO200006010-A2.  
 PD 06-JAN-2000.  
 PA (INCY) INCYTE PHARM INC.  
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 Best Local Similarity 99.8%; Pred. No. 7.1e-155;  
 RESULT 38  
 ID ABQ61039 standard; cDNA; 1100 BP.  
 DE Human PRO1558 protein encoding sequence.  
 PN WO200231111-A2.  
 PD 18-APR-2002.  
 PA (HYSE) HYSEQ INC.  
 Query Match 99.3%; Score 981.8; DB 6; Length 1100;  
 Best Local Similarity 99.8%; Pred. No. 7.1e-155;  
 RESULT 39  
 ID ADO42272 standard; cDNA; 988 BP.  
 DE Human NOVX polynucleotide #61.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 PA (AGEE) AGEE M L.  
 PA (ALSO) ALSOBROOK J P.  
 PA (ANDE) ANDERSON D W.  
 PA (BERG) BERGHS C.  
 PA (BOLD) BOLDOG F L.  
 PA (BURG) BURGESS C E.  
 PA (CATT) CATTERTON E.  
 PA (DIPI) DIPIPPO V A.  
 PA (EDIN) EDINGER S R.  
 PA (EISE) EISEN A.  
 PA (ELLE) ELLERMAN K.  
 PA (GANG) GANGOLLI E A.  
 PA (GERL) GERLACH V.  
 PA (GORM) GORMAN L.  
 PA (ROTH) ROTHBERG B G.  
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 PA (JIWV) JI W.  
 PA (KEKU) KEKUDA R.  
 PA (KHRA) KHRAMTSOV N V.  
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 PA (LEPL) LEFLEY D M.  
 PA (LILL) LI L.  
 PA (MACD) MACDOUGALL J R.  
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 PA (ORTT) ORT T.  
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 PA (PATT) PATURAJAN M.  
 PA (PENA) PENA C E A.  
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 PA (TAUP) TAUPIER R J.  
 PA (VERN) VERNET C A M.  
 PA (VOSS) VOSS E Z.  
 PA (ZHON) ZHONG M.  
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 ID AAH33455 standard; cDNA; 967 BP.  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 PA (HUMA) HUMAN GENOME SCI INC.  
 Query Match 94.9%; Score 938.2; DB 4; Length 967;  
 Best Local Similarity 99.4%; Pred. No. 1.3e-147;  
 RESULT 41  
 ID AAC76634 standard; cDNA; 812 BP.



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DE Human OREF ORF2189 polynucleotide sequence SEQ ID NO:4377.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP. 80.9%; Score 799.8; DB 3; Length 812;
Query Match 99.1%; Pred. No. 1.6e-124;
Best Local Similarity
RESULT 42
ID ABA05420 standard; cDNA; 789 BP.
DE Human O-methyltransferase family member 25692 coding sequence.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC. 79.8%; Score 789; DB 6; Length 789;
Query Match 100.0%; Pred. No. 1e-122;
Best Local Similarity
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ID AAD56372 standard; DNA; 876 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 71.0%; Score 701.8; DB 9; Length 876;
Query Match 86.5%; Pred. No. 3.4e-108;
Best Local Similarity
RESULT 44
ID AAD56361 standard; DNA; 885 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 70.9%; Score 701; DB 9; Length 885;
Query Match 86.2%; Pred. No. 4.7e-108;
Best Local Similarity
RESULT 45
ID ADO42274 standard; cDNA; 787 BP.
DE Human NOVX polynucleotide #62.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JTWV/) JI W.
PA (KEKU/) KEKUDA R.
PA (KIRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.

PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 59.0%; Score 583.6; DB 12; Length 787;
Best Local Similarity 90.1%; Pred. No. 1.8e-88;
RESULT 46
ID ACH35195 standard; cDNA; 474 BP.
DE Human endothelial cell cDNA #3328.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W. 42.7%; Score 422; DB 9; Length 474;
Query Match 100.0%; Pred. No. 1.6e-61;
Best Local Similarity
RESULT 47
ID ACH35890 standard; cDNA; 458 BP.
DE Human endothelial cell cDNA #4023.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W. 41.8%; Score 413; DB 9; Length 458;
Query Match 100.0%; Pred. No. 4.9e-60;
Best Local Similarity
RESULT 48
ID ADD34178 standard; DNA; 770 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY. 40.9%; Score 404.4; DB 10; Length 770;
Query Match 80.4%; Pred. No. 1.3e-58;
Best Local Similarity
RESULT 49
ID ABN94134 standard; DNA; 326 BP.
DE Gene #632 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC. 31.5%; Score 312; DB 6; Length 326;
Query Match 99.7%; Pred. No. 3.4e-43;
Best Local Similarity
RESULT 50
ID ADM80035 standard; DNA; 11171 BP.
DE Spiramycin biosynthesis related DNA, SEQ ID 2.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS CENT NAT RECH SCI. 19.7%; Score 194.8; DB 12; Length 11171;
Query Match 55.1%; Pred. No. 1.1e-23;
Best Local Similarity
RESULT 51
ID ADN97551 standard; DNA; 11171 BP.
DE S ambotaciens spiramycin biosynthetic enzyme genomic region #2.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS. 19.7%; Score 194.8; DB 12; Length 11171;
Query Match 55.1%; Pred. No. 1.1e-23;
Best Local Similarity
RESULT 52
ID ADM80044 standard; DNA; 675 BP.
DE Spiramycin biosynthesis orf5*, SEQ ID 11.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS CENT NAT RECH SCI. 19.6%; Score 193.8; DB 12; Length 675;
Query Match 58.1%; Pred. No. 1.7e-23;
Best Local Similarity

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RESULT 53  
ID ADN97560 standard; DNA; 675 BP.  
DE S ambotaciens spiramycin biosynthetic gene ORFs\*.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 19.6%; Score 193.8; DB 12; Length 675;  
Best Local Similarity 58.1%; Pred. No. 1.7e-23;  
RESULT 54  
ID ABD04592 standard; DNA; 846 BP.  
DE Pseudomonas aeruginosa polynucleotide #3196.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 19.1%; Score 189; DB 11; Length 846;  
Best Local Similarity 56.0%; Pred. No. 1.1e-22;  
RESULT 55  
ID AAQ4449 standard; DNA; 2381 BP.  
DE 3-acylating enzyme coding sequence.  
PN JP06038750-A.  
PD 15-FEB-1994.  
PA (MEIJ ) MEIJI SEIKA KAISHA.  
Query Match 18.8%; Score 185.8; DB 2; Length 2381;  
Best Local Similarity 57.3%; Pred. No. 3.6e-22;  
RESULT 56  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 18.8%; Score 185.8; DB 12; Length 84428;  
Best Local Similarity 57.3%; Pred. No. 3.2e-22;  
RESULT 57  
ID ADI39159 standard; DNA; 85692 BP.  
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.4%; Score 182.4; DB 12; Length 85692;  
Best Local Similarity 57.4%; Pred. No. 1.2e-21;  
RESULT 58  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.1%; Score 179.2; DB 12; Length 86941;  
Best Local Similarity 57.9%; Pred. No. 4.1e-21;  
RESULT 59  
ID AAC89765 standard; cDNA; 178 BP.  
DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
PN WO200073324-A2.  
PD 07-DEC-2000.  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
Query Match 17.7%; Score 174.8; DB 4; Length 178;  
Best Local Similarity 98.9%; Pred. No. 2.6e-20;  
RESULT 60  
ID ABS63429 standard; cDNA; 953 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 16.4%; Score 161.8; DB 6; Length 953;  
Best Local Similarity 55.1%; Pred. No. 3.7e-18;  
RESULT 61  
ID ABS63428 standard; cDNA; 1049 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.

PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 16.1%; Score 159.2; DB 6; Length 1049;  
Best Local Similarity 54.8%; Pred. No. 9.9e-18;  
RESULT 62  
ID ABS63413 standard; cDNA; 997 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 16.0%; Score 158.6; DB 6; Length 997;  
Best Local Similarity 54.2%; Pred. No. 1.2e-17;  
RESULT 63  
ID ADA71076 standard; DNA; 1338 BP.  
DE Rice gene, SEQ ID 4399.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 16.0%; Score 158.6; DB 8; Length 1338;  
Best Local Similarity 55.2%; Pred. No. 1.2e-17;  
RESULT 64  
ID ABS63427 standard; cDNA; 1078 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 15.9%; Score 157.2; DB 6; Length 1078;  
Best Local Similarity 57.1%; Pred. No. 2.1e-17;  
RESULT 65  
ID ABS63424 standard; cDNA; 1018 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 15.7%; Score 155.6; DB 6; Length 1018;  
Best Local Similarity 56.6%; Pred. No. 3.9e-17;  
RESULT 66  
ID ABS63407 standard; cDNA; 891 BP.  
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 15.6%; Score 154; DB 6; Length 891;  
Best Local Similarity 56.7%; Pred. No. 7.3e-17;  
RESULT 67  
ID AAA14651 standard; DNA; 77536 BP.  
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
PN WO2003000906-A2.  
Query Match 15.5%; Score 153; DB 3; Length 77536;  
Best Local Similarity 55.4%; Pred. No. 9.5e-17;  
RESULT 68  
ID ADA49019 standard; DNA; 1112 BP.  
DE Wheat gene conferring disease resistance in plants.  
PN WO2003000906-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 15.4%; Score 152.8; DB 9; Length 1112;  
Best Local Similarity 58.3%; Pred. No. 1.2e-16;  
RESULT 69  
ID AAX25215 standard; cDNA; 1218 BP.  
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
PN WO9910498-A2.  
PD 04-MAR-1999.  
PA (PION-) PIONEER HI-BRED INT INC.



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Query Match 15.4%; Score 152.4; DB 2; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.3e-16;  
 RESULT 70  
 ID AAD05742 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA-3-O-methyltransferase (CCoA-OMT) cDNA.  
 PN WO200134817-A2.  
 PD 17-MAY-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.4%; Score 152.4; DB 5; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.3e-16;  
 RESULT 71  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum aneamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 15.3%; Score 151.4; DB 8; Length 82746;  
 Best Local Similarity 57.3%; Pred. No. 1.8e-16;  
 RESULT 72  
 ID ABZ40101 standard; DNA; 666 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 15.1%; Score 149.2; DB 10; Length 666;  
 Best Local Similarity 53.5%; Pred. No. 4.7e-16;  
 RESULT 73  
 ID AX25210 standard; cDNA; 1003 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.1%; Score 149.2; DB 2; Length 1003;  
 Best Local Similarity 58.0%; Pred. No. 4.6e-16;  
 RESULT 74  
 ID ADM49212 standard; DNA; 798 BP.  
 DE Maize gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 15.0%; Score 148; DB 9; Length 798;  
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;  
 RESULT 75  
 ID ABS63425 standard; cDNA; 1118 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1118;  
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;  
 RESULT 76  
 ID ABS63408 standard; cDNA; 1146 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1146;  
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;  
 RESULT 77  
 ID ADD34177 standard; DNA; 407 BP.  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
 PN WO2003020220-A2.  
 PD 13-MAR-2003.  
 PA (UYEW-) UNIV EMORY.  
 Query Match 14.9%; Score 147.4; DB 10; Length 407;  
 Best Local Similarity 73.3%; Pred. No. 9.4e-16;  
 RESULT 78  
 ID AAA81501 standard; DNA; 48275 BP.  
 DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.

PN WO20022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 48275;  
 Best Local Similarity 53.1%; Pred. No. 1e-15;  
 RESULT 79  
 ID AAA81489 standard; DNA; 837096 BP.  
 DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.  
 PN WO20022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 110000;  
 Best Local Similarity 53.1%; Pred. No. 1e-15;  
 RESULT 80  
 ID RAF21610 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match 14.8%; Score 146.8; DB 3; Length 349980;  
 Best Local Similarity 53.1%; Pred. No. 9.8e-16;  
 RESULT 81  
 ID AAL61190 standard; DNA; 504 BP.  
 DE Actinosynnema pretiosum O-methyltransferase gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 14.8%; Score 146.6; DB 8; Length 504;  
 Best Local Similarity 57.7%; Pred. No. 1.3e-15;  
 RESULT 82  
 ID AAX25208 standard; cDNA; 1160 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 14.8%; Score 146.4; DB 2; Length 1160;  
 Best Local Similarity 53.5%; Pred. No. 1.3e-15;  
 RESULT 83  
 ID ABS63409 standard; cDNA; 1057 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.6%; Score 144.4; DB 6; Length 1057;  
 Best Local Similarity 57.3%; Pred. No. 2.9e-15;  
 RESULT 84  
 ID ADA71075 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4398.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.3%; Score 141.8; DB 8; Length 783;  
 Best Local Similarity 57.4%; Pred. No. 7.9e-15;  
 RESULT 85  
 ID ACL23248 standard; DNA; 509 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13239.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Query Match 14.2%; Score 140.8; DB 9; Length 509;  
 Best Local Similarity 60.3%; Pred. No. 1.2e-14;  
 RESULT 86  
 ID ABS63412 standard; cDNA; 1058 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.2%; Score 140.6; DB 6; Length 1058;



Best Local Similarity 50.6%; Pred. No. 1.2e-14;  
 RESULT 87  
 ID ADA70823 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4146.  
 PN WO200300089-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.2%; Score 140; DB 8; Length 783;  
 Best Local Similarity 52.9%; Pred. No. 1.6e-14;  
 RESULT 88  
 ID ABN87118 standard; cDNA; 1103 BP.  
 DE Lolium perenne LpCCoAMTB nucleotide sequence SEQ ID NO:12.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135.6; DB 6; Length 1103;  
 Best Local Similarity 57.0%; Pred. No. 8.5e-14;  
 RESULT 89  
 ID ABN87121 standard; cDNA; 773 BP.  
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 773;  
 Best Local Similarity 56.9%; Pred. No. 1.1e-13;  
 RESULT 90  
 ID ABN87122 standard; cDNA; 789 BP.  
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 789;  
 Best Local Similarity 56.9%; Pred. No. 1.1e-13;  
 RESULT 91  
 ID ABN87120 standard; cDNA; 693 BP.  
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:15.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.3%; Score 131.6; DB 6; Length 693;  
 Best Local Similarity 56.9%; Pred. No. 4e-13;  
 RESULT 92  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.  
 Query Match 12.9%; Score 127.4; DB 5; Length 109519;  
 Best Local Similarity 55.8%; Pred. No. 1.7e-12;  
 RESULT 93  
 ID ABN87126 standard; cDNA; 689 BP.  
 DE Lolium perenne LpCCoAMTB nucleotide sequence SEQ ID NO:21.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.8%; Score 126.8; DB 6; Length 689;  
 Best Local Similarity 57.1%; Pred. No. 2.5e-12;  
 RESULT 94  
 ID ABS63410 standard; cDNA; 923 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Query Match 12.7%; Score 126; DB 6; Length 923;  
 Best Local Similarity 56.6%; Pred. No. 3.4e-12;  
 RESULT 95  
 ID AAX25209 standard; cDNA; 944 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.

PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 12.7%; Score 126; DB 2; Length 944;  
 Best Local Similarity 56.6%; Pred. No. 3.4e-12;  
 RESULT 96  
 ID ADA48371 standard; DNA; 835 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 12.7%; Score 125.4; DB 9; Length 835;  
 Best Local Similarity 55.0%; Pred. No. 4.3e-12;  
 RESULT 97  
 ID ADC68436 standard; cDNA; 1051 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.6%; Score 125; DB 10; Length 1051;  
 Best Local Similarity 54.0%; Pred. No. 5e-12;  
 RESULT 98  
 ID ADC68544 standard; cDNA; 1059 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.5%; Score 123.4; DB 10; Length 1059;  
 Best Local Similarity 53.9%; Pred. No. 9.2e-12;  
 RESULT 99  
 ID ADC68545 standard; cDNA; 1063 BP.  
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.4%; Score 122.6; DB 10; Length 1063;  
 Best Local Similarity 54.2%; Pred. No. 1.3e-11;  
 RESULT 100  
 ID ABN87112 standard; cDNA; 765 BP.  
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:6.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.0%; Score 118.4; DB 6; Length 765;  
 Best Local Similarity 53.7%; Pred. No. 6.3e-11;  
 RESULT 101  
 ID AAQ14978 standard; DNA; 1810 BP.  
 DE ACYA gene.  
 PN EP459525-A.  
 PD 04-DEC-1991.  
 PA (SAOC) MERCIAN CORP.  
 Query Match 11.9%; Score 118; DB 2; Length 1810;  
 Best Local Similarity 57.8%; Pred. No. 7.2e-11;  
 RESULT 102  
 ID ABN87245 standard; cDNA; 1161 BP.  
 DE Lolium perenne CCoAMTB cDNA sequence SEQ ID NO:168.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.9%; Score 117.8; DB 6; Length 1161;  
 Best Local Similarity 53.7%; Pred. No. 7.9e-11;  
 RESULT 103  
 ID ABN87110 standard; cDNA; 758 BP.  
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:4.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.7%; Score 115.6; DB 6; Length 758;  
 Best Local Similarity 53.7%; Pred. No. 7.9e-11;



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Best Local Similarity 52.8%; Pred. No. 1.9e-10;  
 RESULT 104  
 ID ABN87115 standard; cDNA; 793 BP.  
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:9.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.7%; Score 115.6; DB 6; Length 793;  
 Best Local Similarity 52.8%; Pred. No. 1.9e-10;  
 RESULT 105  
 ID ABN87108 standard; cDNA; 1113 BP.  
 DE Lolium perenne LpCCoAMTa nucleotide sequence SEQ ID NO:1.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.6%; Score 115; DB 6; Length 1113;  
 Best Local Similarity 52.8%; Pred. No. 2.3e-10;  
 RESULT 106  
 ID ABN87246 standard; cDNA; 1199 BP.  
 DE Lolium perenne CCoAMT2 cDNA sequence SEQ ID NO:170.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.6%; Score 115; DB 6; Length 1199;  
 Best Local Similarity 52.8%; Pred. No. 2.3e-10;  
 RESULT 107  
 ID ABN87111 standard; cDNA; 774 BP.  
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:5.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.5%; Score 113.8; DB 6; Length 774;  
 Best Local Similarity 53.0%; Pred. No. 3.7e-10;  
 RESULT 108  
 ID ABN87113 standard; cDNA; 777 BP.  
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:7.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.4%; Score 113.2; DB 6; Length 777;  
 Best Local Similarity 52.2%; Pred. No. 4.7e-10;  
 RESULT 109  
 ID ABN87114 standard; cDNA; 792 BP.  
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:8.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 11.1%; Score 110; DB 6; Length 792;  
 Best Local Similarity 51.9%; Pred. No. 1.6e-09;  
 RESULT 110  
 ID AA24153 standard; cDNA to mRNA; 111 BP.  
 DE Human gene signature HUMG06156.  
 PN WO9514772-A1.  
 PD 01-JUN-1995.  
 PA (MATS/) MATSUBARA K.  
 PA (OKUB/) OKUBO K.  
 Query Match 10.8%; Score 106.8; DB 2; Length 111;  
 Best Local Similarity 97.3%; Pred. No. 5.7e-09;  
 RESULT 111  
 ID ABK62368 standard; cDNA; 343 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #275.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 10.5%; Score 103.6; DB 6; Length 343;  
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;  
 RESULT 112

ID ADB55662 standard; DNA; 343 BP.  
 DE Toxicity-related gene, SEQ ID 688.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 10.5%; Score 103.6; DB 10; Length 343;  
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;  
 RESULT 113  
 ID ABT40596 standard; DNA; 343 BP.  
 DE Toxicity modelling related rat gene SEQ ID NO 298.  
 PN WO200295000-A2.  
 PD 28-NOV-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 10.5%; Score 103.6; DB 10; Length 343;  
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;  
 RESULT 114  
 ID AAA68001 standard; DNA; 1012 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 3; Length 1012;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 115  
 ID ADD41751 standard; DNA; 1012 BP.  
 DE O-methyl transferase DNA #9.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 9.8%; Score 96.8; DB 10; Length 1012;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 116  
 ID AAV23912 standard; DNA; 1026 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 117  
 ID AA206875 standard; cDNA; 1026 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 1.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 118  
 ID AAA67913 standard; DNA; 1026 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 9.8%; Score 96.8; DB 3; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 119  
 ID ADD41663 standard; DNA; 1026 BP.  
 DE O-methyl transferase DNA #1.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 9.8%; Score 96.8; DB 10; Length 1026;  
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;  
 RESULT 120  
 ID ABN87119 standard; cDNA; 628 BP.  
 DE Lolium perenne LpCCoAMTb partial nucleotide sequence SEQ ID NO:14.  
 PN WO200226994-A1.



PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 9.6%; Score 95.4; DB 6; Length 628;  
Best Local Similarity 53.7%; Pred. No. 4.4e-07;  
RESULT 121  
ID AC123249 standard; DNA; 542 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13240.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UTYNI-) UNIV JAPAN OKAYAMA.  
Query Match 9.6%; Score 95.2; DB 9; Length 542;  
Best Local Similarity 50.9%; Pred. No. 4.7e-07;  
RESULT 122  
ID ADK69906 standard; DNA; 1180 BP.  
DE Maize P4 CCoAOMT2 gene, seq id 3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.6%; Score 95.2; DB 10; Length 1180;  
Best Local Similarity 58.5%; Pred. No. 4.6e-07;  
RESULT 123  
ID ADK69926 standard; DNA; 1199 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #4.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.6%; Score 95.2; DB 10; Length 1199;  
Best Local Similarity 58.5%; Pred. No. 4.6e-07;  
RESULT 124  
ID AB000975 standard; DNA; 675 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 6750.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 93.4; DB 11; Length 675;  
Best Local Similarity 52.3%; Pred. No. 9.4e-07;  
RESULT 125  
ID ADK69918 standard; DNA; 1172 BP.  
DE Maize W64A CCoAOMT2 gene deletion mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1172;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 126  
ID ADK69927 standard; DNA; 1178 BP.  
DE Maize W64A CCoAOMT2 gene deletion mutant #2.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1178;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 127  
ID ADK69919 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 128  
ID ADK69920 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #2.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 129  
ID ADK69928 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #7.  
PN FR2833615-A1.

PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 130  
ID ADK69923 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #5.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 131  
ID ADK69904 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene, seq id 1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 132  
ID ADK69922 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #4.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 133  
ID ADK69924 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #6.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 134  
ID ADK69929 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #8.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 135  
ID ADK69931 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #10.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 136  
ID ADK69921 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 137  
ID ADK69930 standard; DNA; 1181 BP.  
DE Maize W64A CCoAOMT2 gene substitution mutant #9.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 138  
ID ADK69917 standard; DNA; 1186 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.



PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 8.5%; Score 84; DB 12; Length 780;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 147  
ID ADN73162 standard; cDNA; 780 BP.  
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Query Match 8.5%; Score 84; DB 12; Length 780;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 148  
ID AAC45547 standard; DNA; 1032 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1032;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 149  
ID AAC42559 standard; DNA; 1033 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1033;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 150  
ID ABN98364 standard; DNA; 1072 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYI/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHIEU A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 8.5%; Score 84; DB 6; Length 1072;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 151  
ID AAC44172 standard; DNA; 1180 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1180;  
Best Local Similarity 51.9%; Pred. No. 3.4e-05;  
RESULT 152  
ID ABS63417 standard; cDNA; 980 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.0%; Score 79.2; DB 6; Length 980;  
Best Local Similarity 51.2%; Pred. No. 0.00022;  
RESULT 153  
ID AAV23845 standard; DNA; 760 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1186;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 139  
ID ADK69925 standard; DNA; 1196 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1196;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 140  
ID ADK69932 standard; DNA; 1199 BP.  
DE Maize W64A CCoAOMT2 gene insertion mutant #5.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1199;  
Best Local Similarity 59.7%; Pred. No. 1.1e-06;  
RESULT 141  
ID ABS63415 standard; cDNA; 931 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.9%; Score 88; DB 6; Length 931;  
Best Local Similarity 50.7%; Pred. No. 7.4e-06;  
RESULT 142  
ID ABS63430 standard; cDNA; 534 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.9%; Score 87.8; DB 6; Length 534;  
Best Local Similarity 54.1%; Pred. No. 8.1e-06;  
RESULT 143  
ID ABS63418 standard; cDNA; 962 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.7%; Score 85.6; DB 6; Length 962;  
Best Local Similarity 52.2%; Pred. No. 1.9e-05;  
RESULT 144  
ID ABS63419 standard; cDNA; 1023 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.7%; Score 85.6; DB 6; Length 1023;  
Best Local Similarity 52.2%; Pred. No. 1.8e-05;  
RESULT 145  
ID AAQ32259 standard; cDNA; 1258 BP.  
DE Caffeoyl-CoA-3-O-methyltransferase gene (pl2-4).  
PN DE411747-A.  
PD 03-DEC-1992.  
PA (FARB) BAYER AG.  
Query Match 8.5%; Score 84.4; DB 2; Length 1258;  
Best Local Similarity 49.8%; Pred. No. 2.9e-05;  
RESULT 146  
ID ADN74200 standard; cDNA; 780 BP.  
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.



PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00069;  
RESULT 154  
ID AA206846 standard; cDNA; 760 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
PN US5952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00069;  
RESULT 155  
ID AA659584 standard; cDNA; 760 BP.  
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00069;  
RESULT 156  
ID AA67932 standard; cDNA; 760 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00069;  
RESULT 157  
ID AD041682 standard; cDNA; 760 BP.  
DE O-methyl transferase DNA #5.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 7.7%; Score 76.2; DB 10; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00069;  
RESULT 158  
ID ABS63416 standard; cDNA; 929 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAROON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAPALSKI J A.  
Query Match 7.5%; Score 74.4; DB 6; Length 929;  
Best Local Similarity 50.5%; Pred. No. 0.0014;  
RESULT 159  
ID ABS54112 standard; cDNA; 870 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UTGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 7.4%; Score 73.2; DB 6; Length 870;  
Best Local Similarity 48.4%; Pred. No. 0.0022;  
RESULT 160  
ID AAQ13306 standard; cDNA; 1107 BP.  
DE Human catechol-O-methyltransferase gene.  
PN WO911513-A.  
PD 08-AUG-1991.  
PA (ORIN) ORION YHTYMAE OY.  
Query Match 7.2%; Score 71; DB 2; Length 1107;  
Best Local Similarity 50.7%; Pred. No. 0.005;  
RESULT 161  
ID AAC77872 standard; cDNA; 1350 BP.  
DE Human cancer associated gene sequence SEQ ID NO:266.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 70.6; DB 3; Length 1350;  
Best Local Similarity 50.4%; Pred. No. 0.0058;

RESULT 162  
ID ABS54113 standard; cDNA; 811 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAMT-2) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UTGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 7.1%; Score 70; DB 6; Length 811;  
Best Local Similarity 47.9%; Pred. No. 0.0074;  
RESULT 163  
ID ADH02845 standard; cDNA; 888 BP.  
DE Petunia E20 cDNA #SEQ ID 4.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.6; DB 10; Length 888;  
Best Local Similarity 50.3%; Pred. No. 0.0086;  
RESULT 164  
ID ADH02842 standard; cDNA; 969 BP.  
DE Petunia diffe cDNA #SEQ ID 1.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.6; DB 10; Length 969;  
Best Local Similarity 50.3%; Pred. No. 0.0086;  
RESULT 165  
ID AB283278 standard; cDNA; 1024 BP.  
DE Toxicologically relevant human nucleotide sequence #437.  
PN WO2003016500-A2.  
PD 27-FEB-2003.  
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
Query Match 7.0%; Score 69.4; DB 10; Length 1024;  
Best Local Similarity 50.4%; Pred. No. 0.0093;  
RESULT 166  
ID ADE84973 standard; cDNA; 1206 BP.  
DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
PN WO2003038129-A2.  
PD 08-MAY-2003.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 7.0%; Score 69.4; DB 10; Length 1206;  
Best Local Similarity 50.4%; Pred. No. 0.0092;  
RESULT 167  
ID ABX63642 standard; cDNA; 1327 BP.  
DE Human cDNA #642 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Query Match 7.0%; Score 69.4; DB 8; Length 1327;  
Best Local Similarity 50.4%; Pred. No. 0.0092;  
RESULT 168  
ID ADH02882 standard; cDNA; 841 BP.  
DE Fuchsia FMT (3282) cDNA #SEQ ID 41.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.2; DB 10; Length 841;  
Best Local Similarity 49.5%; Pred. No. 0.01;  
RESULT 169  
ID ADH02884 standard; cDNA; 943 BP.  
DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 7.0%; Score 69.2; DB 10; Length 943;  
Best Local Similarity 49.5%; Pred. No. 0.01;  
RESULT 170  
ID AAC42096 standard; cDNA; 1186 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.9%; Score 68.6; DB 3; Length 1186;  
Best Local Similarity 46.7%; Pred. No. 0.013;  
RESULT 171  
ID ADH02852 standard; cDNA; 1006 BP.



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DE Torenia TMT5.nt cdna #SEQ ID 11.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 6.8%; Score 67.4; DB 10; Length 1006;  
 Best Local Similarity 50.1%; Pred. No. 0.02;  
 RESULT 172  
 ID ABA90338 standard; cDNA; 1149 BP.  
 DE Human polynucleotide #13.  
 PN WO200181363-A1.  
 PD 01-NOV-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 Query Match 6.8%; Score 67; DB 6; Length 1149;  
 Best Local Similarity 51.5%; Pred. No. 0.023;  
 RESULT 173  
 ID AAV23874 standard; DNA; 1074 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 174  
 ID AAZ06877 standard; cDNA; 1074 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 3.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 175  
 ID RAA67961 standard; DNA; 1074 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 176  
 ID ADD41711 standard; DNA; 1074 BP.  
 DE O-methyl transferase DNA #7.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 177  
 ID AAV23875 standard; DNA; 1075 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 178  
 ID AAZ06878 standard; cDNA; 1075 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 4.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 179  
 ID AAA67962 standard; DNA; 1075 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
 PN WO200022099-A1.

PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 180  
 ID ADD41712 standard; DNA; 1075 BP.  
 DE O-methyl transferase DNA #8.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.025;  
 RESULT 181  
 ID AAX53491 standard; DNA; 114955 BP.  
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
 PN WO9913886-A1.  
 PD 25-MAR-1999.  
 PA (UVEC-) UNIV EAST CAROLINA.  
 Query Match 6.7%; Score 66.6; DB 2; Length 114955;  
 Best Local Similarity 33.8%; Pred. No. 0.024;  
 RESULT 182  
 ID AAD19545 standard; cDNA; 744 BP.  
 DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.  
 PN WO200173090-A2.  
 PD 04-OCT-2001.  
 PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.  
 Query Match 6.7%; Score 66.4; DB 4; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.03;  
 RESULT 183  
 ID ADI30327 standard; cDNA; 744 BP.  
 DE Alfalfa harvest inducible cDNA sequence H12.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.03;  
 RESULT 184  
 ID ADI30333 standard; DNA; 1906 BP.  
 DE Alfalfa harvest inducible H12 gene genomic DNA sequence.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 1906;  
 Best Local Similarity 49.3%; Pred. No. 0.029;  
 RESULT 185  
 ID ABS63420 standard; cDNA; 912 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 6.7%; Score 66.2; DB 6; Length 912;  
 Best Local Similarity 47.9%; Pred. No. 0.032;  
 RESULT 186  
 ID ABS44115 standard; DNA; 967 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Query Match 6.6%; Score 64.8; DB 6; Length 967;  
 Best Local Similarity 49.0%; Pred. No. 0.054;  
 RESULT 187  
 ID ABQ55289 standard; cDNA; 553 BP.  
 DE Human ovarian antigen HCOX38 cDNA, SEQ ID NO:1169.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.5%; Score 64.6; DB 6; Length 553;  
 Best Local Similarity 49.5%; Pred. No. 0.06;  
 RESULT 188



ID AAC11287 standard; cDNA; 143 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 15362.  
PN EPI03401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GNSSET.  
Query Match 6.5%; Score 64.4; DB 3; Length 143;  
Best Local Similarity 98.5%; Pred. No. 0.067;  
RESULT 189  
ID ABS63426 standard; cDNA; 600 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 6.5%; Score 64.2; DB 6; Length 600;  
Best Local Similarity 53.4%; Pred. No. 0.069;  
RESULT 190  
ID ABS63411 standard; cDNA; 510 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 6.4%; Score 63.6; DB 6; Length 510;  
Best Local Similarity 45.9%; Pred. No. 0.088;  
RESULT 191  
ID AD019501 standard; DNA; 135005 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.4%; Score 63; DB 12; Length 135005;  
Best Local Similarity 47.8%; Pred. No. 0.095;  
RESULT 192  
ID ABX09141 standard; DNA; 75216 BP.  
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV230.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP ) INST PASTEUR.  
Query Match 6.3%; Score 62.8; DB 6; Length 75216;  
Best Local Similarity 46.4%; Pred. No. 0.1;  
RESULT 193  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.1;  
RESULT 194  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.1;  
RESULT 195  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.12;  
RESULT 196  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.12;  
RESULT 197  
ID ABS54114 standard; DNA; 845 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 6.2%; Score 61.6; DB 6; Length 845;  
Best Local Similarity 48.5%; Pred. No. 0.19;  
RESULT 198  
ID AAX53491 standard; DNA; 114955 BP.  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
PN WO9913886-A1.  
PD 25-MAR-1999.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 6.2%; Score 61.2; DB 2; Length 114955;  
Best Local Similarity 31.2%; Pred. No. 0.19;  
RESULT 199  
ID AAQ61817 standard; DNA; 1578 BP.

DE Open reading frame of pseudorabies virus.  
PN WO9408000-A1.  
PD 14-APR-1994.  
PA (ALKU ) AKZO NV.  
Query Match 6.1%; Score 60.8; DB 2; Length 1578;  
Best Local Similarity 45.3%; Pred. No. 0.25;  
RESULT 200  
ID ABQ81846 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
PN EPI227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Query Match 6.1%; Score 60.4; DB 6; Length 349980;  
Best Local Similarity 49.0%; Pred. No. 0.25;  
RESULT 201  
ID AB214595 standard; DNA; 729 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.1%; Score 60; DB 6; Length 729;  
Best Local Similarity 48.5%; Pred. No. 0.35;  
RESULT 202  
ID AAC45004 standard; DNA; 917 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 60; DB 3; Length 917;  
Best Local Similarity 48.5%; Pred. No. 0.34;  
RESULT 203  
ID ABS63422 standard; cDNA; 982 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 6.1%; Score 60; DB 6; Length 982;  
Best Local Similarity 48.7%; Pred. No. 0.34;  
RESULT 204  
ID ADH02867 standard; cDNA; 1079 BP.  
DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 6.1%; Score 60; DB 10; Length 1079;  
Best Local Similarity 48.7%; Pred. No. 0.34;  
RESULT 205  
ID ACA38007 standard; DNA; 1143 BP.  
DE Prokaryotic essential gene #19664.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 60; DB 8; Length 1143;  
Best Local Similarity 45.4%; Pred. No. 0.34;  
RESULT 206  
ID AAA68101 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 6.0%; Score 59.6; DB 3; Length 399;  
Best Local Similarity 55.2%; Pred. No. 0.41;  
RESULT 207  
ID ADD41851 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #2.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 6.0%; Score 59.6; DB 10; Length 399;



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Best Local Similarity 55.2%; Pred. No. 0.41;  
RESULT 208  
ID AD123934 standard; DNA; 7185 BP.  
DE Streptomyces refuineus 024A locus ORF7.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 7185;  
Best Local Similarity 46.9%; Pred. No. 0.38;  
RESULT 209  
ID AD123920 standard; DNA; 61944 BP.  
DE Streptomyces refuineus 024A locus (NRRL 3143).  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 61944;  
Best Local Similarity 46.9%; Pred. No. 0.36;  
RESULT 210  
ID ADQ22939 standard; DNA; 4667 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.0%; Score 59.2; DB 12; Length 4667;  
Best Local Similarity 44.6%; Pred. No. 0.45;  
RESULT 211  
ID ADQ22939 standard; DNA; 4667 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.0%; Score 59; DB 6; Length 10800;  
Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 213  
ID ADO10046 standard; cDNA; 10800 BP.  
DE Novel human protein Nov1c cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU/) KEKUDA R.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (GROS/) GROSSE W M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (EDIN/) EDINGER S R.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ROTH/) ROTHENBERG M E.  
PA (STON/) STONE D J.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (ANDE/) ANDERSON D W.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (EISE/) EISEN A.  
Query Match 6.0%; Score 59; DB 6; Length 10800;  
Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 215  
ID ADO10042 standard; cDNA; 10809 BP.  
DE Novel human protein Nov1a cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU/) KEKUDA R.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (GROS/) GROSSE W M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (EDIN/) EDINGER S R.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ROTH/) ROTHENBERG M E.  
PA (STON/) STONE D J.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (ANDE/) ANDERSON D W.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (EISE/) EISEN A.  
Query Match 6.0%; Score 59; DB 12; Length 10809;  
Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 216  
ID ADH02847 standard; cDNA; 1077 BP.  
DE Petunia E33 cDNA #SEQ ID 5.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITEL-) INT FLOWER DEV PTY LTD.  
Query Match 5.9%; Score 58.8; DB 10; Length 1077;  
Best Local Similarity 48.5%; Pred. No. 0.54;  
RESULT 217  
ID AAF25795 standard; DNA; 3849 BP.  
DE S. chrysomallus acm-C DNA.  
PN DE19928313-A1.  
PD 21-DEC-2000.  
PA (KELL/) KELLER U.  
Query Match 5.9%; Score 58.8; DB 4; Length 3849;  
Best Local Similarity 45.9%; Pred. No. 0.52;  
RESULT 218  
ID AAD5726 standard; DNA; 5858 BP.  
DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.9%; Score 58.8; DB 8; Length 5858;  
Best Local Similarity 48.3%; Pred. No. 0.52;  
RESULT 219  
ID ADA71279 standard; DNA; 897 BP.  
DE Rice gene, SEQ ID 4602.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.9%; Score 58; DB 8; Length 897;

Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 214  
ID ABQ93879 standard; DNA; 10809 BP.  
DE Human laminin alpha-5-like NOV1a DNA, SEQ ID NO:1.  
PN WO200253742-A2.  
PD 11-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.0%; Score 59; DB 6; Length 10809;  
Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 215  
ID ADO10042 standard; cDNA; 10809 BP.  
DE Novel human protein Nov1a cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU/) KEKUDA R.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (GROS/) GROSSE W M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (EDIN/) EDINGER S R.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ROTH/) ROTHENBERG M E.  
PA (STON/) STONE D J.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (ANDE/) ANDERSON D W.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (EISE/) EISEN A.  
Query Match 6.0%; Score 59; DB 12; Length 10809;  
Best Local Similarity 46.8%; Pred. No. 0.47;  
RESULT 216  
ID ADH02847 standard; cDNA; 1077 BP.  
DE Petunia E33 cDNA #SEQ ID 5.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITEL-) INT FLOWER DEV PTY LTD.  
Query Match 5.9%; Score 58.8; DB 10; Length 1077;  
Best Local Similarity 48.5%; Pred. No. 0.54;  
RESULT 217  
ID AAF25795 standard; DNA; 3849 BP.  
DE S. chrysomallus acm-C DNA.  
PN DE19928313-A1.  
PD 21-DEC-2000.  
PA (KELL/) KELLER U.  
Query Match 5.9%; Score 58.8; DB 4; Length 3849;  
Best Local Similarity 45.9%; Pred. No. 0.52;  
RESULT 218  
ID AAD5726 standard; DNA; 5858 BP.  
DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.9%; Score 58.8; DB 8; Length 5858;  
Best Local Similarity 48.3%; Pred. No. 0.52;  
RESULT 219  
ID ADA71279 standard; DNA; 897 BP.  
DE Rice gene, SEQ ID 4602.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.9%; Score 58; DB 8; Length 897;



Best Local Similarity 44.9%; Pred. No. 0.74;  
RESULT 220  
ID AAL40781 standard; DNA; 88421 BP.  
DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.  
PN WO200231155-A2.  
PD 18-APR-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.9%; Score 58; DB 6; Length 88421;  
Best Local Similarity 44.5%; Pred. No. 0.65;  
RESULT 221  
ID ABN87109 standard; CDNA; 557 BP.  
DE Lolium perenne LpCCOAMTA partial nucleotide sequence SEQ ID NO:3.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 5.8%; Score 57.8; DB 6; Length 557;  
Best Local Similarity 49.7%; Pred. No. 0.81;  
RESULT 222  
ID AB222145 standard; DNA; 1029 BP.  
DE Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.  
PN JP2002247985-A.  
PD 03-SEP-2002.  
PA (RIKA-) RIKAGAKU KENKYUSHO.  
Query Match 5.8%; Score 57.4; DB 8; Length 1029;  
Best Local Similarity 48.6%; Pred. No. 0.93;  
RESULT 223  
ID ADO42841 standard; DNA; 1275 BP.  
DE Pseudomonas aurantiaca S-4380 levansucrase encoding sequence.  
PN KR2003005996-A.  
PD 23-JAN-2003.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
PA (REAL-) REAL BIOTECH CO LTD.  
Query Match 5.8%; Score 57.4; DB 11; Length 1275;  
Best Local Similarity 45.6%; Pred. No. 0.92;  
RESULT 224  
ID ADA48866 standard; DNA; 584 BP.  
DE Banana gene conferring disease resistance in plants.  
PN WO200300906-A2.  
PD 03-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.8%; Score 57.2; DB 9; Length 584;  
Best Local Similarity 60.1%; Pred. No. 1;  
RESULT 225  
ID ADB74275 standard; DNA; 38494 BP.  
DE Mycobacterium leprae DNA #2.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38494;  
Best Local Similarity 50.9%; Pred. No. 0.98;  
RESULT 226  
ID ADB74386 standard; DNA; 38675 BP.  
DE Mycobacterium leprae DNA #20.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38675;  
Best Local Similarity 50.9%; Pred. No. 0.98;  
RESULT 227  
ID AAD14507 standard; DNA; 1182 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme DNA #3.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 228  
ID ADD26448 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus ORF6 DNA.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 229  
ID ADG47793 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus 15 kb gene ORF6 DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 230  
ID ACA62930 standard; DNA; 1182 BP.  
DE DNA encoding clavulanic acid synthesis associated protein #6.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 231  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.7%; Score 56.8; DB 8; Length 2000;  
Best Local Similarity 10.5%; Pred. No. 1.1;  
RESULT 232  
ID AAD14501 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 233  
ID ADD26442 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 11.6 kb genomic fragment.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 234  
ID ADG47787 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 15 kb gene fragment DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 235  
ID ACA62924 standard; DNA; 11604 BP.  
DE Clavulanic acid synthesis associated DNA.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 236  
ID AAQ91580 standard; DNA; 15079 BP.  
DE S. clavuligerus cla gene region.  
PN CA2108113-A.  
PD 09-APR-1995.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 2; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 237  
ID AAD14499 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15 kb genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 15079;



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Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 238  
ID ACA62922 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15kb genomic DNA sequence.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 239  
ID ADD26455 standard; DNA; 15120 BP.  
DE Streptomyces clavuligerus 15 kb genomic fragment.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 240  
ID ADG47775 standard; DNA; 15120 BP.  
DE Streptomyces clavuligerus 15 kb gene.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 241  
ID AAX83426 standard; DNA; 22976 BP.  
DE Genomic region containing human lipolysis stimulated receptor gene.  
PN WO9907737-A2.  
PD 18-FEB-1999.  
PA (GSET) GENSET.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 5.7%; Score 56.8; DB 2; Length 22976;  
Best Local Similarity 45.6%; Pred. No. 1.1;  
RESULT 242  
ID AAD36874 standard; DNA; 29870 BP.  
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 8; Length 29870;  
Best Local Similarity 43.6%; Pred. No. 1.1;  
RESULT 243  
ID ABL67924 standard; DNA; 41936 BP.  
DE Ovary cancer related gene sequence SEQ ID NO:6261.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AYAL-) AYALON PHARM.  
Query Match 5.7%; Score 56.8; DB 6; Length 41936;  
Best Local Similarity 45.6%; Pred. No. 1.1;  
RESULT 244  
ID ADA71360 standard; DNA; 2450 BP.  
DE Rice gene, SEQ ID 4683.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.7%; Score 56.6; DB 8; Length 2450;  
Best Local Similarity 43.1%; Pred. No. 1.2;  
RESULT 245  
ID ADJ11693 standard; DNA; 3414 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 329.  
PN US200313588-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
Query Match 5.7%; Score 56.6; DB 11; Length 3414;  
Best Local Similarity 43.1%; Pred. No. 1.2;  
RESULT 246  
ID AAD54235 standard; DNA; 25085 BP.  
DE Streptomyces amphibiosporus lactimidomycin ORF5 DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.7%; Score 56.6; DB 10; Length 25085;  
Best Local Similarity 45.1%; Pred. No. 1.2;  
RESULT 247  
ID AAD54230 standard; DNA; 50543 BP.  
DE Streptomyces amphibiosporus lactimidomycin DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.7%; Score 56.6; DB 10; Length 50543;  
Best Local Similarity 45.1%; Pred. No. 1.1;  
RESULT 248  
ID AAA09686 standard; DNA; 3957 BP.  
DE HSV-2 immediate early protein ICP4 DNA sequence.  
PN WO9516779-A1.  
PD 22-JUN-1995.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 5.7%; Score 56.4; DB 5; Length 3957;  
Best Local Similarity 49.8%; Pred. No. 1.3;  
RESULT 249  
ID ADG75121 standard; DNA; 3957 BP.  
DE Human herpesvirus 2 ICP4 ORF DNA - SEQ ID 193.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56.4; DB 10; Length 3957;  
Best Local Similarity 49.8%; Pred. No. 1.3;  
RESULT 250  
ID ADI23932 standard; DNA; 15738 BP.  
DE Streptomyces refuineus 024A locus ORF6.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.7%; Score 56.4; DB 10; Length 15738;  
Best Local Similarity 51.7%; Pred. No. 1.3;  
RESULT 251  
ID AAD25519 standard; DNA; 154746 BP.  
DE Human herpesvirus 2 complete DNA genome.  
PN WO200176643-A1.  
PD 18-OCT-2001.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
Best Local Similarity 49.8%; Pred. No. 1.2;  
RESULT 252  
ID AAD25519 standard; DNA; 154746 BP.  
DE Human herpesvirus 2 complete DNA genome.  
PN WO200176643-A1.  
PD 18-OCT-2001.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
Best Local Similarity 49.8%; Pred. No. 1.2;  
RESULT 253  
ID ABZ66780 standard; DNA; 1143 BP.  
DE Orthomycin biosynthetic polynucleotide SEQ ID NO 222.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.7%; Score 56.2; DB 10; Length 1143;  
Best Local Similarity 45.6%; Pred. No. 1.5;  
RESULT 254  
ID AAQ98470 standard; cDNA; 2744 BP.  
DE MISP1-containing plasmid pMiss1.  
PN WO9525165-A1.



PD 21-SEP-1995.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.7%; Score 56.2; DB 2; Length 2744;  
Best Local Similarity 48.0%; Pred. No. 1.4;  
RESULT 255  
ID ABL50559 standard; DNA; 14186 BP.  
DE Micromonospora carbonacea evernimycin locus nucleotide contig 5.  
PN WO200155180-A2.  
PD 02-AUG-2001.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
PA (FARN/) FARNET C.  
Query Match 5.7%; Score 56.2; DB 4; Length 14186;  
Best Local Similarity 45.6%; Pred. No. 1.4;  
RESULT 256  
ID AB266811 standard; DNA; 48221 BP.  
DE Orthosmycin biosynthetic gene cluster SEQ ID NO 280.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.7%; Score 56.2; DB 10; Length 48221;  
Best Local Similarity 45.6%; Pred. No. 1.3;  
RESULT 257  
ID ACH44935 standard; cDNA; 494 BP.  
DE Human foetal brain cDNA #5660.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 5.7%; Score 56; DB 9; Length 494;  
Best Local Similarity 51.2%; Pred. No. 1.6;  
RESULT 258  
ID ABD15803 standard; DNA; 1098 BP.  
DE Pseudomonas aeruginosa polynucleotide #14407.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 56; DB 11; Length 1098;  
Best Local Similarity 49.7%; Pred. No. 1.6;  
RESULT 259  
ID ACA42208 standard; DNA; 1473 BP.  
DE Prokaryotic essential gene #23865.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.7%; Score 56; DB 8; Length 1473;  
Best Local Similarity 49.7%; Pred. No. 1.6;  
RESULT 260  
ID ABD15660 standard; DNA; 1566 BP.  
DE Pseudomonas aeruginosa polynucleotide #14264.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 56; DB 11; Length 1566;  
Best Local Similarity 49.7%; Pred. No. 1.6;  
RESULT 261  
ID ABD15749 standard; DNA; 1908 BP.  
DE Pseudomonas aeruginosa polynucleotide #14353.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 56; DB 11; Length 1908;  
Best Local Similarity 49.7%; Pred. No. 1.6;  
RESULT 262  
ID AA207194 standard; cDNA; 2109 BP.  
DE Human lung tumour protein SAL-50 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56; DB 2; Length 2109;  
Best Local Similarity 49.3%; Pred. No. 1.6;

RESULT 263  
ID AAC79147 standard; cDNA; 2109 BP.  
DE Human lung tumour-specific cDNA #100.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56; DB 3; Length 2109;  
Best Local Similarity 49.3%; Pred. No. 1.6;  
RESULT 264  
ID AAD23222 standard; cDNA; 2109 BP.  
DE Human lung tumour-specific protein SAL-50 cDNA.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56; DB 4; Length 2109;  
Best Local Similarity 49.3%; Pred. No. 1.6;  
RESULT 265  
ID AD066461 standard; cDNA; 2109 BP.  
DE Human lung tumour-specific related cDNA, SEQ ID NO 153.  
PN WO200292001-A2.  
PD 21-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56; DB 10; Length 2109;  
Best Local Similarity 49.3%; Pred. No. 1.6;  
RESULT 266  
ID ADE87715 standard; cDNA; 2109 BP.  
DE Human lung tumour antigen cDNA #100.  
PN US2003118599-A1.  
PD 26-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.7%; Score 56; DB 10; Length 2109;  
Best Local Similarity 49.3%; Pred. No. 1.6;  
RESULT 267  
ID AAH15254 standard; cDNA; 2142 BP.  
DE Human cDNA sequence SEQ ID NO:11376.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.7%; Score 56; DB 4; Length 2142;  
Best Local Similarity 51.2%; Pred. No. 1.6;  
RESULT 268  
ID AAH14344 standard; cDNA; 2198 BP.  
DE Human cDNA sequence SEQ ID NO:11730.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.7%; Score 56; DB 4; Length 2198;  
Best Local Similarity 51.2%; Pred. No. 1.6;  
RESULT 269  
ID AAX61221 standard; DNA; 2392 BP.  
DE Mouse DNA demethylase, dmtase2, coding sequence.  
PN WO9924583-A1.  
PD 20-MAY-1999.  
PA (UYWC-) UNIV MCGILL.  
Query Match 5.7%; Score 56; DB 2; Length 2392;  
Best Local Similarity 51.2%; Pred. No. 1.6;  
RESULT 270  
ID ADD14651 standard; cDNA; 2392 BP.  
DE Human src biomarker polynucleotide SEQ ID NO:45.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.7%; Score 56; DB 10; Length 2392;  
Best Local Similarity 51.2%; Pred. No. 1.6;  
RESULT 271  
ID AAV68520 standard; DNA; 4257 BP.  
DE The nucleotide sequence of the Herpes simplex virus ICP4.  
PN WO9846637-A2.  
PD 22-OCT-1998.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 5.7%; Score 56; DB 2; Length 4257;  
Best Local Similarity 45.6%; Pred. No. 1.5;  
RESULT 272



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DE Gene #3953 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC. 5.7%; Score 56; DB 6; Length 43058;  
Query Match  
Best Local Similarity 45.5%; Pred. No. 1.4;  
RESULT 282  
ID ADH02862 standard; cDNA; 780 BP.  
DE Fuchsia FMT CDNA #SEQ ID 21.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD. 5.6%; Score 55.8; DB 10; Length 780;  
Query Match  
Best Local Similarity 49.1%; Pred. No. 1.7;  
RESULT 283  
ID ADA70053 standard; DNA; 1152 BP.  
DE Rice gene, SEQ ID 3376.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG. 5.6%; Score 55.8; DB 8; Length 1152;  
Query Match  
Best Local Similarity 45.5%; Pred. No. 1.7;  
RESULT 284  
ID ADJ11565 standard; DNA; 1152 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing seqID 201.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T. 5.6%; Score 55.8; DB 8; Length 1152;  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KEEPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICE D. 5.6%; Score 55.8; DB 11; Length 1152;  
Query Match  
Best Local Similarity 45.5%; Pred. No. 1.7;  
RESULT 285  
ID AAS0254 standard; DNA; 1926 BP.  
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.  
PN WO200047778-A1.  
PD 17-AUG-2000.  
PA (PHAR-) PHARMACOEPIA INC. 5.6%; Score 55.8; DB 3; Length 1926;  
Query Match  
Best Local Similarity 46.7%; Pred. No. 1.7;  
RESULT 286  
ID AAF82902 standard; DNA; 1926 BP.  
DE EBV tethering protein EBNA1 encoding DNA.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN. 5.6%; Score 55.8; DB 4; Length 1926;  
Query Match  
Best Local Similarity 46.7%; Pred. No. 1.7;  
RESULT 287  
ID ADK65580 standard; DNA; 1926 BP.  
DE Human herpesvirus 4 nuclear antigen-1 coding sequence.  
PN DE10207135-A1.  
PD 11-SEP-2003.  
PA (EURO-) EUROIMMUN GMBH. 5.6%; Score 55.8; DB 10; Length 1926;  
Query Match  
Best Local Similarity 46.7%; Pred. No. 1.7;  
RESULT 288  
ID AAA75454 standard; DNA; 2580 BP.  
DE Nucleotide sequence of the Epstein Barr nuclear antigen.  
PN US6114111-A.  
PD 05-SEP-2000.  
PA (RIGE-) RIGEL PHARM INC. 5.6%; Score 55.8; DB 3; Length 2580;  
Query Match  
Best Local Similarity 46.7%; Pred. No. 1.7;

ID AAV10362 standard; cDNA; 4257 BP.  
DE Infected cell protein number 4 alpha-4 gene.  
PN WO9804709-A2.  
PD 05-FEB-1998.  
PA (ARCH-) ARCH DEV CORP. 5.7%; Score 56; DB 2; Length 4257;  
Query Match  
Best Local Similarity 45.6%; Pred. No. 1.5;  
RESULT 273  
ID ADCS9464 standard; DNA; 4943 BP.  
DE DNA sequence encoding novel human tyrosine kinase protein.  
PN JP2003024075-A.  
PD 28-JAN-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO. 5.7%; Score 56; DB 10; Length 4943;  
Query Match  
Best Local Similarity 49.3%; Pred. No. 1.5;  
RESULT 274  
ID AAD34321 standard; cDNA; 4988 BP.  
DE Human PKIN-24 CDNA.  
PN WO200218557-A2.  
PD 07-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC. 5.7%; Score 56; DB 6; Length 4988;  
Query Match  
Best Local Similarity 49.3%; Pred. No. 1.5;  
RESULT 275  
ID AAQ76213 standard; DNA; 12001 BP.  
DE HSV L/ST region.  
PN WO9428156-A1.  
PD 08-DEC-1994.  
PA (DAND) DANA FARBER CANCER INST INC. 5.7%; Score 56; DB 2; Length 12001;  
Query Match  
Best Local Similarity 45.6%; Pred. No. 1.5;  
RESULT 276  
ID AAL02789 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5477.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. 5.7%; Score 56; DB 4; Length 13862;  
Query Match  
Best Local Similarity 49.3%; Pred. No. 1.5;  
RESULT 277  
ID AAL07516 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 10204.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. 5.7%; Score 56; DB 4; Length 13862;  
Query Match  
Best Local Similarity 49.3%; Pred. No. 1.5;  
RESULT 278  
ID ABA08208 standard; DNA; 13862 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. 5.7%; Score 56; DB 4; Length 13862;  
Query Match  
Best Local Similarity 49.3%; Pred. No. 1.5;  
RESULT 279  
ID ABL64982 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3319.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM. 5.7%; Score 56; DB 6; Length 43058;  
Query Match  
Best Local Similarity 45.5%; Pred. No. 1.4;  
RESULT 280  
ID ABL65219 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3556.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM. 5.7%; Score 56; DB 6; Length 43058;  
Query Match  
Best Local Similarity 45.5%; Pred. No. 1.4;  
RESULT 281  
ID ABN97455 standard; DNA; 43058 BP.



RESULT 289  
ID AAI64275 standard; DNA; 2580 BP.  
DE Epstein-Barr virus nuclear antigen coding sequence.  
PN US6316223-B1.  
PD 13-NOV-2001.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 5.6%; Score 55.8; DB 6; Length 2580;  
Best Local Similarity 46.7%; Pred. No. 1.7;  
RESULT 290  
ID AAX90923 standard; DNA; 5452 BP.  
DE Anti-sense strand of pCMVEBNA plasmid.  
PN WO9947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 5452;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 291  
ID AA233778 standard; DNA; 8705 BP.  
DE Vector pShuttle DNA.  
PN WO9950457-A1.  
PD 07-OCT-1999.  
PA (UTAH) UNIV UTAH RES FOUND.  
Query Match 5.6%; Score 55.8; DB 2; Length 8705;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 292  
ID ADM10659 standard; DNA; 8705 BP.  
DE Expression vector pShuttle.  
PN US2004077082-A1.  
PD 22-APR-2004.  
PA (KORH/) KOHN R K.  
PA (RUFF/) RUFFNER D E.  
PA (PRAK/) PRAKASH R K.  
Query Match 5.6%; Score 55.8; DB 12; Length 8705;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 293  
ID ADP64415 standard; DNA; 9482 BP.  
DE Vector pCEFPu nucleotide sequence SEQ ID NO:1.  
PN WO2004053137-A2.  
PD 24-JUN-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 9482;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 294  
ID AA222301 standard; cDNA; 9551 BP.  
DE cDNA encoding a human trichohyalin (TRHY) protein.  
PN US5958752-A.  
PD 28-SEP-1999.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.6%; Score 55.8; DB 2; Length 9551;  
Best Local Similarity 49.9%; Pred. No. 1.6;  
RESULT 295  
ID AAV21683 standard; DNA; 9600 BP.  
DE Vector plasmid pCMVkmITR-EPI.  
PN WO9806437-A2.  
PD 19-FEB-1998.  
PA (CHIR) CHIRON CORP.  
Query Match 5.6%; Score 55.8; DB 2; Length 9600;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 296  
ID ABS71027 standard; DNA; 10285 BP.  
DE pCEP-Xa-Fc construct DNA sequence.  
PN WO200256905-A2.  
PD 25-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 297  
ID ABS66453 standard; DNA; 10285 BP.  
DE Plasmid pCEP-Xa-Fc\* expressing human IgG/protease cleavage site.  
PN WO200256907-A2.  
PD 25-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.  
PA (LECH/) LECHNER F.  
PA (ORTM/) ORTMANN R.  
PA (LUEO/) LUEOEND R.  
PA (STAU/) STAUPENBIEL M.  
PA (FREY/) FREY P.  
Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 298  
ID ADL67154 standard; DNA; 10330 BP.  
DE Plasmid pCEP-mB7-H6(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:24.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10330;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 299  
ID AA222248 standard; DNA; 10380 BP.  
DE Nucleotide sequence of pCEP4 vector.  
PN WO9947921-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10380;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 300  
ID ADL67152 standard; DNA; 10477 BP.  
DE Plasmid pCEP-mB7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:22.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10477;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 301  
ID ADL67150 standard; DNA; 10516 BP.  
DE Plasmid pCEP-hsb7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:20.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10516;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 302  
ID ADL67148 standard; DNA; 10561 BP.  
DE Plasmid pCEP-hsb7-H4(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:18.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10561;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 303  
ID AAQ51731 standard; DNA; 10596 BP.  
DE Plasmid pCisEBON for subcloning huHGF variants.  
PN WO9323541-A1.  
PD 25-NOV-1993.  
PA (GETH) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 304  
ID AAX15650 standard; DNA; 10596 BP.  
DE Nucleotide sequence of plasmid pCIS.EBON.  
PN US879910-A.  
PD 09-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 305  
ID AA40348 standard; DNA; 10596 BP.  
DE Plasmid pCisEBON for expression of hepatocyte growth factor.  
PN US5547856-A.  
PD 20-AUG-1996.  
PA (GETH) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.6;  
RESULT 306



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ADL67175 standard; DNA; 10615 BP.  
 ID Plasmid pCEP-hsB7-H6-COMP-FLAG nucleotide sequence SEQ ID NO:45.  
 DE WO2004022594-A2.  
 PN PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10615;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 307  
 ID ADL67153 standard; DNA; 10774 BP.  
 DE Plasmid pCEP-mB7-H6(ECD)-FC nucleotide sequence SEQ ID NO:23.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10774;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 308  
 ID ADL67151 standard; DNA; 10921 BP.  
 DE Plasmid pCEP-mB7-H5(ECD)-FC nucleotide sequence SEQ ID NO:21.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10921;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 309  
 ID ADL67149 standard; DNA; 10961 BP.  
 DE Plasmid pCEP-hsB7-H5(ECD)-FC nucleotide sequence SEQ ID NO:19.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10961;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 310  
 ID ADL67147 standard; DNA; 11006 BP.  
 DE Plasmid pCEP-hsB7-H4(ECD)-FC nucleotide sequence SEQ ID NO:17.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11006;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 311  
 ID ADL67176 standard; DNA; 11059 BP.  
 DE Plasmid pCEP-hsB7-H6-Xa1-FC\* nucleotide sequence SEQ ID NO:46.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11059;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 312  
 ID AD007395 standard; DNA; 11924 BP.  
 DE Modified human hepsin plasmid pCEP4W/hep36.  
 PN WO2004033630-A2.  
 PD 22-APR-2004.  
 PA (SCHD) SCHERING AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 11924;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 313  
 ID AD007394 standard; DNA; 12242 BP.  
 DE Modified human hepsin plasmid pCEP4W/hepEK.  
 PN WO2004033630-A2.  
 PD 22-APR-2004.  
 PA (SCHD) SCHERING AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 12242;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 314  
 ID AAA59553 standard; DNA; 16080 BP.  
 DE DNA clone pCEK Cl.127 encoding a human beta-secretase enzyme.  
 PN WO200047618-A2.  
 PD 17-AUG-2000.  
 PA (ELAN-) ELAN PHARM INC.  
 Query Match 5.6%; Score 55.8; DB 3; Length 16080;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 315  
 ID ADL71910 standard; cDNA; 17753 BP.  
 DE Expression vector pCytts-OPE.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 17753;  
 Best Local Similarity 46.7%; Pred. No. 1.6;  
 RESULT 316  
 ID ADN12161 standard; DNA; 172281 BP.  
 DE Epstein-Barr virus genome B95-8.  
 PN WO2004027036-A2.  
 PD 01-APR-2004.  
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 Query Match 5.6%; Score 55.8; DB 12; Length 172281;  
 Best Local Similarity 46.7%; Pred. No. 1.5;  
 RESULT 317  
 ID AAH03407 standard; cDNA; 726 BP.  
 DE Human cDNA clone (5'-primer) SEQ ID NO:242.  
 PN EPI074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.6%; Score 55.6; DB 4; Length 726;  
 Best Local Similarity 53.5%; Pred. No. 1.9;  
 RESULT 318  
 ID AAL61200 standard; DNA; 1026 BP.  
 DE Actinosynnema pretiosum glucose 1-dehydrogenase gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 5.6%; Score 55.6; DB 8; Length 1026;  
 Best Local Similarity 46.2%; Pred. No. 1.9;  
 RESULT 319  
 ID ABD11061 standard; DNA; 774 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9665.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.6%; Score 55.4; DB 11; Length 774;  
 Best Local Similarity 45.2%; Pred. No. 2;  
 RESULT 320  
 ID ABX56066 standard; DNA; 3033 BP.  
 DE M. echinospora calicheamicin biosynthesis gene orfVI.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.6%; Score 55.4; DB 8; Length 3033;  
 Best Local Similarity 44.4%; Pred. No. 1.9;  
 RESULT 321  
 ID AAQ46806 standard; DNA; 29879 BP.  
 DE eryA region of S. erythraea chromosome.  
 PN WO9313663-A1.  
 PD 22-JUL-1993.  
 PA (ABBO) ABBOTT LAB.  
 Query Match 5.6%; Score 55.4; DB 2; Length 29879;  
 Best Local Similarity 49.3%; Pred. No. 1.8;  
 RESULT 322  
 ID ADM45913 standard; DNA; 84428 BP.  
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
 PN JP2004049100-A.  
 PD 19-FEB-2004.  
 PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
 Query Match 5.6%; Score 55.4; DB 12; Length 84428;  
 Best Local Similarity 48.3%; Pred. No. 1.8;  
 RESULT 323  
 ID ABZ78139 standard; cDNA; 1679 BP.  
 DE Human cancer-related coding sequence, 187p3f2.  
 PN WO200283921-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Query Match 5.6%; Score 55.2; DB 8; Length 1679;  
 Best Local Similarity 46.9%; Pred. No. 2.1;  
 RESULT 324  
 ID ACC00700 standard; cDNA; 1885 BP.  
 DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:149.



PN WO2003002751-A2.  
 PD 09-JAN-2003.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.6%; Score 55.2; DB 8; Length 1885;  
 Best Local Similarity 47.8%; Pred. No. 2.1;  
 RESULT 325  
 ID ACA38134 standard; DNA; 1887 BP.  
 DE Prokaryotic essential gene #19791.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.6%; Score 55.2; DB 8; Length 1887;  
 Best Local Similarity 45.0%; Pred. No. 2.1;  
 RESULT 326  
 ID AAAG3350 standard; DNA; 21185 BP.  
 DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.  
 PN WO200040596-A1.  
 PD 13-JUL-2000.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 5.6%; Score 55.2; DB 3; Length 21185;  
 Best Local Similarity 50.3%; Pred. No. 2;  
 RESULT 327  
 ID AAAG3348 standard; DNA; 63164 BP.  
 DE Streptomyces globisporus C-1027 gene cluster.  
 PN WO200040596-A1.  
 PD 13-JUL-2000.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 5.6%; Score 55.2; DB 3; Length 63164;  
 Best Local Similarity 50.3%; Pred. No. 1.9;  
 RESULT 328  
 ID ADK1938 standard; DNA; 2559 BP.  
 DE Human methyl-CpG-binding protein DNA #11.  
 PN US6709817-B1.  
 PD 23-MAR-2004.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Query Match 5.6%; Score 55; DB 12; Length 2559;  
 Best Local Similarity 53.5%; Pred. No. 2.3;  
 RESULT 329  
 ID ADQ19517 standard; DNA; 2559 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2336.  
 PN WO20004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 5.6%; Score 55; DB 12; Length 2559;  
 Best Local Similarity 53.5%; Pred. No. 2.3;  
 RESULT 330  
 ID ADM80034 standard; DNA; 30943 BP.  
 DE Spiramycin biosynthesis related DNA, SEQ ID 1.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Query Match 5.6%; Score 55; DB 12; Length 30943;  
 Best Local Similarity 44.9%; Pred. No. 2.1;  
 RESULT 331  
 ID ADN97550 standard; DNA; 30943 BP.  
 DE S ambotfaciens spiramycin biosynthetic enzyme genomic region.  
 PN WO20004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 PA (CNRS) CNRS.  
 Query Match 5.6%; Score 55; DB 12; Length 30943;  
 Best Local Similarity 44.9%; Pred. No. 2.1;  
 RESULT 332  
 ID AA21187 standard; DNA; 53789 BP.  
 DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
 PN WO9807868-A1.  
 PD 26-FEB-1998.  
 PA (NOVS) NOVARTIS AG.  
 Query Match 5.6%; Score 55; DB 2; Length 53789;  
 Best Local Similarity 47.9%; Pred. No. 2.1;  
 RESULT 333  
 ID AAA68012 standard; DNA; 594 BP.  
 DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 5.5%; Score 54.8; DB 3; Length 594;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 334  
 ID ADD41762 standard; DNA; 594 BP.  
 DE O-methyl transferase DNA #11.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 5.5%; Score 54.8; DB 10; Length 594;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 335  
 ID AAV23843 standard; DNA; 607 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 5.5%; Score 54.8; DB 2; Length 607;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 336  
 ID AA206844 standard; cDNA; 607 BP.  
 DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.  
 PN US9592486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 5.5%; Score 54.8; DB 2; Length 607;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 337  
 ID AA69594 standard; cDNA; 607 BP.  
 DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 5.5%; Score 54.8; DB 3; Length 607;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 338  
 ID AA67930 standard; DNA; 607 BP.  
 DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 5.5%; Score 54.8; DB 3; Length 607;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 339  
 ID ADD41680 standard; DNA; 607 BP.  
 DE O-methyl transferase DNA #3.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 5.5%; Score 54.8; DB 10; Length 607;  
 Best Local Similarity 57.6%; Pred. No. 2.6;  
 RESULT 340  
 ID AB277318 standard; cDNA; 2684 BP.  
 DE Nucleotide sequence of a murine ADC33 polypeptide.  
 PN WO20003008557-A2.  
 PD 30-JAN-2003.  
 PA (UYFL) UNIV FLORIDA.  
 Query Match 5.5%; Score 54.8; DB 8; Length 2684;  
 Best Local Similarity 50.6%; Pred. No. 2.5;  
 RESULT 341  
 ID ADA69536 standard; DNA; 980 BP.  
 DE Rice gene, SEQ ID 2859.



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PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 54.6; DB 8; Length 980;
Best Local Similarity 48.5%; Pred. No. 2.7;
RESULT 342
ID AAV19115 standard; DNA; 1308 BP.
DE Human secreted apoptosis-related protein hSARP2 DNA.
PN WO9813493-A2.
PD 02-APR-1998.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match 5.5%; Score 54.6; DB 2; Length 1308;
Best Local Similarity 45.5%; Pred. No. 2.7;
RESULT 343
ID ADF11997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET ) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 39949;
Best Local Similarity 45.6%; Pred. No. 2.9;
RESULT 344
ID ADF11998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET ) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 48200;
Best Local Similarity 45.6%; Pred. No. 2.9;
RESULT 345
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (EJAE/) EJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 65140;
Best Local Similarity 51.9%; Pred. No. 2.8;
RESULT 346
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 125401;
Best Local Similarity 51.9%; Pred. No. 2.8;
RESULT 347
ID ACA23654 standard; DNA; 897 BP.
DE Prokaryotic essential gene #5311.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 54; DB 8; Length 897;
Best Local Similarity 44.4%; Pred. No. 3.4;
RESULT 348
ID ACC00684 standard; cDNA; 1118 BP.
DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:117.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.5%; Score 54; DB 8; Length 1118;
Best Local Similarity 46.2%; Pred. No. 3.4;
RESULT 349
ID ADC23596 standard; cDNA; 1118 BP.
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 101).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.5%; Score 54; DB 10; Length 1118;
Best Local Similarity 46.2%; Pred. No. 3.4;
RESULT 350
ID ABK12029 standard; DNA; 1217 BP.
DE DNA encoding aminoglycoside multidrug resistance protein.
PN KX99074514-A.
PD 05-OCT-1999.
PA (DONG-) DONGWHA PHARM IND CO LTD.
PA (SUHJ/) SUH J W.
Query Match 5.5%; Score 54; DB 3; Length 1217;
Best Local Similarity 46.3%; Pred. No. 3.4;
RESULT 351
ID AAV67187 standard; DNA; 1380 BP.
DE M. luteus salt-resistant glutaminase encoding DNA.
PN JPI0243787-A.
PD 14-SEP-1998.
PA (FUND-) FUNDOKIN SHOYU KK.
Query Match 5.5%; Score 54; DB 2; Length 1380;
Best Local Similarity 47.1%; Pred. No. 3.4;
RESULT 352
ID AAS85408 standard; cDNA; 4056 BP.
DE DNA encoding novel human diagnostic protein #21212.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 54; DB 5; Length 4056;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 353
ID ABZ11999 standard; cDNA; 4530 BP.
DE Human polynucleotide SEQ ID NO 881.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 54; DB 6; Length 4530;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 354
ID ADM44517 standard; cDNA; 4530 BP.
DE Novel human arginine-rich protein cDNA #881.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 5.5%; Score 54; DB 12; Length 4530;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 355
ID AAA31496 standard; DNA; 451 BP.
DE Plant microsatellite marker #457.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 5.4%; Score 53.8; DB 3; Length 451;
Best Local Similarity 57.1%; Pred. No. 3.8;
RESULT 356
ID ADM80038 standard; DNA; 1272 BP.
DE Spiramycin biosynthesis orf2*c, SEQ ID 5.
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PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
Best Local Similarity 48.0%; Pred. No. 3.7;  
RESULT 357  
ID ADN97554 standard; DNA; 1272 BP.  
DE S ambofaciens spiramycin biosynthetic gene ORF2\*c.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
Best Local Similarity 48.0%; Pred. No. 3.7;  
RESULT 358  
ID ABA95453 standard; DNA; 2082 BP.  
DE Thermus thermophilus uvrD coding sequence.  
PN WO200173052-A2.  
PD 04-OCT-2001.  
PA (MCHE/) MCHENRY C S.  
Query Match 5.4%; Score 53.8; DB 4; Length 2082;  
Best Local Similarity 48.1%; Pred. No. 3.6;  
RESULT 359  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
Best Local Similarity 48.0%; Pred. No. 3.5;  
RESULT 360  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
Best Local Similarity 48.0%; Pred. No. 3.5;  
RESULT 361  
ID AAR80414 standard; DNA; 44377 BP.  
DE Platenolide synthase gene cluster.  
PN EP791655-A2.  
PD 27-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
Best Local Similarity 48.0%; Pred. No. 3.3;  
RESULT 362  
ID AAT78508 standard; DNA; 44377 BP.  
DE Platenolide synthase gene cluster.  
PN EP791656-A2.  
PD 27-AUG-1997.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
Best Local Similarity 48.0%; Pred. No. 3.3;  
RESULT 363  
ID ADK16023 standard; DNA; 64492 BP.  
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
PN US2004053274-A1.  
PD 18-MAR-2004.  
PA (TOKD ) TOKYO INST TECHNOLOGY.  
Query Match 5.4%; Score 53.8; DB 12; Length 64492;  
Best Local Similarity 50.6%; Pred. No. 3.3;  
RESULT 364  
ID AAD08215 standard; DNA; 114793 BP.  
DE Human genome from BAC clone, hbml68.  
PN WO200142434-A1.  
PD 14-JUN-2001.  
PA (MERI ) MERCK & CO INC.  
Query Match 5.4%; Score 53.8; DB 4; Length 114793;  
Best Local Similarity 47.2%; Pred. No. 3.2;

RESULT 365  
ID AAZ32020 standard; DNA; 38734 BP.  
DE Human METH1 related EST AL021529.  
PN WO9937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
Query Match 5.4%; Score 53.6; DB 2; Length 38734;  
Best Local Similarity 44.9%; Pred. No. 3.6;  
RESULT 366  
ID AACS0077 standard; DNA; 38734 BP.  
DE AL021529 cDNA clone.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Query Match 5.4%; Score 53.6; DB 5; Length 38734;  
Best Local Similarity 44.9%; Pred. No. 3.6;  
RESULT 367  
ID AAL61221 standard; DNA; 1554 BP.  
DE Actinosynnema pretiosum transcriptional activator gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 5.4%; Score 53.4; DB 8; Length 1554;  
Best Local Similarity 48.5%; Pred. No. 4.3;  
RESULT 368  
ID AAZ50651 standard; cDNA; 2248 BP.  
DE Corn starch synthase SSB DNA fragment inserted in pSPB47.  
PN WO200006755-A2.  
PD 10-FEB-2000.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 5.4%; Score 53.4; DB 3; Length 2248;  
Best Local Similarity 50.2%; Pred. No. 4.2;  
RESULT 369  
ID AAQ14183 standard; cDNA; 2338 BP.  
DE N-clavipes dragline silk protein coding sequence.  
PN EP452925-A.  
PD 23-OCT-1991.  
PA (UYWY-) UNIV OF WYOMING.  
Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.2;  
RESULT 370  
ID AAV23249 standard; cDNA; 2338 BP.  
DE Nephila clavipes spider silk protein encoding cDNA.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.2;  
RESULT 371  
ID AAZ38195 standard; cDNA; 2338 BP.  
DE N. clavipes spider silk protein 1 encoding cDNA.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 5.4%; Score 53.4; DB 3; Length 2338;  
Best Local Similarity 45.5%; Pred. No. 4.2;  
RESULT 372  
ID AA157831 standard; cDNA; 4176 BP.  
DE Human polynucleotide SEQ ID NO 34.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.



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Query Match      5.4%; Score 53.4; DB 4; Length 4176;
Best Local Similarity 48.9%; Pred. No. 4.1;
RESULT 373
ID AAT61225 standard; DNA; 11905 BP.
DE Actinosynnema pretiosum anamitocin biosynthetic gene cluster II.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW ) UNIV WASHINGTON.
Query Match      5.4%; Score 53.4; DB 8; Length 11905;
Best Local Similarity 48.5%; Pred. No. 4;
RESULT 374
Query Match      5.4%; Score 53.4; DB 11; Length 110000;
Best Local Similarity 45.7%; Pred. No. 5.8;
RESULT 375
ID ACA26842 standard; DNA; 900 BP.
DE Prokaryotic essential gene #8499.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      5.4%; Score 53.2; DB 8; Length 900;
Best Local Similarity 49.6%; Pred. No. 4.7;
RESULT 376
ID ABX34289 standard; DNA; 135638 BP.
DE S. atroolivaceus leinamycin biosynthesis gene cluster.
PN WO200277179-A2.
PD 03-OCT-2002.
PA (REGC ) UNIV CALIFORNIA.
PA (KYOW ) KYOWA HAKKO KOGYO KK.
Query Match      5.4%; Score 53.2; DB 10; Length 135638;
Best Local Similarity 47.9%; Pred. No. 4.1;
RESULT 377
ID ADJ27274 standard; cDNA; 1929 BP.
DE Mouse HSP70.1 coding sequence.
PN WO2003061684-A2.
PD 31-JUL-2003.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match      5.4%; Score 53; DB 11; Length 1929;
Best Local Similarity 44.3%; Pred. No. 4.9;
RESULT 378
ID AAT45060 standard; cDNA; 1236 BP.
DE Maize T22 cDNA nucleotide sequence.
PN WO9505732-A1.
PD 02-MAR-1995.
PA (UYIA ) UNIV YALE.
Query Match      5.3%; Score 52.8; DB 2; Length 1236;
Best Local Similarity 47.3%; Pred. No. 5.4;
RESULT 379
ID ACA38386 standard; DNA; 2712 BP.
DE Prokaryotic essential gene #20043.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      5.3%; Score 52.8; DB 8; Length 2712;
Best Local Similarity 46.8%; Pred. No. 5.3;
RESULT 380
ID ACA40526 standard; DNA; 2715 BP.
DE Prokaryotic essential gene #22183.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      5.3%; Score 52.8; DB 8; Length 2715;
Best Local Similarity 46.8%; Pred. No. 5.3;
RESULT 381
ID ADP90617 standard; DNA; 34719 BP.
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.
PN JP2004180638-A.
PD 02-JUL-2004.
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.
Query Match      5.3%; Score 52.8; DB 12; Length 34719;
Best Local Similarity 50.4%; Pred. No. 4.9;
RESULT 382
Query Match      5.3%; Score 52.8; DB 4; Length 110000;
Best Local Similarity 46.8%; Pred. No. 4.8;
RESULT 383
Query Match      5.3%; Score 52.8; DB 4; Length 110000;
Best Local Similarity 46.8%; Pred. No. 4.8;
RESULT 384
ID ADJ39074 standard; cDNA; 447 BP.
DE Plant cDNA #74.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW ) BUDWORTH P.
PA (MOUG ) MOUGHAMER T.
PA (BRIG ) BRIGGS S P.
PA (COOP ) COOPER B.
PA (GLAZ ) GLAZEBROOK J.
PA (GOFF ) GOFF S A.
PA (KATA ) KATAGIRI F.
PA (KREP ) KREPS J.
PA (PROV ) PROVART N.
PA (RICK ) RICKES D.
PA (ZHUT ) ZHU T.
Query Match      5.3%; Score 52.6; DB 12; Length 447;
Best Local Similarity 47.4%; Pred. No. 6;
RESULT 385
ID ACA03588 standard; DNA; 1275 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #71.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR ) CHIRON CORP.
Query Match      5.3%; Score 52.6; DB 8; Length 1275;
Best Local Similarity 43.1%; Pred. No. 5.8;
RESULT 386
ID ADC13276 standard; DNA; 1275 BP.
DE DNA of HIV construct tatRevNef-opt-native_ZA SEQ ID NO 55.
PN WO2003004620-A2.
PD 16-JAN-2003.
PA (CHIR ) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.
Query Match      5.3%; Score 52.6; DB 10; Length 1275;
Best Local Similarity 43.1%; Pred. No. 5.8;
RESULT 387
ID ACA38006 standard; DNA; 1368 BP.
DE Prokaryotic essential gene #19663.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      5.3%; Score 52.6; DB 8; Length 1368;
Best Local Similarity 43.9%; Pred. No. 5.8;
RESULT 388
ID ADG73813 standard; cDNA; 2466 BP.
DE Human variant subtilase-like serine protease polynucleotide.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match      5.3%; Score 52.6; DB 12; Length 2466;
Best Local Similarity 45.8%; Pred. No. 5.7;
RESULT 389
ID AAH26500 standard; cDNA; 2561 BP.
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match      5.3%; Score 52.6; DB 5; Length 2561;
Best Local Similarity 47.3%; Pred. No. 5.7;
RESULT 390
ID ACA03550 standard; DNA; 3624 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #33.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR ) CHIRON CORP.
Query Match      5.3%; Score 52.6; DB 8; Length 3624;
Best Local Similarity 43.1%; Pred. No. 5.7;
RESULT 391
ID ADC13268 standard; DNA; 3624 BP.
DE DNA of HIV construct p2PolTatRevNef-opt-native_C SEQ ID NO 47.
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PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 5.3%; Score 52.6; DB 10; Length 3624;  
Best Local Similarity 43.1%; Pred. No. 5.7;  
RESULT 392  
ID ADG73810 standard; cDNA; 3705 BP.  
DE Human subtilase-like serine protease polynucleotide.  
PN WO2003106667-A2.  
PD 24-DEC-2003.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 5.3%; Score 52.6; DB 12; Length 3705;  
Best Local Similarity 45.8%; Pred. No. 5.7;  
RESULT 393  
ID ADO58090 standard; DNA; 4199 BP.  
DE Thermus thermophilus V1 ATPase gene operon.  
PN WO2004046350-A1.  
PD 03-JUN-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
Query Match 5.3%; Score 52.6; DB 12; Length 4199;  
Best Local Similarity 55.1%; Pred. No. 5.6;  
RESULT 394  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.1;  
RESULT 395  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.1;  
RESULT 396  
ID ABU61294 standard; DNA; 1227 BP.  
DE N. uniformis p-hydroxymandelate oxidase DNA.  
PN WO200234921-A2.  
PD 02-MAY-2002.  
PA (STAM ) DSM NV.  
PA (STAM ) DSM BIOTECH GMBH.  
PA (UJO ) UNIV JOHNS HOPKINS.  
Query Match 5.3%; Score 52.4; DB 6; Length 1227;  
Best Local Similarity 45.0%; Pred. No. 6.3;  
RESULT 397  
ID ABL69280 standard; DNA; 1891 BP.  
DE Prostate cancer related gene sequence SEQ ID NO:7617.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 6.2;  
RESULT 398  
ID ABV94243 standard; cDNA; 1891 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:234.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 6.2;  
RESULT 399  
ID ABK84580 standard; cDNA; 1891 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1151.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 6.2;  
RESULT 400  
ID AAA53918 standard; cDNA; 3978 BP.  
DE Adenyl cyclase type I-C1 C1 alpha domain coding sequence.  
PN US61076-A.  
PD 22-AUG-2000.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 5.3%; Score 52.4; DB 3; Length 3978;  
Best Local Similarity 47.8%; Pred. No. 6.1;  
RESULT 401  
ID ADL15099 standard; DNA; 5117 BP.  
DE Human male brain KIAA0533 protein DNA for cancer treatment.

PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 5.3%; Score 52.4; DB 10; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.1;  
RESULT 402  
ID ADN95659 standard; DNA; 5117 BP.  
DE Human BEC/LEC-related gene sequence SeqID583.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 5.3%; Score 52.4; DB 11; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.1;  
RESULT 403  
ID ABQ93882 standard; DNA; 5204 BP.  
DE Human laminin alpha-5-like NOVId DNA, SEQ ID NO:7.  
PN WO200253742-A2.  
PD 11-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.3%; Score 52.4; DB 6; Length 5204;  
Best Local Similarity 50.0%; Pred. No. 6.1;  
RESULT 404  
ID ADM87490 standard; cDNA; 5403 BP.  
DE Human EST derived nucleotide sequence. SEQ ID NO:583.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 5.3%; Score 52.4; DB 12; Length 5403;  
Best Local Similarity 50.0%; Pred. No. 6;  
RESULT 405  
ID AAI58165 standard; cDNA; 5640 BP.  
DE Human polynucleotide SEQ ID NO 368.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.3%; Score 52.4; DB 4; Length 5640;  
Best Local Similarity 50.0%; Pred. No. 6;  
RESULT 406  
ID ADQ98371 standard; cDNA; 5640 BP.  
DE DNA encoding human GPCR-like protein seqid 41.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.3%; Score 52.4; DB 5; Length 5640;  
Best Local Similarity 50.0%; Pred. No. 6;  
RESULT 407  
ID AD848131 standard; cDNA; 5640 BP.  
DE Novel human cDNA SEQ ID NO 41.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 5.3%; Score 52.4; DB 9; Length 5640;  
Best Local Similarity 50.0%; Pred. No. 6;  
RESULT 408  
ID ABQ72930 standard; cDNA; 8296 BP.  
DE Human laminin alpha 5 2743 N-terminal amino acids cDNA SEQ ID NO:35.  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PA (BIOS-) BIOSTRATUM INC.  
Query Match 5.3%; Score 52.4; DB 6; Length 8296;  
Best Local Similarity 50.0%; Pred. No. 6;  
RESULT 409  
ID AAD27805 standard; DNA; 11091 BP.  
DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #2.  
PN WO200198342-A1.  
PD 27-DEC-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.



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PA (GLAX ) GLAXO GROUP LTD.  
 Query Match 5.3%; Score 52.4; DB 6; Length 11091;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 410  
 ID AAD27804 standard; DNA; 11118 BP.  
 DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #1.  
 PN WO200198342-A1.  
 PD 27-DEC-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Query Match 5.3%; Score 52.4; DB 6; Length 11118;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 411  
 ID AAD5817 standard; DNA; 11238 BP.  
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #7.  
 PN CA2391131-A1.  
 PD 19-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.3%; Score 52.4; DB 10; Length 11238;  
 Best Local Similarity 45.6%; Pred. No. 5.9;  
 RESULT 412  
 ID ABQ72906 standard; cDNA; 11350 BP.  
 DE Human laminin alpha 5 encoding cDNA SEQ ID NO:1.  
 PN WO200250111-A2.  
 PD 27-JUN-2002.  
 PA (BIOS-) BIOSTRATUM INC.  
 Query Match 5.3%; Score 52.4; DB 6; Length 11350;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 413  
 ID ADI28066 standard; cDNA; 11367 BP.  
 DE ECMCAD gene clone 638272CB1.  
 PN WO200202634-A2.  
 PD 10-JAN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.3%; Score 52.4; DB 6; Length 11367;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 414  
 ID ADN04477 standard; cDNA; 11426 BP.  
 DE Antiporiatic cDNA sequence #440.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 5.3%; Score 52.4; DB 12; Length 11426;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 415  
 ID ADM87010 standard; cDNA; 11640 BP.  
 DE Human protein encoding cDNA SEQ ID NO:103.  
 PN WO2004009834-A2.  
 PD 29-JAN-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 5.3%; Score 52.4; DB 12; Length 11640;  
 Best Local Similarity 50.0%; Pred. No. 5.9;  
 RESULT 416  
 ID AAD5810 standard; DNA; 60196 BP.  
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.  
 PN CA2391131-A1.  
 PD 19-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.3%; Score 52.4; DB 10; Length 60196;  
 Best Local Similarity 45.6%; Pred. No. 5.7;  
 RESULT 417  
 ID AAC47161 standard; DNA; 738 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.3%; Score 52.2; DB 3; Length 738;  
 Best Local Similarity 47.8%; Pred. No. 6.9;  
 RESULT 418  
 ID AAC47930 standard; DNA; 833 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.

Query Match 5.3%; Score 52.2; DB 3; Length 833;  
 Best Local Similarity 47.8%; Pred. No. 6.9;  
 RESULT 419  
 ID AAT85356 standard; DNA; 2004 BP.  
 DE Nephila clavipes spider silk protein 2 Kb DNA sequence.  
 PN WO9708315-A1.  
 PD 06-MAR-1997.  
 PA (BASE/) BASEL R M.  
 PA (ELIO/) ELION G R.  
 Query Match 5.3%; Score 52.2; DB 2; Length 2004;  
 Best Local Similarity 47.2%; Pred. No. 6.7;  
 RESULT 420  
 ID ACA38157 standard; DNA; 2757 BP.  
 DE Prokaryotic essential gene #19814.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.3%; Score 52.2; DB 8; Length 2757;  
 Best Local Similarity 46.7%; Pred. No. 6.7;  
 RESULT 421  
 ID ADC30607 standard; cDNA; 4542 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:689.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.3%; Score 52.2; DB 10; Length 4542;  
 Best Local Similarity 47.6%; Pred. No. 6.6;  
 RESULT 422  
 ID AAD54236 standard; DNA; 6297 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.3%; Score 52.2; DB 10; Length 6297;  
 Best Local Similarity 47.2%; Pred. No. 6.5;  
 RESULT 423  
 ID ABQ77491 standard; DNA; 67459 BP.  
 DE S. aurantiaca DNA containing sti gene cluster.  
 PN DE10128661-A1.  
 PD 19-DEC-2002.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.3%; Score 52.2; DB 8; Length 67459;  
 Best Local Similarity 43.5%; Pred. No. 6.1;  
 RESULT 424  
 ID AD059147 standard; DNA; 70782 BP.  
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.  
 PN DE10241152-A1.  
 PD 18-MAR-2004.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.3%; Score 52.2; DB 12; Length 70782;  
 Best Local Similarity 44.2%; Pred. No. 6.1;  
 RESULT 425  
 ID ACF06127 standard; DNA; 1218 BP.  
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:37.  
 PN WO2003052050-A2.  
 PD 26-JUN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 5.3%; Score 52; DB 9; Length 1218;  
 Best Local Similarity 50.6%; Pred. No. 7.3;  
 RESULT 426  
 ID ABD03077 standard; DNA; 1248 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1681.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.3%; Score 52; DB 11; Length 1248;  
 Best Local Similarity 50.4%; Pred. No. 7.3;  
 RESULT 427  
 ID ASD02833 standard; DNA; 1302 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1437.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.



Query Match  
Best Local Similarity 5.3%; Score 52; DB 11; Length 1302;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 428  
ID ABL40020 standard; DNA; 1491 BP.  
DE Synthetic Gag polynucleotide sequence SEQ ID NO:99.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match  
Best Local Similarity 5.3%; Score 52; DB 6; Length 1491;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 429  
ID ADW73833 standard; DNA; 1491 BP.  
DE HIV-1 polynucleotide #68.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBERG E J V.  
Query Match  
Best Local Similarity 5.3%; Score 52; DB 12; Length 1491;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 430  
ID ABD02890 standard; DNA; 1956 BP.  
DE Pseudomonas aeruginosa polynucleotide #1494.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.3%; Score 52; DB 11; Length 1956;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 431  
ID ADP69917 standard; DNA; 3078 BP.  
DE Mammalian codon optimised E. coli LacZ gene.  
PN WO2004050872-A1.  
PD 17-JUN-2004.  
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
Query Match  
Best Local Similarity 5.3%; Score 52; DB 12; Length 3078;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 432  
ID ABD11785 standard; DNA; 498 BP.  
DE Pseudomonas aeruginosa polynucleotide #10389.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 11; Length 498;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 433  
ID ABD11976 standard; DNA; 561 BP.  
DE Pseudomonas aeruginosa polynucleotide #10580.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 11; Length 561;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 434  
ID ABD12080 standard; DNA; 1053 BP.  
DE Pseudomonas aeruginosa polynucleotide #10684.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 11; Length 1053;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 435  
ID ACA27206 standard; DNA; 1227 BP.  
DE Prokaryotic essential gene #8863.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 8; Length 1227;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 436  
ID ABD04500 standard; DNA; 1233 BP.  
DE Pseudomonas aeruginosa polynucleotide #3104.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 11; Length 1233;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 437  
ID ABD04263 standard; DNA; 1386 BP.  
DE Pseudomonas aeruginosa polynucleotide #2867.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 11; Length 1386;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 438  
ID ABZ81830 standard; DNA; 2072 BP.  
DE Receptor FZD10 nucleic acid sequence.  
PN WO2003012082-A2.  
PD 13-FEB-2003.  
PA (AXOR-) AXORDIA LTD.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 8; Length 2072;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 439  
ID AAD17401 standard; DNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP) gene.  
PN WO200164717-A1.  
PD 07-SEP-2001.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 4; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 440  
ID ABV73022 standard; cDNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP)-1 encoding cDNA.  
PN WO200255547-A2.  
PD 18-JUL-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (SVIN) ST VINCENTS INST MEDICAL RES.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 6; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 441  
ID ABX75330 standard; cDNA; 2075 BP.  
DE Human cDNA encoding Frizzled-8.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 8; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 442  
ID AAD52558 standard; DNA; 2075 BP.  
DE FRP DNA.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 8; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 443  
ID ADC71197 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein (sFRP) cDNA.  
PN US6600018-B1.  
PD 29-JUL-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 10; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 444  
ID ADH43319 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein 1 (sFRP-1) cDNA.  
PN US2003187223-A1.  
PD 02-OCT-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (UYMA-) UNIV MASSACHUSETTS.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match  
Best Local Similarity 5.2%; Score 51.8; DB 12; Length 2075;  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
RESULT 445



DE Gene encoding a subunit of cellulose synthase.  
 PN JP2000060568-A.  
 PD 29-FEB-2000.  
 PA (MIZU/) MIZUNO K.  
 PA (OJIP) OJI PAPER CO.  
 Query Match 5.2%; Score 51.8; DB 3; Length 10732;  
 Best Local Similarity 13.2%; Pred. No. 7.5;  
 RESULT 455  
 ID AAL61170 standard; DNA; 14055 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #1.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 5.2%; Score 51.8; DB 8; Length 14055;  
 Best Local Similarity 44.1%; Pred. No. 7.4;  
 RESULT 456  
 ID AAD54645 standard; DNA; 113193 BP.  
 DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.  
 PN WO200297082-A2.  
 PD 05-DEC-2002.  
 PA (UYDU-) UNIV COLLEGE DUBLIN.  
 Query Match 5.2%; Score 51.8; DB 8; Length 113193;  
 Best Local Similarity 46.9%; Pred. No. 7;  
 RESULT 457  
 ID ACC0687 standard; cDNA; 893 BP.  
 DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:123.  
 PN WO2003002751-A2.  
 PD 09-JAN-2003.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 8.6;  
 RESULT 458  
 ID ADC23602 standard; cDNA; 893 BP.  
 DE cDNA encodes protein used to alter plant oil phenotype (SeqID 107).  
 PN WO2003001902-A2.  
 PD 09-JAN-2003.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 10; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 8.6;  
 RESULT 459  
 ID ACA38013 standard; DNA; 1242 BP.  
 DE Prokaryotic essential gene #19670.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 1242;  
 Best Local Similarity 44.5%; Pred. No. 8.6;  
 RESULT 460  
 ID ABD15461 standard; DNA; 1311 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14065.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 1311;  
 Best Local Similarity 43.9%; Pred. No. 8.5;  
 RESULT 461  
 ID ABD15601 standard; DNA; 2850 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14205.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 2850;  
 Best Local Similarity 43.9%; Pred. No. 8.4;  
 RESULT 462  
 ID ACA26098 standard; DNA; 2853 BP.  
 DE Prokaryotic essential gene #7755.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 2853;  
 Best Local Similarity 45.4%; Pred. No. 8.4;  
 ID AAA10594 standard; DNA; 10732 BP.

DE AC43985 standard; DNA; 2145 BP.  
 PN Prokaryotic essential gene #25642.  
 PD WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.8; DB 8; Length 2145;  
 Best Local Similarity 44.4%; Pred. No. 7.8;  
 RESULT 446  
 ID AAK94307 standard; cDNA; 2525 BP.  
 DE Human full-length cDNA, SEQ ID NO: 2971.  
 PN EP1130094-A2.  
 PD 05-SEP-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.2%; Score 51.8; DB 4; Length 2525;  
 Best Local Similarity 43.0%; Pred. No. 7.8;  
 RESULT 447  
 ID ADL30938 standard; cDNA; 2525 BP.  
 DE Full length human cDNA clone SeqID 2971.  
 PN EP1396543-A2.  
 PD 10-MAR-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 5.2%; Score 51.8; DB 12; Length 2525;  
 Best Local Similarity 43.0%; Pred. No. 7.8;  
 RESULT 448  
 ID ABS78645 standard; cDNA; 2597 BP.  
 DE Human cDNA encoding CGDD3, INCYTE 3089944CB1.  
 PN WO200272830-A2.  
 PD 19-SEP-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 2597;  
 Best Local Similarity 43.0%; Pred. No. 7.8;  
 RESULT 449  
 ID ABX77526 standard; cDNA; 4462 BP.  
 DE Differentially expressed breast cancer associated cDNA #21.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4462;  
 Best Local Similarity 45.0%; Pred. No. 7.7;  
 RESULT 450  
 ID AAS12954 standard; cDNA; 4469 BP.  
 DE Human Frizzled Related Protein (FRP-1) cDNA.  
 PN WO200164949-A2.  
 PD 07-SEP-2001.  
 PA (ALCO-) ALCON LAB INC.  
 Query Match 5.2%; Score 51.8; DB 4; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 7.7;  
 RESULT 451  
 ID ABT10165 standard; cDNA; 4469 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 299.  
 PN WO200259271-A2.  
 PD 01-AUG-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 7.7;  
 RESULT 452  
 ID AB34845 standard; cDNA; 4469 BP.  
 DE Coding sequence SEQ ID 203, differentially expressed in osteogenesis.  
 PN WO200281745-A2.  
 PD 17-OCT-2002.  
 PA (AVET) AVENTIS PHARMA SA.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 7.7;  
 RESULT 453  
 ID ADP21417 standard; DNA; 4469 BP.  
 DE Gene SFRP1 for screening for cardiac therapeutic preparation.  
 PN WO2004050894-A2.  
 PD 17-JUN-2004.  
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
 Query Match 5.2%; Score 51.8; DB 12; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 7.7;  
 RESULT 454  
 ID AAA10594 standard; DNA; 10732 BP.



RESULT 463  
ID ABX09933 standard; DNA; 2865 BP.  
DE DNA encoding maize Starch synthase Iia.  
PN WO200279410-A2.  
PD 10-OCT-2002.  
PA (BADI) BASF PLANT SCI GMBH.  
Query Match 5.2%; Score 51.6; DB 8; Length 2865;  
Best Local Similarity 49.6%; Pred. No. 8.4;  
RESULT 464  
ID ADG75175 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 8.1;  
RESULT 465  
ID ADG75118 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 8.1;  
RESULT 466  
ID AAV62154 standard; DNA; 21034 BP.  
DE HSV-2 strain SB5 Contig ID 10 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 21034;  
Best Local Similarity 44.9%; Pred. No. 7.9;  
RESULT 467  
ID AAV62134 standard; DNA; 26338 BP.  
DE HSV-2 strain SB5 Contig ID 104 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 26338;  
Best Local Similarity 44.9%; Pred. No. 7.9;  
RESULT 468  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.2%; Score 51.6; DB 12; Length 76994;  
Best Local Similarity 44.5%; Pred. No. 7.6;  
RESULT 469  
ID AAD54645 standard; DNA; 113193 BP.  
DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (UVDU-) UNIV COLLEGE DUBLIN.  
Query Match 5.2%; Score 51.6; DB 8; Length 113193;  
Best Local Similarity 44.0%; Pred. No. 7.6;  
RESULT 470  
ID AAV62176 standard; DNA; 117213 BP.  
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (FARB) BAYER AG.  
Query Match 5.2%; Score 51.6; DB 6; Length 813;  
Best Local Similarity 44.7%; Pred. No. 9.4;  
RESULT 471  
ID ABA99457 standard; DNA; 813 BP.  
DE Actinoplanes sp DNA encoding acarbose synthase AcbOAsp.  
PN DE10021667-A1.  
PD 08-NOV-2001.  
PA (FARB) BAYER AG.  
Query Match 5.2%; Score 51.4; DB 10; Length 4725;  
Best Local Similarity 50.6%; Pred. No. 8.9;  
RESULT 472  
ID AAR29167 standard; cDNA; 1106 BP.  
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.  
PN WO200032757-A2.

PD 08-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 5.2%; Score 51.4; DB 3; Length 1106;  
Best Local Similarity 45.0%; Pred. No. 9.3;  
RESULT 473  
ID ADG36364 standard; DNA; 1197 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:232.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1197;  
Best Local Similarity 43.9%; Pred. No. 9.3;  
RESULT 474  
ID ADG36374 standard; DNA; 1411 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:242.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1411;  
Best Local Similarity 43.9%; Pred. No. 9.2;  
RESULT 475  
ID ADJ27276 standard; cDNA; 1926 BP.  
DE Mouse HSP70.3 coding sequence.  
PN WO2003061684-A2.  
PD 31-JUL-2003.  
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 5.2%; Score 51.4; DB 11; Length 1926;  
Best Local Similarity 44.1%; Pred. No. 9.1;  
RESULT 476  
ID AAS10678 standard; cDNA; 1929 BP.  
DE Murine hsp70 cDNA sequence.  
PN WO200151081-A1.  
PD 19-JUL-2001.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
Query Match 5.2%; Score 51.4; DB 4; Length 1929;  
Best Local Similarity 44.1%; Pred. No. 9.1;  
RESULT 477  
ID ACA23299 standard; DNA; 2307 BP.  
DE Prokaryotic essential gene #4956.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.4; DB 8; Length 2307;  
Best Local Similarity 49.8%; Pred. No. 9.1;  
RESULT 478  
ID ADQ18001 standard; DNA; 2526 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 818.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2526;  
Best Local Similarity 44.1%; Pred. No. 9.1;  
RESULT 479  
ID ADQ22602 standard; DNA; 2652 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5422.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2652;  
Best Local Similarity 44.1%; Pred. No. 9.1;  
RESULT 480  
ID AAD55818 standard; DNA; 4725 BP.  
DE Micronospora carbonacea polyketide synthase (PKS) type I gene #8.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.2%; Score 51.4; DB 10; Length 4725;  
Best Local Similarity 50.6%; Pred. No. 8.9;  
RESULT 481  
ID AB211709 standard; cDNA; 7847 BP.  
DE Human polynucleotide SEQ ID NO 591.  
PN WO200270539-A2.



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PD 12-SEP-2002.
PA (HYSE-) HYSE INC. 5.2%; Score 51.4; DB 6; Length 7847;
Query Match
Best Local Similarity 50.2%; Pred. No. 8.8;
RESULT 482
ID ADM44227 standard; cDNA; 7847 BP.
DE Novel human arginine-rich protein cDNA #591.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRNA/) DRMANAC R T.
Query Match
Best Local Similarity 50.2%; Score 51.4; DB 12; Length 7847;
Pred. No. 8.8;
RESULT 483
ID ADP90617 standard; DNA; 34719 BP.
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.
PN JP2004180638-A.
PD 02-JUL-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match
Best Local Similarity 47.1%; Score 51.4; DB 12; Length 34719;
Pred. No. 8.4;
RESULT 484
ID ABA99469 standard; DNA; 38064 BP.
DE Actinoplanes sp SE 50/110 (CBS614.71) DNA encoding acarbose operon.
PN DE10021667-A1.
PD 08-NOV-2001.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 44.7%; Score 51.4; DB 6; Length 38064;
Pred. No. 8.4;
RESULT 485
ID ABX04971 standard; DNA; 103599 BP.
DE S. cinamonensis monensis type I polyketide synthase gene cluster.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIORICA TECHNOLOGY LTD.
Query Match
Best Local Similarity 44.8%; Score 51.4; DB 4; Length 103599;
Pred. No. 8.2;
RESULT 486
ID ADP95323 standard; cDNA; 447 BP.
DE Cotton expressed sequence tag, EST, #4334.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match
Best Local Similarity 50.8%; Score 51.2; DB 12; Length 447;
Pred. No. 10;
RESULT 487
ID AB213934 standard; DNA; 699 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 47.5%; Score 51.2; DB 6; Length 699;
Pred. No. 10;
RESULT 488
ID ADG87603 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 47.5%; Score 51.2; DB 6; Length 699;
Pred. No. 10;
RESULT 489
ID ADG87604 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.
PN WO200222675-A2.

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PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 6; Length 699;
Pred. No. 10;
RESULT 490
ID ADA67907 standard; DNA; 699 BP.
DE Arabidopsis thaliana gene, SEQ ID 151.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 8; Length 699;
Pred. No. 10;
RESULT 491
ID ABN9073 standard; DNA; 792 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 6; Length 792;
Pred. No. 10;
RESULT 492
ID ACA26840 standard; DNA; 1107 BP.
DE Prokaryotic essential gene #8497.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 8; Length 1107;
Pred. No. 10;
RESULT 493
ID AAD55811 standard; DNA; 1683 BP.
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.
PN CA2391131-A1.
PD 19-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 10; Length 1683;
Pred. No. 9.9;
RESULT 494
ID AAS54365 standard; DNA; 2034 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #496.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.2%; Score 51.2; DB 4; Length 2034;
Pred. No. 9.8;
RESULT 495
ID AAV13836 standard; cDNA; 2277 BP.
DE Homo sapiens mammalian codon-optimized telomerase protein p105 gene.
PN WO9801543-A1.
PD 15-JAN-1998.

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PA (TULA-) TULARIK INC.  
Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
Best Local Similarity 46.4%; Pred. No. 9.8;  
RESULT 496  
ID AAV05372 standard; RNA; 2277 BP.  
DE Human telomerase p105 subunit mammalian optimised synthetic RNA.  
PN WO9801542-A1.  
PD 15-JAN-1998.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
Best Local Similarity 46.4%; Pred. No. 9.8;  
RESULT 497  
ID AAV07385 standard; DNA; 4467 BP.  
DE Heterosigma akashiwo Nat-Atrase gene.  
PN JP2000050874-A.  
PD 22-FEB-2000.  
PA (NORO ) NORINSUISANGSHO KOKUSAI NORIN SUITSANGYO.  
Query Match 5.2%; Score 51.2; DB 3; Length 4467;  
Best Local Similarity 44.1%; Pred. No. 9.6;  
RESULT 498  
ID AAA58471 standard; DNA; 58857 BP.  
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.  
PN WO200040704-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.2%; Score 51.2; DB 3; Length 58857;  
Best Local Similarity 45.2%; Pred. No. 9;  
RESULT 499  
ID ADP03244 standard; DNA; 473 BP.  
DE S. fradiae IF012773 L-glutamine DOI aminotransferase partial DNA.  
PN JP2004089151-A.  
PD 25-MAR-2004.  
PA (TOKD ) TOKYO INST TECHNOLOGY.  
Query Match 5.2%; Score 51; DB 12; Length 473;  
Best Local Similarity 44.4%; Pred. No. 11;  
RESULT 500  
ID ABD13343 standard; DNA; 501 BP.  
DE Pseudomonas aeruginosa polynucleotide #11947.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51; DB 11; Length 501;  
Best Local Similarity 48.5%; Pred. No. 11;  
RESULT 501  
ID AAV55831 standard; DNA; 799 BP.  
DE Nucleotide sequence of the stabilising sequence-encoding insert.  
PN WO9822577-A1.  
PD 28-MAY-1998.  
PA (MASU/) MASUCCI M G.  
Query Match 5.2%; Score 51; DB 2; Length 799;  
Best Local Similarity 46.1%; Pred. No. 11;  
RESULT 502  
ID ACA37639 standard; DNA; 1497 BP.  
DE Prokaryotic essential gene #19296.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51; DB 8; Length 1497;  
Best Local Similarity 48.0%; Pred. No. 11;  
RESULT 503  
ID ABD13303 standard; DNA; 1500 BP.  
DE Pseudomonas aeruginosa polynucleotide #11907.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51; DB 11; Length 1500;  
Best Local Similarity 48.5%; Pred. No. 11;  
RESULT 504  
ID ADJ40244 standard; cDNA; 1503 BP.  
DE Plant cDNA #1244.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
PA (ZHUT/) ZHU T.  
Query Match 5.2%; Score 51; DB 12; Length 1503;  
Best Local Similarity 47.6%; Pred. No. 11;  
RESULT 505  
ID AAL44275 standard; DNA; 1632 BP.  
DE Micrococcus luteus crtI gene sequence.  
PN WO200241833-A2.  
PD 30-MAY-2002.  
PA (CRGI ) CARGILL INC.  
Query Match 5.2%; Score 51; DB 6; Length 1632;  
Best Local Similarity 42.9%; Pred. No. 11;  
RESULT 506  
ID ADG93408 standard; DNA; 1632 BP.  
DE Maize lipoxygenase (LOX) DNA #20.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.2%; Score 51; DB 10; Length 1632;  
Best Local Similarity 45.9%; Pred. No. 11;  
RESULT 507  
ID AAL61149 standard; DNA; 1713 BP.  
DE Human mutant ARX gene #2.  
PN WO2003045989-A1.  
PD 05-JUN-2003.  
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
Query Match 5.2%; Score 51; DB 9; Length 1713;  
Best Local Similarity 46.2%; Pred. No. 11;  
RESULT 508  
ID ADG93406 standard; DNA; 1803 BP.  
DE Maize lipoxygenase (LOX) DNA #19.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.2%; Score 51; DB 10; Length 1803;  
Best Local Similarity 45.9%; Pred. No. 11;  
RESULT 509  
ID AAH26500 standard; cDNA; 2561 BP.  
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.2%; Score 51; DB 5; Length 2561;  
Best Local Similarity 47.3%; Pred. No. 11;  
RESULT 510  
ID ABN85324 standard; cDNA; 2710 BP.  
DE Human cytoskeleton-associated protein, CSAP-15, coding sequence.  
PN WO200253719-A2.  
PD 11-JUL-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.2%; Score 51; DB 6; Length 2710;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 511  
ID AAL44298 standard; DNA; 6941 BP.  
DE Micrococcus luteus C50 carotenoid producing operon.  
PN WO200241833-A2.  
PD 30-MAY-2002.  
PA (CRGI ) CARGILL INC.  
Query Match 5.2%; Score 51; DB 6; Length 6941;  
Best Local Similarity 42.9%; Pred. No. 10;  
RESULT 512  
ID AAQ73500 standard; DNA; 8438 BP.  
DE DNA encoding Pseudorabies virus large latency transcript.  
PN US5352596-A.  
PD 04-OCT-1994.



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PA (USDA ) US SEC OF AGRIC.  
Query Match 5.1%; Score 50.8; DB 8; Length 1173;  
Best Local Similarity 43.9%; Pred. No. 12;  
RESULT 522  
ID ADJ39706 standard; cDNA; 1173 BP.  
DE Plant cDNA #706.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KEP/) KRIPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICK D.  
PA (ZHUT/) ZHU T.  
Query Match 5.1%; Score 50.8; DB 12; Length 1173;  
Best Local Similarity 43.9%; Pred. No. 12;  
RESULT 523  
ID AAS51566 standard; DNA; 1317 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #151.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.1%; Score 50.8; DB 4; Length 1317;  
Best Local Similarity 51.0%; Pred. No. 12;  
RESULT 524  
ID ACAL9467 standard; DNA; 1317 BP.  
DE Prokaryotic essential gene #1124.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.1%; Score 50.8; DB 8; Length 1317;  
Best Local Similarity 51.0%; Pred. No. 12;  
RESULT 525  
ID ADA71150 standard; DNA; 1479 BP.  
DE Rice gene, SEQ ID 4473.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.1%; Score 50.8; DB 8; Length 1479;  
Best Local Similarity 46.7%; Pred. No. 12;  
RESULT 526  
ID AAL51696 standard; cDNA; 1682 BP.  
DE Argiope trifasciata spider silk protein coding sequence #1.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWV-) UNIV WYOMING.  
Query Match 5.1%; Score 50.8; DB 8; Length 1682;  
Best Local Similarity 45.8%; Pred. No. 12;  
RESULT 527  
ID ABS78661 standard; DNA; 5760 BP.  
DE M. echinospira DNA encoding PKSE protein.  
PN CA2387401-A1.  
PD 04-SEP-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.8; DB 6; Length 5760;  
Best Local Similarity 45.0%; Pred. No. 11;  
RESULT 528  
ID ABS63414 standard; cDNA; 508 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 5.1%; Score 50.6; DB 6; Length 508;  
Best Local Similarity 54.6%; Pred. No. 13;  
RESULT 529  
ID AAF74867 standard; DNA; 1313 BP.  
DE Leishmania major PPG nucleotide sequence.

PA (USDA ) US SEC OF AGRIC.  
Query Match 5.2%; Score 51; DB 2; Length 8438;  
Best Local Similarity 44.6%; Pred. No. 10;  
RESULT 513  
ID ABX56062 standard; DNA; 741 BP.  
DE M. echinospira calicheamicin biosynthesis gene orfII.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETERING INST CANCER RES.  
Query Match 5.1%; Score 50.8; DB 8; Length 741;  
Best Local Similarity 45.8%; Pred. No. 12;  
RESULT 514  
ID ACA43508 standard; DNA; 1125 BP.  
DE Prokaryotic essential gene #25165.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.1%; Score 50.8; DB 8; Length 1125;  
Best Local Similarity 50.0%; Pred. No. 12;  
RESULT 515  
ID AAT91453 standard; DNA; 1155 BP.  
DE Mycobacterium tuberculosis antigen TbrA28 encoding DNA.  
PN WO9709429-A2.  
PD 13-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 516  
ID AAT91517 standard; DNA; 1155 BP.  
DE Mycobacterium tuberculosis antigen TbrA28 encoding DNA.  
PN WO9709428-A2.  
PD 13-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 517  
ID AAV44350 standard; DNA; 1155 BP.  
DE Mycobacterium tuberculosis antigen TbrA28 DNA.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 518  
ID AAV64458 standard; DNA; 1155 BP.  
DE M. tuberculosis immunogenic polypeptide TbrA28 DNA.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 519  
ID AAZ19048 standard; DNA; 1155 BP.  
DE M. tuberculosis recombinant antigen DNA encoding TbrA28.  
PN WO9942118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 520  
ID AAZ19260 standard; DNA; 1155 BP.  
DE M. tuberculosis antigen TbrA28 DNA sequence.  
PN WO9942076-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
Best Local Similarity 49.3%; Pred. No. 12;  
RESULT 521  
ID ADA70376 standard; DNA; 1173 BP.  
DE Rice gene, SEQ ID 3699.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.



PN CN1272542-A.  
 PD 08-NOV-2000.  
 PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.  
 Query Match 5.1%; Score 50.6; DB 4; Length 1313;  
 Best Local Similarity 47.1%; Pred. No. 13;  
 RESULT 530  
 ID ACA37566 standard; DNA; 1371 BP.  
 DE Prokaryotic essential gene #19223.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.6; DB 8; Length 1371;  
 Best Local Similarity 43.7%; Pred. No. 13;  
 RESULT 531  
 ID AA192870 standard; cDNA; 2564 BP.  
 DE Human polynucleotide SEQ ID NO 12930.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.1%; Score 50.6; DB 4; Length 2564;  
 Best Local Similarity 48.6%; Pred. No. 12;  
 RESULT 532  
 ID ADQ21323 standard; DNA; 4233 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4143.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 5.1%; Score 50.6; DB 12; Length 4233;  
 Best Local Similarity 47.3%; Pred. No. 12;  
 RESULT 533  
 ID ADQ25196 standard; DNA; 4244 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8016.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 5.1%; Score 50.6; DB 12; Length 4244;  
 Best Local Similarity 47.3%; Pred. No. 12;  
 RESULT 534  
 ID ADJ39239 standard; cDNA; 549 BP.  
 DE Plant cDNA #239.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW-) BUDWORTH P.  
 PA (MOUG-) MOUGHAMER T.  
 PA (BRIG-) BRIGGS S P.  
 PA (COOP-) COOPER B.  
 PA (GLAZ-) GLAZEBROOK J.  
 PA (GOFF-) GOFF S A.  
 PA (KATA-) KATAGIRI F.  
 PA (KREP-) KREPS J.  
 PA (PROV-) PROVART N.  
 PA (RICK-) RICHE D.  
 PA (ZHUT-) ZHU T.  
 Query Match 5.1%; Score 50.4; DB 12; Length 549;  
 Best Local Similarity 47.6%; Pred. No. 14;  
 RESULT 535  
 ID ABZ66752 standard; DNA; 669 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 166.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.4; DB 10; Length 669;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 536  
 ID AAV62138 standard; DNA; 980 BP.  
 DE HSV-2 strain SB5 Contig ID 53 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK-) SMITHKLINE BEECHAM CORP.  
 Query Match 5.1%; Score 50.4; DB 2; Length 980;  
 Best Local Similarity 49.0%; Pred. No. 14;  
 RESULT 537  
 ID AD142416 standard; DNA; 1159 BP.  
 DE Plant transcription factor polynucleotide #544.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER-) SHERMAN B K.  
 PA (RIEC-) RIECHMANN J L.  
 PA (JIAN-) JIANG C.  
 PA (HEAR-) HEARD J B.  
 PA (HAAK-) HAAKE V.  
 PA (CREE-) CREELMAN R A.  
 PA (RATC-) RATCLIFFE O.  
 PA (ADAM-) ADAM L J.  
 PA (REUB-) REUBER T L.  
 PA (KEDD-) KEDDIE J.  
 PA (BROU-) BROUN P E.  
 PA (PILG-) PILGRIM M L.  
 PA (DUBE-) DUBELL A N.  
 PA (PINE-) PINEDA O.  
 PA (YUGG-) YU G.  
 Query Match 5.1%; Score 50.4; DB 12; Length 1159;  
 Best Local Similarity 47.0%; Pred. No. 14;  
 RESULT 538  
 ID ADC36273 standard; DNA; 1209 BP.  
 DE Weed controller metabolism associated gene SEQ ID NO:141.  
 PN WO2003040370-A1.  
 PD 15-MAY-2003.  
 PA (SUMO-) SUMITOMO CHEM CO LTD.  
 Query Match 5.1%; Score 50.4; DB 10; Length 1209;  
 Best Local Similarity 47.0%; Pred. No. 14;  
 RESULT 539  
 ID ADC36278 standard; DNA; 1473 BP.  
 DE Weed controller metabolism associated gene SEQ ID NO:146.  
 PN WO2003040370-A1.  
 PD 15-MAY-2003.  
 PA (SUMO-) SUMITOMO CHEM CO LTD.  
 Query Match 5.1%; Score 50.4; DB 10; Length 1473;  
 Best Local Similarity 47.0%; Pred. No. 14;  
 RESULT 540  
 ID AAL61177 standard; DNA; 2247 BP.  
 DE Actinosynema pretiosum ABC transporter gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW-) UNIV WASHINGTON.  
 Query Match 5.1%; Score 50.4; DB 8; Length 2247;  
 Best Local Similarity 43.7%; Pred. No. 13;  
 RESULT 541  
 ID AAF81370 standard; DNA; 6390 BP.  
 DE Quorum sensing controlled gene qsc107 ORF.  
 PN WO200118248-A2.  
 PD 15-MAR-2001.  
 PA (IOWA-) UNIV IOWA RES FOUND.  
 PA (QUOR-) QUORUM SCI INC.  
 Query Match 5.1%; Score 50.4; DB 4; Length 6390;  
 Best Local Similarity 50.7%; Pred. No. 13;  
 RESULT 542  
 ID ABZ75344 standard; DNA; 23673 BP.  
 DE Human R1128 gene cluster.  
 PN US6340774-B1.  
 PD 22-JAN-2002.  
 PA (STRD-) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.1%; Score 50.4; DB 6; Length 23673;  
 Best Local Similarity 47.7%; Pred. No. 13;  
 RESULT 543  
 ID ABZ66808 standard; DNA; 45055 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 277.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.4; DB 10; Length 45055;  
 Best Local Similarity 44.7%; Pred. No. 12;  
 RESULT 544  
 Query Match 5.1%; Score 50.4; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 12;  
 RESULT 545



ID ADJ42262 standard; cDNA; 595 BP.  
 DE Plant cDNA #3262.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAWER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.1%; Score 50.2; DB 12; Length 595;  
 Best Local Similarity 50.5%; Pred. No. 15;  
 RESULT 546  
 ID ACA26748 standard; DNA; 841 BP.  
 DE Prokaryotic essential gene #8405.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.2; DB 8; Length 841;  
 Best Local Similarity 46.7%; Pred. No. 15;  
 RESULT 547  
 ID ABD12328 standard; DNA; 864 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10932.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 864;  
 Best Local Similarity 47.1%; Pred. No. 15;  
 RESULT 548  
 ID AAF61096 standard; DNA; 1545 BP.  
 DE P. putida KT2440-associated DNA ORF11200.  
 PN DE19335088-A1.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Query Match 5.1%; Score 50.2; DB 4; Length 1545;  
 Best Local Similarity 44.2%; Pred. No. 15;  
 RESULT 549  
 ID ABD12652 standard; DNA; 2211 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11256.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2211;  
 Best Local Similarity 47.1%; Pred. No. 14;  
 RESULT 550  
 ID ABD12391 standard; DNA; 2289 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10995.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2289;  
 Best Local Similarity 47.1%; Pred. No. 14;  
 RESULT 551  
 ID AAH14472 standard; cDNA; 3269 BP.  
 DE Human cDNA sequence SEQ ID NO:11967.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.1%; Score 50.2; DB 4; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 14;  
 RESULT 552  
 ID AAL61173 standard; DNA; 9975 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 5.1%; Score 50.2; DB 8; Length 9975;  
 Best Local Similarity 46.0%; Pred. No. 14;  
 RESULT 553  
 ID ABX48858 standard; cDNA; 390 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #14023.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 5.1%; Score 50; DB 8; Length 390;  
 Best Local Similarity 52.2%; Pred. No. 16;  
 RESULT 554  
 ID AAZ52552 standard; cDNA; 888 BP.  
 DE Human secreted protein clone yd61\_1 nucleotide sequence SEQ ID NO:155.  
 PN WO9958642-A2.  
 PD 18-NOV-1999.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 5.1%; Score 50; DB 3; Length 888;  
 Best Local Similarity 49.4%; Pred. No. 16;  
 RESULT 555  
 ID AD000480 standard; cDNA; 1149 BP.  
 DE Novel human cDNA sequence #1295.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1149;  
 Best Local Similarity 47.8%; Pred. No. 16;  
 RESULT 556  
 ID ADN98911 standard; cDNA; 1149 BP.  
 DE Novel human cDNA sequence #511.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1149;  
 Best Local Similarity 47.8%; Pred. No. 16;  
 RESULT 557  
 ID ACA25880 standard; DNA; 1365 BP.  
 DE Prokaryotic essential gene #7537.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50; DB 8; Length 1365;  
 Best Local Similarity 45.4%; Pred. No. 16;  
 RESULT 558  
 ID ADP28824 standard; DNA; 1470 BP.  
 DE Human secreted protein encoding sequence SEQ ID #822.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1470;  
 Best Local Similarity 47.8%; Pred. No. 16;  
 RESULT 559  
 ID ADI23924 standard; DNA; 1806 BP.  
 DE Streptomyces refulneus 024A locus ORF2.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 10; Length 1806;  
 Best Local Similarity 46.3%; Pred. No. 16;  
 RESULT 560  
 ID ADG98257 standard; DNA; 1806 BP.  
 DE Acyl-specific C-domain DNA #13.  
 PN US2003211567-A1.  
 PD 13-NOV-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1806;  
 Best Local Similarity 46.3%; Pred. No. 16;  
 RESULT 561  
 ID AAZ87297 standard; DNA; 13842 BP.



DE S. venezuelae macrolide biosynthetic gene pikAI, SEQ ID NO:30.  
 PN WO200000620-A2.  
 PA (MINU) UNIV MINNESOTA.  
 Query Match 5.1%; Score 50; DB 3; Length 13842;  
 Best Local Similarity 44.7%; Pred. No. 15;  
 RESULT 562  
 ID ADL1915 standard; DNA; 13842 BP.  
 DE Streptomyces macrolide biosynthetic protein (pikR2) coding sequence.  
 PN US2003194784-A1.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.  
 Query Match 5.1%; Score 50; DB 12; Length 13842;  
 Best Local Similarity 44.7%; Pred. No. 15;  
 RESULT 563  
 ID ADI23898 standard; DNA; 15738 BP.  
 DE Streptomyces fradiiae A541 locus ORF5.  
 PN US2003198981-A1.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 10; Length 15738;  
 Best Local Similarity 43.1%; Pred. No. 15;  
 RESULT 564  
 ID ADOS1695 standard; DNA; 32329 BP.  
 DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
 PN US2004038250-A1.  
 PD 26-FEB-2004.  
 PA (ASTU-) ASTUR-PHARMA SA.  
 PA (UYOV-) UNIV OVIEDO.  
 Query Match 5.1%; Score 50; DB 12; Length 32329;  
 Best Local Similarity 48.5%; Pred. No. 14;  
 RESULT 565  
 ID AA287318 standard; DNA; 36778 BP.  
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU) UNIV MINNESOTA.  
 Query Match 5.1%; Score 50; DB 3; Length 36778;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 566  
 ID ADL1933 standard; DNA; 36778 BP.  
 DE Streptomyces venezuelae pik gene cluster coding sequence.  
 PN US2003194784-A1.  
 PD 16-OCT-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.  
 Query Match 5.1%; Score 50; DB 12; Length 36778;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 567  
 ID ADI23892 standard; DNA; 37360 BP.  
 DE Streptomyces fradiiae A541 locus contig 2.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 10; Length 37360;  
 Best Local Similarity 43.1%; Pred. No. 14;  
 RESULT 568  
 ID AA287285 standard; DNA; 37948 BP.  
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU) UNIV MINNESOTA.  
 Query Match 5.1%; Score 50; DB 3; Length 37948;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 569  
 ID AAA75633 standard; DNA; 38506 BP.  
 DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.  
 PN US6117659-A.

PD 12-SEP-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 3; Length 38506;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 570  
 ID AA256001 standard; DNA; 38506 BP.  
 DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.  
 PN WO9961599-A2.  
 PD 02-DEC-1999.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 3; Length 38506;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 571  
 ID ADA09418 standard; DNA; 38506 BP.  
 DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.  
 PN US6509455-B1.  
 PD 21-JAN-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 8; Length 38506;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 572  
 ID ADH53462 standard; DNA; 38506 BP.  
 DE S. venezuelae pKOS023-27 cosmid DNA.  
 PN US2003162262-A1.  
 PD 28-AUG-2003.  
 PA (ASHL/) ASHLEY G.  
 PA (BETL/) BETLACH M C.  
 PA (BETL/) BETLACH M.  
 PA (MCDA/) MCDANIEL R.  
 PA (TANG/) TANG L.  
 Query Match 5.1%; Score 50; DB 10; Length 38506;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 573  
 ID ABS56090 standard; DNA; 38506 BP.  
 DE S. venezuelae DNA inserted into cosmid pKOS023-27.  
 PN WO200297082-A2.  
 PD 05-DEC-2002.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 10; Length 38506;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 574  
 ID ABQ74179 standard; DNA; 229354 BP.  
 DE Human cytomegalovirus strain AD169 genomic sequence SEQ ID NO:64.  
 PN WO200257437-A2.  
 PD 25-JUL-2002.  
 PA (SCRI) SCRIPPS RES INST.  
 Query Match 5.1%; Score 50; DB 6; Length 229354;  
 Best Local Similarity 46.1%; Pred. No. 14;  
 RESULT 575  
 ID ABQ90211 standard; DNA; 825 BP.  
 DE M. capsulatus gene #196 for DNA array.  
 PN WO200255655-A2.  
 PD 18-JUL-2002.  
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.  
 Query Match 5.0%; Score 49.8; DB 6; Length 825;  
 Best Local Similarity 49.2%; Pred. No. 17;  
 RESULT 576  
 ID ABK34330 standard; cDNA; 856 BP.  
 DE Human cDNA for novel secreted protein, SEQ ID 99.  
 PN WO200177290-A2.  
 PD 18-OCT-2001.  
 PA (GEMV) GENETICS INST INC.  
 Query Match 5.0%; Score 49.8; DB 6; Length 856;  
 Best Local Similarity 50.5%; Pred. No. 17;  
 RESULT 577  
 ID AB266685 standard; DNA; 1272 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 32.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.0%; Score 49.8; DB 10; Length 1272;  
 Best Local Similarity 45.5%; Pred. No. 17;



RESULT 578  
ID AAD53025 standard; DNA; 1293 BP.  
DE Streptomyces platensis ema9 gene.  
PN WO200292801-A2.  
PD 21-NOV-2002.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49.8; DB 8; Length 1293;  
Best Local Similarity 48.7%; Pred. No. 17;  
RESULT 579  
ID ACA26585 standard; DNA; 1374 BP.  
DE Prokaryotic essential gene #8242.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.8; DB 8; Length 1374;  
Best Local Similarity 51.1%; Pred. No. 17;  
RESULT 580  
ID ADA70992 standard; DNA; 1458 BP.  
DE Rice gene, SEQ ID 4315.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49.8; DB 8; Length 1458;  
Best Local Similarity 48.1%; Pred. No. 17;  
RESULT 581  
ID ADI27212 standard; DNA; 1581 BP.  
DE Rabbit LRP binding family protein DNA #1.  
PN WO2003106657-A2.  
PD 24-DEC-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match 5.0%; Score 49.8; DB 12; Length 1581;  
Best Local Similarity 46.2%; Pred. No. 17;  
RESULT 582  
ID ABV94776 standard; cDNA; 1814 BP.  
DE Human pancreatic cancer expressed cDNA SEQ ID NO 182.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.8; DB 6; Length 1814;  
Best Local Similarity 47.5%; Pred. No. 17;  
RESULT 583  
ID ADP10373 standard; DNA; 1837 BP.  
DE Reference mRNA sequences for marker probe #50.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 5.0%; Score 49.8; DB 12; Length 1837;  
Best Local Similarity 47.5%; Pred. No. 17;  
RESULT 584  
ID AAF26295 standard; DNA; 2048 BP.  
DE Pseudomonas sp Type II (xcp) secretion system DNA ORF04962a.  
PN WO200107622-A2.  
PD 01-FEB-2001.  
PA (TIGR-) TIGR INST GENOMIC RES.  
PA (QUIA-) QUIAGEN GMBH.  
PA (GEF) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
Query Match 5.0%; Score 49.8; DB 4; Length 2048;  
Best Local Similarity 43.1%; Pred. No. 17;  
RESULT 585  
ID ADA71072 standard; DNA; 2136 BP.  
DE Rice gene, SEQ ID 4395.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49.8; DB 8; Length 2136;  
Best Local Similarity 47.8%; Pred. No. 17;  
RESULT 586  
ID ABL61822 standard; DNA; 2520 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:159.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (CORI-) CORIXA CORP.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
Best Local Similarity 48.7%; Pred. No. 17;  
RESULT 587  
ID ABK84011 standard; cDNA; 2520 BP.  
DE Human cDNA differentially expressed in granulocytic cells #582.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
Best Local Similarity 48.7%; Pred. No. 17;  
RESULT 588  
ID ABD16186 standard; DNA; 3003 BP.  
DE Pseudomonas aeruginosa polynucleotide #14790.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.8; DB 11; Length 3003;  
Best Local Similarity 49.1%; Pred. No. 17;  
RESULT 589  
ID AAD28566 standard; DNA; 3113 BP.  
DE Herpes simplex virus type 2 UL46frag11f5 DNA.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.8; DB 6; Length 3113;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 590  
ID ADG74980 standard; DNA; 3113 BP.  
DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 52.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.8; DB 10; Length 3113;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 591  
ID ABD15936 standard; DNA; 3132 BP.  
DE Pseudomonas aeruginosa polynucleotide #14540.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.8; DB 11; Length 3132;  
Best Local Similarity 49.1%; Pred. No. 17;  
RESULT 592  
ID AAT86704 standard; DNA; 3147 BP.  
DE DNA encoding thermostable esterase TspA E101.  
PN WO9725058-A1.  
PD 17-JUL-1997.  
PA (THER-) THERMOGEN INC.  
Query Match 5.0%; Score 49.8; DB 2; Length 3147;  
Best Local Similarity 46.4%; Pred. No. 17;  
RESULT 593  
ID AAS03399 standard; DNA; 3147 BP.  
DE Thermus DNA encoding a thermostable esterase, TspA/E101.  
PN US6218163-B1.  
PD 17-APR-2001.  
PA (THER-) THERMOGEN INC.  
Query Match 5.0%; Score 49.8; DB 4; Length 3147;  
Best Local Similarity 46.4%; Pred. No. 17;  
RESULT 594  
ID AAD28565 standard; DNA; 3345 BP.  
DE Herpes simplex virus type 2 full length HSV-2 UL37 gene.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.8; DB 6; Length 3345;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 595  
ID ADG75117 standard; DNA; 3345 BP.  
DE Human herpesvirus 2 UL37 ORF DNA - SEQ ID 189.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.



Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 596  
ID ADG74977 standard; DNA; 3345 BP.  
DE Human herpesvirus 2 UL37 DNA - SEQ ID 49.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 597  
ID ABD16219 standard; DNA; 3411 BP.  
DE Pseudomonas aeruginosa polynucleotide #14823.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.8; DB 11; Length 3411;  
Best Local Similarity 49.1%; Pred. No. 17;  
RESULT 598  
ID AD085407 standard; DNA; 3540 BP.  
DE Streptomyces Phok/Phor operon containing DNA fragment, seq id 1.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.8; DB 12; Length 3540;  
Best Local Similarity 44.5%; Pred. No. 17;  
RESULT 599  
ID AAV62148 standard; DNA; 3663 BP.  
DE HSV-2 strain SB5 Contig ID 94 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49.8; DB 2; Length 3663;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 600  
ID AC38707 standard; DNA; 4323 BP.  
DE Prokaryotic essential gene #20364.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.8; DB 8; Length 4323;  
Best Local Similarity 43.3%; Pred. No. 17;  
RESULT 601  
ID AD085409 standard; DNA; 4440 BP.  
DE Streptomyces phor:omegaac mutant, seq id 4.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.8; DB 12; Length 4440;  
Best Local Similarity 44.5%; Pred. No. 16;  
RESULT 602  
ID ABZ66810 standard; DNA; 37116 BP.  
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 10; Length 37116;  
Best Local Similarity 45.5%; Pred. No. 16;  
RESULT 603  
ID AAD17184 standard; DNA; 65140 BP.  
DE Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAEVRIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.

PA (VALL/) VALLA S.  
Query Match 5.0%; Score 49.8; DB 4; Length 65140;  
Best Local Similarity 46.4%; Pred. No. 15;  
RESULT 604  
ID AAD17186 standard; DNA; 125401 BP.  
DE Streptomyces noursei nystatin PKS gene cluster DNA.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAEVRIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 5.0%; Score 49.8; DB 4; Length 125401;  
Best Local Similarity 46.4%; Pred. No. 15;  
RESULT 605  
ID ABD03617 standard; DNA; 678 BP.  
DE Pseudomonas aeruginosa polynucleotide #2221.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.6; DB 11; Length 678;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 606  
ID ABD03778 standard; DNA; 753 BP.  
DE Pseudomonas aeruginosa polynucleotide #2382.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.6; DB 11; Length 753;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 607  
ID ACA45724 standard; DNA; 1362 BP.  
DE Prokaryotic essential gene #27381.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.6; DB 8; Length 1362;  
Best Local Similarity 48.3%; Pred. No. 18;  
RESULT 608  
ID ADB58045 standard; DNA; 1531 BP.  
DE Toxicity-related gene, SEQ ID 3071.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.6; DB 10; Length 1531;  
Best Local Similarity 47.2%; Pred. No. 18;  
RESULT 609  
ID ADB52519 standard; DNA; 1531 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.6; DB 10; Length 1531;  
Best Local Similarity 47.2%; Pred. No. 18;  
RESULT 610  
ID AAQ13305 standard; DNA; 1591 BP.  
DE Rat catechol-O-methyltransferase gene.  
PN WO9111513-A.  
PD 08-AUG-1991.  
PA (ORIN) ORION YHTYMAE OY.  
Query Match 5.0%; Score 49.6; DB 2; Length 1591;  
Best Local Similarity 47.2%; Pred. No. 18;  
RESULT 611  
ID ADG75153 standard; DNA; 1765 BP.  
DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 225.  
PN WO2003086308-A2.



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PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP. 5.0%; Score 49.6; DB 10; Length 1765;  
 Query Match  
 Best Local Similarity 45.6%; Pred. No. 18;  
 RESULT 612  
 ID AAS51445 standard; DNA; 2040 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #30.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 44.6%; Pred. No. 18;  
 RESULT 613  
 ID ACA19446 standard; DNA; 2040 BP.  
 DE Prokaryotic essential gene #1103.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 44.6%; Pred. No. 18;  
 RESULT 614  
 ID ADM03489 standard; cDNA; 2218 BP.  
 DE Human cDNA of the invention SEQ ID NO:2174.  
 PN EP1347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match  
 Best Local Similarity 43.5%; Pred. No. 18;  
 RESULT 615  
 ID ABZ35021 standard; cDNA; 2271 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 133.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Query Match  
 Best Local Similarity 47.2%; Pred. No. 18;  
 RESULT 616  
 ID ADR75311 standard; cDNA; 2487 BP.  
 DE Prostate cancer marker cDNA.  
 PN WO2003009814-A2.  
 PD 06-FEB-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 10; Length 2487;  
 RESULT 617  
 ID AAS51581 standard; DNA; 2742 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #166.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 44.8%; Pred. No. 18;  
 RESULT 618  
 ID ACA19538 standard; DNA; 2742 BP.  
 DE Prokaryotic essential gene #1195.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 44.8%; Pred. No. 18;  
 RESULT 619  
 ID ABD03933 standard; DNA; 2814 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2537.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 11; Length 2814;  
 RESULT 620  
 ID ADJ67856 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004038289-A1.  
 PD 26-FEB-2004.

PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 621  
 ID ADJ68068 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004038290-A1.  
 PD 26-FEB-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 622  
 ID ADK01146 standard; DNA; 3729 BP.  
 DE DNA polymerase III-type enzyme subunit DNA #6.  
 PN US2004043415-A1.  
 PD 04-MAR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 623  
 ID ADJ79365 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004043414-A1.  
 PD 04-MAR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 624  
 ID ADJ84805 standard; DNA; 3729 BP.  
 DE T. thermophilus DNA polymerase III alpha subunit gene.  
 PN US2004048309-A1.  
 PD 11-MAR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 625  
 ID ADM77593 standard; DNA; 3729 BP.  
 DE DNA polymerase III-type enzyme related polynucleotide #4.  
 PN US2004077012-A1.  
 PD 22-APR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 626  
 ID ADJ79365 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004043414-A1.  
 PD 04-MAR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 627  
 ID ADJ84805 standard; DNA; 3729 BP.  
 DE T. thermophilus DNA polymerase III alpha subunit gene.  
 PN US2004048309-A1.  
 PD 11-MAR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 628  
 ID ADM77593 standard; DNA; 3729 BP.  
 DE DNA polymerase III-type enzyme related polynucleotide #4.  
 PN US2004077012-A1.  
 PD 22-APR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match  
 Best Local Similarity 5.0%; Score 49.6; DB 12; Length 3729;  
 RESULT 629  
 ID ADJ79365 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004043414-A1.  
 PD 04-MAR-2004.



RESULT 626  
 ID ADM66260 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004081995-A1.  
 PD 29-APR-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
 Best Local Similarity 44.7%; Pred. No. 18;  
 RESULT 627  
 ID ADO04313 standard; DNA; 3729 BP.  
 DE T. thermophilus DNA polymerase III dnaE gene.  
 PN US2004106137-A1.  
 PD 03-JUN-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
 Best Local Similarity 44.7%; Pred. No. 18;  
 RESULT 628  
 ID ADP82390 standard; DNA; 3729 BP.  
 DE Thermus thermophilus dnaE gene.  
 PN US2004110210-A1.  
 PD 10-JUN-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
 Best Local Similarity 44.7%; Pred. No. 18;  
 RESULT 629  
 ID ABN59919 standard; cDNA; 5080 BP.  
 DE Novel human coding sequence SEQ ID NO: 330.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.0%; Score 49.6; DB 6; Length 5080;  
 Best Local Similarity 44.2%; Pred. No. 18;  
 RESULT 630  
 ID ADP82340 standard; DNA; 5081 BP.  
 DE Leukaemia-related DNA sequence #2896.  
 PN WO2003039443-A2.  
 PD 15-MAY-2003.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
 PA (HAFE-) HAFERLACH T.  
 PA (SCHO/) SCHOCH C.  
 PA (KERN/) KERN W.  
 Query Match 5.0%; Score 49.6; DB 10; Length 5081;  
 Best Local Similarity 44.2%; Pred. No. 18;  
 RESULT 631  
 ID ABU68935 standard; DNA; 5181 BP.  
 DE Kidney cancer related gene sequence SEQ ID NO: 7272.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 5.0%; Score 49.6; DB 6; Length 5181;  
 Best Local Similarity 47.2%; Pred. No. 18;  
 RESULT 632  
 ID ADJ11677 standard; DNA; 951 BP.  
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 313.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVANT N.  
 PA (RICK/) RICKE D.  
 Query Match 5.0%; Score 49.4; DB 11; Length 951;  
 Best Local Similarity 44.3%; Pred. No. 20;  
 RESULT 633  
 ID ABZ37556 standard; DNA; 1029 BP.  
 DE Streptomyces viridochromogenes AviG74 encoding polynucleotide.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Query Match 5.0%; Score 49.4; DB 8; Length 1029;  
 Best Local Similarity 47.8%; Pred. No. 20;  
 RESULT 634  
 ID ADP88594 standard; DNA; 1149 BP.  
 DE Human POU domain factor Brn3a gene exon 2.  
 PN WO2004052186-A2.  
 PD 24-JUN-2004.  
 PA (FORS-) FORSYTH INST.  
 Query Match 5.0%; Score 49.4; DB 12; Length 1149;  
 Best Local Similarity 46.7%; Pred. No. 20;  
 RESULT 635  
 ID ACA38093 standard; DNA; 1173 BP.  
 DE Prokaryotic essential gene #19750.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.4; DB 8; Length 1173;  
 Best Local Similarity 45.2%; Pred. No. 20;  
 RESULT 636  
 ID ACA27337 standard; DNA; 1191 BP.  
 DE Prokaryotic essential gene #8994.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.4; DB 8; Length 1191;  
 Best Local Similarity 53.8%; Pred. No. 20;  
 RESULT 637  
 ID AAX09010 standard; cDNA; 1272 BP.  
 DE Brn-3a polynucleotide.  
 PN WO9905272-A1.  
 PD 04-FEB-1999.  
 PA (UNLO) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.4; DB 2; Length 1272;  
 Best Local Similarity 46.7%; Pred. No. 20;  
 RESULT 638  
 ID AAZ9006 standard; cDNA; 1272 BP.  
 DE Human transcription factor Brn-3a coding sequence.  
 PN WO20034466-A1.  
 PD 15-JUN-2000.  
 PA (UNLO) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.4; DB 3; Length 1272;  
 Best Local Similarity 46.7%; Pred. No. 20;  
 RESULT 639  
 ID ADM80093 standard; DNA; 1398 BP.  
 DE Spiramycin biosynthesis orf13c, SEQ ID 60.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Query Match 5.0%; Score 49.4; DB 12; Length 1398;  
 Best Local Similarity 45.0%; Pred. No. 20;  
 RESULT 640  
 ID ADN97609 standard; DNA; 1398 BP.  
 DE S ambofaciens spiramycin biosynthetic gene ORF13c.



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PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET ) AVENTIS PHARMA SA.
PA (CNRS ) CNRS.
Query Match 5.0%; Score 49.4; DB 12; Length 1398;
Best Local Similarity 45.0%; Pred. No. 20;
RESULT 641
ID ABD01548 standard; DNA; 1419 BP.
DE Pseudomonas aeruginosa polynucleotide #152.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1419;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 642
ID ACA40703 standard; DNA; 1587 BP.
DE Prokaryotic essential gene #22360.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 1587;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 643
ID ACA38400 standard; DNA; 1590 BP.
DE Prokaryotic essential gene #20057.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 1590;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 644
ID ABD01553 standard; DNA; 1692 BP.
DE Pseudomonas aeruginosa polynucleotide #157.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1692;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 645
ID ABD01582 standard; DNA; 1698 BP.
DE Pseudomonas aeruginosa polynucleotide #186.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1698;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 646
ID AAT40082 standard; DNA; 1724 BP.
DE M. tuberculosis RNA polymerase Group I sigma subunit sigA gene.
PN GB2298862-A.
PD 18-SEP-1996.
PA (ASTR ) ASTRA AB.
Query Match 5.0%; Score 49.4; DB 2; Length 1724;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 647
ID ADG75006 standard; DNA; 2091 BP.
DE Human herpesvirus 2 UL47 DNA - SEQ ID 78.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2091;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 648
ID ADG75154 standard; DNA; 2091 BP.
DE Human herpesvirus 2 strain HG52 UL47 DNA - SEQ ID 226.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2091;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 649
ID ADG75015 standard; DNA; 2118 BP.
DE Human herpesvirus 2 UL47 coding region DNA - SEQ ID 87.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2118;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 650
ID ADG75014 standard; DNA; 2211 BP.
DE Human herpesvirus 2 UL47-His construct DNA - SEQ ID 86.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2211;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 651
ID AAV22682 standard; DNA; 2214 BP.
DE New DNA sequence isolated from Pinctada fucata.
PN JPI0080285-A.
PD 31-MAR-1998.
PA (MIKI-) MIKIMOTO SEIYAKU KK.
Query Match 5.0%; Score 49.4; DB 2; Length 2214;
Best Local Similarity 47.1%; Pred. No. 20;
RESULT 652
ID ADC30095 standard; cDNA; 2382 BP.
DE Human novel cDNA sequence, SEQ ID NO:177.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 49.4; DB 10; Length 2382;
Best Local Similarity 45.6%; Pred. No. 20;
RESULT 653
ID ACA30032 standard; DNA; 2502 BP.
DE Prokaryotic essential gene #11689.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 2502;
Best Local Similarity 55.6%; Pred. No. 20;
RESULT 654
ID AAQ92657 standard; DNA; 2745 BP.
DE Virulence determinant rpoV gene.
PN WO9517511-A2.
PD 29-JUN-1995.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 655
ID AAQ92656 standard; DNA; 2745 BP.
DE Virulence determinant rpoV gene.
PN WO9517511-A2.
PD 29-JUN-1995.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 656
ID AAV38109 standard; DNA; 2745 BP.
DE Mycobacterium bovis large ORF WAG200 DNA sequence.
PN US5783386-A.
PD 21-JUL-1998.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 657
ID AAV38108 standard; DNA; 2745 BP.
DE Mycobacterium bovis virulence restoring DNA sequence.
PN US5783386-A.
PD 21-JUL-1998.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
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RESULT 658  
 ID AAS14697 standard; DNA; 3038 BP.  
 DE Human cDNA encoding neuroendocrine VGF.  
 PN WO200174298-A2.  
 PD 11-OCT-2001.  
 PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
 PA (HUGH-) HUGHES HOWARD MED INST.  
 Query Match 5.0%; Score 49.4; DB 4; Length 3038;  
 Best Local Similarity 44.2%; Pred. No. 19;  
 RESULT 659  
 ID ADD14800 standard; cDNA; 3038 BP.  
 DE Human src biomarker polynucleotide SEQ ID NO:194.  
 PN WO2003062395-A2.  
 PD 31-JUL-2003.  
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
 Query Match 5.0%; Score 49.4; DB 10; Length 3038;  
 Best Local Similarity 44.2%; Pred. No. 19;  
 RESULT 660  
 ID AAV22683 standard; cDNA to mRNA; 3331 BP.  
 DE New DNA sequence isolated from Pinctada fucata.  
 PN JP10080285-A.  
 PD 31-MAR-1998.  
 PA (MIKI-) MIKIMOTO SEIYAKU KK.  
 Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
 Best Local Similarity 47.1%; Pred. No. 19;  
 RESULT 661  
 ID AA232021 standard; DNA; 3331 BP.  
 DE Human METH1 related EST D86074.  
 PN WO9937660-A1.  
 PD 29-JUL-1999.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
 Best Local Similarity 47.1%; Pred. No. 19;  
 RESULT 662  
 ID AAC90078 standard; DNA; 3331 BP.  
 DE D86074 cDNA clone.  
 PN WO200071577-A1.  
 PD 30-NOV-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK-) SMITHKLINE BEECHAM CORP.  
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 PA (JONA/) JONAK Z L.  
 PA (TRUL/) TRULLI S H.  
 PA (FORN/) FORNWALD J A.  
 PA (TERR/) TERRETT J A.  
 Query Match 5.0%; Score 49.4; DB 5; Length 3331;  
 Best Local Similarity 47.1%; Pred. No. 19;  
 RESULT 663  
 ID AA30290 standard; DNA; 3489 BP.  
 DE Kaposi's sarcoma-associated herpesvirus LANA gene.  
 PN WO20029626-A1.  
 PD 25-MAY-2000.  
 PA (KIEF/) KIEFF E D.  
 PA (BALL/) BALLESTAS M E.  
 PA (KAYE/) KAYE K M.  
 Query Match 5.0%; Score 49.4; DB 3; Length 3489;  
 Best Local Similarity 42.9%; Pred. No. 19;  
 RESULT 664  
 ID AAF82901 standard; DNA; 3489 BP.  
 DE Nucleotide sequence of KSHV tethering protein, LANA.  
 PN WO200125484-A2.  
 PD 12-APR-2001.  
 PA (UNMI-) UNIV MICHIGAN.  
 Query Match 5.0%; Score 49.4; DB 4; Length 3489;  
 Best Local Similarity 42.9%; Pred. No. 19;  
 RESULT 665  
 ID ABA93487 standard; DNA; 3489 BP.  
 DE Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA.

PN US6322792-B1.  
 PD 27-NOV-2001.  
 PA (KIEF/) KIEFF E D.  
 Query Match 5.0%; Score 49.4; DB 6; Length 3489;  
 Best Local Similarity 42.9%; Pred. No. 19;  
 RESULT 666  
 ID ADJ65095 standard; DNA; 3489 BP.  
 DE HHV8 DNA encoding latency-associated nuclear antigen, LANA.  
 PN US2004037847-A1.  
 PD 26-FEB-2004.  
 PA (KIEF/) KIEFF E D.  
 PA (BALL/) BALLESTAS M E.  
 PA (KAYE/) KAYE K M.  
 Query Match 5.0%; Score 49.4; DB 12; Length 3489;  
 Best Local Similarity 42.9%; Pred. No. 19;  
 RESULT 667  
 ID ACA27005 standard; DNA; 4255 BP.  
 DE prokaryotic essential gene #8662.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.4; DB 8; Length 4255;  
 Best Local Similarity 45.5%; Pred. No. 19;  
 RESULT 668  
 ID AAV33912 standard; cDNA; 4524 BP.  
 DE Nucleotide sequence of the SIAx DP2-64 (Oct-T1) gene.  
 PN WO9849299-A1.  
 PD 05-NOV-1998.  
 PA (LUDM-) LUDWIG INST CANCER RES.  
 Query Match 5.0%; Score 49.4; DB 2; Length 4524;  
 Best Local Similarity 47.5%; Pred. No. 19;  
 RESULT 669  
 ID AAV62152 standard; DNA; 10211 BP.  
 DE HSV-2 strain SB5 Contig ID 99 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK-) SMITHKLINE BEECHAM CORP.  
 Query Match 5.0%; Score 49.4; DB 2; Length 10211;  
 Best Local Similarity 45.8%; Pred. No. 19;  
 RESULT 670  
 ID ABV93363 standard; DNA; 14061 BP.  
 DE Human NOV13b coding sequence.  
 PN WO200272771-A2.  
 PD 19-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.0%; Score 49.4; DB 6; Length 14061;  
 Best Local Similarity 44.7%; Pred. No. 19;  
 RESULT 671  
 ID AAV73805 standard; DNA; 32207 BP.  
 DE KSHV LUR DNA (nucleotides 105,301-137,507).  
 PN US5849564-A.  
 PD 15-DEC-1998.  
 PA (UYCO-) UNIV COLUMBIA NEW YORK.  
 Query Match 5.0%; Score 49.4; DB 2; Length 32207;  
 Best Local Similarity 42.9%; Pred. No. 18;  
 RESULT 672  
 ID ADO51695 standard; DNA; 32329 BP.  
 DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
 PN US2004038250-A1.  
 PD 26-FEB-2004.  
 PA (ASTU-) ASTUR-PHARMA SA.  
 PA (UYOV-) UNIV OVIEDO.  
 Query Match 5.0%; Score 49.4; DB 12; Length 32329;  
 Best Local Similarity 44.7%; Pred. No. 18;  
 RESULT 673  
 ID AB237516 standard; DNA; 59816 BP.  
 DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
 Best Local Similarity 47.8%; Pred. No. 18;  
 RESULT 674



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ID ABZ37515 standard; DNA; 59816 BP.  
DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
Best Local Similarity 47.8%; Pred. No. 18;  
RESULT 675  
ID ABX04971 standard; DNA; 103599 BP.  
DE S. cinnamomensis monensin type I polyketide synthase gene cluster.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 18;  
RESULT 676  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 18;  
RESULT 677  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 18;  
RESULT 678  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 18;  
RESULT 679  
ID AAV19941 standard; DNA; 137507 BP.  
DE KSHV long unique coding region and terminal repeat.  
PN WO9804576-A1.  
PD 05-FEB-1998.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 5.0%; Score 49.4; DB 2; Length 137507;  
Best Local Similarity 42.9%; Pred. No. 17;  
RESULT 680  
ID ADN12162 standard; DNA; 137508 BP.  
DE Human herpesvirus 8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match 5.0%; Score 49.4; DB 12; Length 137508;  
Best Local Similarity 42.9%; Pred. No. 17;  
RESULT 681  
ID ABD17309 standard; DNA; 789 BP.  
DE Pseudomonas aeruginosa polynucleotide #15913.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 789;  
Best Local Similarity 48.3%; Pred. No. 22;  
RESULT 682  
ID ABD13248 standard; DNA; 795 BP.  
DE Pseudomonas aeruginosa polynucleotide #11852.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 795;  
Best Local Similarity 46.1%; Pred. No. 22;  
RESULT 683  
ID ABD17908 standard; DNA; 888 BP.  
DE Pseudomonas aeruginosa polynucleotide #16512.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 888;  
Best Local Similarity 50.7%; Pred. No. 22;  
RESULT 684  
ID AAS72681 standard; cDNA; 1074 BP.  
DE DNA encoding novel human diagnostic protein #8485.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. 5.0%; Score 49.2; DB 5; Length 1074;  
Query Match

Best Local Similarity 42.4%; Pred. No. 22;  
RESULT 685  
ID ABD12927 standard; DNA; 1221 BP.  
DE Pseudomonas aeruginosa polynucleotide #11531.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1221;  
Best Local Similarity 46.1%; Pred. No. 22;  
RESULT 686  
ID ABD15054 standard; DNA; 1263 BP.  
DE Pseudomonas aeruginosa polynucleotide #13658.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
Best Local Similarity 45.6%; Pred. No. 22;  
RESULT 687  
ID ABD14863 standard; DNA; 1263 BP.  
DE Pseudomonas aeruginosa polynucleotide #13467.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
Best Local Similarity 45.6%; Pred. No. 22;  
RESULT 688  
ID AAX09011 standard; cDNA; 1266 BP.  
DE Brn-3a polynucleotide.  
PN WO9905272-A1.  
PD 04-FEB-1999.  
PA (UNIO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.2; DB 2; Length 1266;  
Best Local Similarity 47.4%; Pred. No. 22;  
RESULT 689  
ID AAA29007 standard; cDNA; 1266 BP.  
DE Murine transcription factor Brn-3a coding sequence.  
PN WO200034466-A1.  
PD 15-JUN-2000.  
PA (UNIO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.2; DB 3; Length 1266;  
Best Local Similarity 47.4%; Pred. No. 22;  
RESULT 690  
ID ABD17488 standard; DNA; 1512 BP.  
DE Pseudomonas aeruginosa polynucleotide #16092.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1512;  
Best Local Similarity 50.7%; Pred. No. 21;  
RESULT 691  
ID ABD17174 standard; DNA; 1521 BP.  
DE Pseudomonas aeruginosa polynucleotide #15778.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1521;  
Best Local Similarity 48.3%; Pred. No. 21;  
RESULT 692  
ID ABD17253 standard; DNA; 1569 BP.  
DE Pseudomonas aeruginosa polynucleotide #15857.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 1569;  
Best Local Similarity 48.3%; Pred. No. 21;  
RESULT 693  
ID AAD11112 standard; DNA; 1602 BP.  
DE Human small cell lung cancer associated gene, ZIC2.  
PN WO200153349-A2.  
PD 26-JUL-2001.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
PA (CORR) CORNELL RES FOUND INC.



Query Match 5.0%; Score 49.2; DB 4; Length 1602;  
Best Local Similarity 53.0%; Pred. No. 21;  
RESULT 694  
ID AAS61863 standard; cDNA; 1602 BP.  
DE Lung small cell carcinoma antigen, cDNA #404.  
PN WO200177168-A2.  
PD 18-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.2; DB 6; Length 1602;  
Best Local Similarity 53.0%; Pred. No. 21;  
RESULT 695  
ID ADD15207 standard; DNA; 1602 BP.  
DE DNA encoding the human zinc finger protein ZIC2.  
PN WO2003039490-A2.  
PD 15-MAY-2003.  
PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.  
Query Match 5.0%; Score 49.2; DB 10; Length 1602;  
Best Local Similarity 53.0%; Pred. No. 21;  
RESULT 696  
ID ADQ03085 standard; DNA; 1713 BP.  
DE P. aeruginosa virulence gene, VIR17.  
PN US2004122212-A1.  
PD 24-JUN-2004.  
PA (COSS/) COSSON P.  
PA (KOH/) KOHLER T.  
PA (BENG/) BENGHEZAL M.  
PA (MARC/) MARCHETTI A.  
PA (DELD/) DELDEN C V.  
Query Match 5.0%; Score 49.2; DB 12; Length 1713;  
Best Local Similarity 43.8%; Pred. No. 21;  
RESULT 697  
ID ADP88591 standard; DNA; 2160 BP.  
DE Murine class V POU transcription factor Brn3a gene.  
PN WO2004052186-A2.  
PD 24-JUN-2004.  
PA (FORS-) FORSYTH INST.  
Query Match 5.0%; Score 49.2; DB 12; Length 2160;  
Best Local Similarity 47.4%; Pred. No. 21;  
RESULT 698  
ID ABD17387 standard; DNA; 2400 BP.  
DE Pseudomonas aeruginosa polynucleotide #15991.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.2; DB 11; Length 2400;  
Best Local Similarity 50.7%; Pred. No. 21;  
RESULT 699  
ID ABR63479 standard; cDNA; 2455 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1386.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.2; DB 6; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 700  
ID ADB58687 standard; DNA; 2455 BP.  
DE Toxicity-related gene, SEQ ID 3713.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.2; DB 10; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 701  
ID ADB53374 standard; DNA; 2455 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3916.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.2; DB 10; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 702  
ID ADF30464 standard; cDNA; 2455 BP.  
DE Rat angiogenesis modulating protein cDNA #9.

PN US2003162706-A1.  
PD 28-AUG-2003.  
PA (PROC) PROCTER & GAMBLE CO.  
Query Match 5.0%; Score 49.2; DB 10; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 703  
ID ABR42262 standard; DNA; 2455 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1964.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.2; DB 10; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 704  
ID ADP72601 standard; DNA; 2455 BP.  
DE Renal toxin progression gene marker #1190.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.0%; Score 49.2; DB 12; Length 2455;  
Best Local Similarity 43.7%; Pred. No. 21;  
RESULT 705  
ID ADE25609 standard; cDNA; 2607 BP.  
DE Human cDNA differentially expressed in foam cells #13.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.0%; Score 49.2; DB 10; Length 2607;  
Best Local Similarity 42.4%; Pred. No. 21;  
RESULT 706  
ID ADK70215 standard; cDNA; 2680 BP.  
DE Human oesophageal cancer antigen cDNA SEQ ID NO:11.  
PN JP2003259872-A.  
PD 16-SEP-2003.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 5.0%; Score 49.2; DB 12; Length 2680;  
Best Local Similarity 53.0%; Pred. No. 21;  
RESULT 707  
ID ADQ25191 standard; DNA; 2717 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8011.  
PN WO2004048918-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.0%; Score 49.2; DB 12; Length 2717;  
Best Local Similarity 53.0%; Pred. No. 21;  
RESULT 708  
ID ABA02191 standard; cDNA; 3318 BP.  
DE Human C/EBP alpha-encoding cDNA.  
PN US6306655-B1.  
PD 23-OCT-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 5.0%; Score 49.2; DB 6; Length 3318;  
Best Local Similarity 42.4%; Pred. No. 21;  
RESULT 709  
ID ADI39068 standard; DNA; 3597 BP.  
DE S. coelicolor meth DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI) BASF AG.  
Query Match 5.0%; Score 49.2; DB 10; Length 3597;  
Best Local Similarity 47.0%; Pred. No. 21;  
RESULT 710  
ID ADI39145 standard; DNA; 8787 BP.  
DE Plasmid pCPshd meth\_Sc DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI) BASF AG.  
Query Match 5.0%; Score 49.2; DB 10; Length 8787;  
Best Local Similarity 47.0%; Pred. No. 20;  
RESULT 711  
ID ABI50991 standard; DNA; 35133 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 nucleotide sequence.  
PN KR2001019888-A.



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PA (OTOG-) OTOGENE AG.  
Query Match 5.0%; Score 49; DB 6; Length 1355;  
Best Local Similarity 50.2%; Pred. No. 23;  
RESULT 721  
ID AAH26499 standard; DNA; 1614 BP.  
DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.0%; Score 49; DB 5; Length 1614;  
Best Local Similarity 43.7%; Pred. No. 23;  
RESULT 722  
ID ABS58306 standard; cDNA; 1852 BP.  
DE Spider dragline cDNA repetitive nucleotide sequence.  
PN US2002137211-A1.  
PD 26-SEP-2002.  
PA (YISI-) UNIV SICHUAN TIANYOU BIOLOGIC ENG CO LTD.  
Query Match 5.0%; Score 49; DB 10; Length 1852;  
Best Local Similarity 46.6%; Pred. No. 23;  
RESULT 723  
ID ADM47862 standard; DNA; 1891 BP.  
DE Polynucleotide sequence #280 useful in producing transgenic plants.  
PN US200233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 5.0%; Score 49; DB 12; Length 1891;  
Best Local Similarity 50.6%; Pred. No. 23;  
RESULT 724  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49; DB 8; Length 2000;  
Best Local Similarity 9.7%; Pred. No. 23;  
RESULT 725  
ID AAH98717 standard; cDNA; 4486 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 574.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49; DB 4; Length 4486;  
Best Local Similarity 47.5%; Pred. No. 22;  
RESULT 726  
ID AAV62153 standard; DNA; 7361 BP.  
DE HSV-2 strain SB5 Contig ID 1 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49; DB 2; Length 7361;  
Best Local Similarity 42.8%; Pred. No. 22;  
RESULT 727  
ID AAV62130 standard; DNA; 8952 BP.  
DE HSV-2 strain SB5 Contig ID 100 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49; DB 2; Length 8952;  
Best Local Similarity 42.8%; Pred. No. 22;  
RESULT 728  
ID AAL61171 standard; DNA; 9222 BP.  
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 5.0%; Score 49; DB 8; Length 9222;  
Best Local Similarity 46.0%; Pred. No. 22;  
RESULT 729  
ID AAH26495 standard; DNA; 12425 BP.  
DE Human low density lipoprotein binding protein 2 (LBP-2) gene.  
PN WO200164874-A2.

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match 5.0%; Score 49.2; DB 4; Length 35133;  
Best Local Similarity 44.4%; Pred. No. 20;  
RESULT 712  
ID AB150990 standard; DNA; 35134 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 SEQ ID NO:1.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match 5.0%; Score 49.2; DB 4; Length 35134;  
Best Local Similarity 44.4%; Pred. No. 20;  
RESULT 713  
ID ADP74816 standard; DNA; 137560 BP.  
DE Parapoxvirus ovis genome DNA sequence Seg1D1.  
PN US2002079465-A2.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 5.0%; Score 49; DB 10; Length 399;  
Best Local Similarity 57.5%; Pred. No. 24;  
RESULT 715  
ID ADD41850 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #1.  
PN US2003113173-A1.  
PD 10-JUL-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 5.0%; Score 49; DB 3; Length 399;  
Best Local Similarity 57.5%; Pred. No. 24;  
RESULT 716  
ID ACA37827 standard; DNA; 717 BP.  
DE Prokaryotic essential gene #19484.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49; DB 8; Length 717;  
Best Local Similarity 44.8%; Pred. No. 24;  
RESULT 717  
ID ABX56042 standard; DNA; 843 BP.  
DE M. echinospora calicheamicin biosynthesis gene calR.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 5.0%; Score 49; DB 8; Length 843;  
Best Local Similarity 47.9%; Pred. No. 23;  
RESULT 718  
ID AAZ51697 standard; DNA; 1044 BP.  
DE Burkholderia cepacia reca gene (1).  
PN WO200014274-A1.  
PD 16-MAR-2000.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 5.0%; Score 49; DB 3; Length 1044;  
Best Local Similarity 43.8%; Pred. No. 23;  
RESULT 719  
ID AAT44494 standard; cDNA; 1355 BP.  
DE Murine cyclin-dependent kinase inhibitor p57KIP2 cDNA.  
PN WO9631534-A1.  
PD 10-OCT-1996.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 5.0%; Score 49; DB 2; Length 1355;  
Best Local Similarity 50.2%; Pred. No. 23;  
RESULT 720  
ID AAI72395 standard; cDNA; 1355 BP.  
DE P57-KIP2 cDNA.  
PN WO200204605-A2.  
PD 17-JAN-2002.  
PA (OTOG-) OTOGENE USA INC.



PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.0%; Score 49; DB 5; Length 12425;  
Best Local Similarity 43.7%; Pred. No. 22;  
RESULT 730  
ID AAA14651 standard; DNA; 77536 BP.  
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
Query Match 5.0%; Score 49; DB 3; Length 77536;  
Best Local Similarity 44.4%; Pred. No. 21;  
RESULT 731  
Query Match 5.0%; Score 49; DB 4; Length 110000;  
Best Local Similarity 50.6%; Pred. No. 21;  
RESULT 732  
Query Match 5.0%; Score 49; DB 4; Length 110000;  
Best Local Similarity 45.0%; Pred. No. 21;  
RESULT 733  
Query Match 5.0%; Score 49; DB 4; Length 110000;  
Best Local Similarity 45.0%; Pred. No. 21;  
RESULT 734  
ID AAV62176 standard; DNA; 117213 BP.  
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
Query Match 5.0%; Score 49; DB 2; Length 117213;  
Best Local Similarity 42.8%; Pred. No. 20;  
RESULT 735  
ID ABD09003 standard; DNA; 852 BP.  
DE Pseudomonas aeruginosa polynucleotide #7607.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 852;  
Best Local Similarity 49.2%; Pred. No. 25;  
RESULT 736  
ID ABD10213 standard; DNA; 1083 BP.  
DE Pseudomonas aeruginosa polynucleotide #8817.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 1083;  
Best Local Similarity 50.3%; Pred. No. 25;  
RESULT 737  
ID ADC36141 standard; DNA; 1188 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:8.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 4.9%; Score 48.8; DB 10; Length 1188;  
Best Local Similarity 47.1%; Pred. No. 25;  
RESULT 738  
ID ACF06125 standard; DNA; 1194 BP.  
DE Bacterial P450 enzyme encoding DNA SEQ ID NO:33.  
PN WO2003052050-A2.  
PD 26-JUN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 4.9%; Score 48.8; DB 9; Length 1194;  
Best Local Similarity 44.8%; Pred. No. 25;  
RESULT 739  
ID AAS09830 standard; DNA; 1209 BP.  
DE Pseudorabies virus DNA encoding glycoprotein 50, gp50.  
PN US6251634-B1.  
PD 26-JUN-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 4.9%; Score 48.8; DB 4; Length 1209;  
Best Local Similarity 44.9%; Pred. No. 25;  
RESULT 740  
ID ABD10628 standard; DNA; 1227 BP.  
DE Pseudomonas aeruginosa polynucleotide #9232.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 1227;  
Best Local Similarity 50.3%; Pred. No. 25;  
RESULT 741  
ID ABZ66800 standard; DNA; 1272 BP.

DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 262.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.8; DB 10; Length 1272;  
Best Local Similarity 47.6%; Pred. No. 25;  
RESULT 742  
ID ABD10546 standard; DNA; 1296 BP.  
DE Pseudomonas aeruginosa polynucleotide #9150.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 1296;  
Best Local Similarity 50.3%; Pred. No. 25;  
RESULT 743  
ID ADC36144 standard; DNA; 1418 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:11.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 4.9%; Score 48.8; DB 10; Length 1418;  
Best Local Similarity 47.1%; Pred. No. 25;  
RESULT 744  
ID ADC36202 standard; DNA; 1418 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:69.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 4.9%; Score 48.8; DB 10; Length 1418;  
Best Local Similarity 47.1%; Pred. No. 25;  
RESULT 745  
ID ACC47259 standard; cDNA; 1427 BP.  
DE Human SCAP encoding cDNA-Incyte Id. 6891852CB1.  
PN WO2003008625-A2.  
PD 30-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.9%; Score 48.8; DB 8; Length 1427;  
Best Local Similarity 48.0%; Pred. No. 25;  
RESULT 746  
ID ABD13152 standard; DNA; 2232 BP.  
DE Pseudomonas aeruginosa polynucleotide #11756.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 2232;  
Best Local Similarity 43.4%; Pred. No. 25;  
RESULT 747  
ID ABD13005 standard; DNA; 2274 BP.  
DE Pseudomonas aeruginosa polynucleotide #11609.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 2274;  
Best Local Similarity 43.4%; Pred. No. 25;  
RESULT 748  
ID ABD13232 standard; DNA; 2613 BP.  
DE Pseudomonas aeruginosa polynucleotide #11836.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 2613;  
Best Local Similarity 43.4%; Pred. No. 25;  
RESULT 749  
ID ABD10111 standard; DNA; 2715 BP.  
DE Pseudomonas aeruginosa polynucleotide #8715.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.8; DB 11; Length 2715;  
Best Local Similarity 50.3%; Pred. No. 25;  
RESULT 750  
ID ABX93509 standard; DNA; 4826 BP.  
DE DNA fragment containing poly-beta-hydroxybutyrate, PHB, synthesis genes.



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PN US2002146785-A1.
PD 10-OCT-2002.
PA (MAHI/) MAHISHI L H.
PA (TRIP/) TRIPATHI G.
PA (RAMC/) RAMCHANDER T V N.
PA (RAWA/) RAWAL S K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 8; Length 4826;
Best Local Similarity 45.7%; Pred. No. 24;

RESULT 751
ID ABK91609 standard; DNA; 7897 BP.
DE Modified HIV protein-encoding plasmid DNA #161.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 7897;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 752
ID ABK91616 standard; DNA; 9166 BP.
DE Modified HIV protein-encoding plasmid DNA #168.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9166;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 753
ID ABK91619 standard; DNA; 9167 BP.
DE Modified HIV protein-encoding plasmid DNA #171.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9167;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 754
ID ABK91617 standard; DNA; 9169 BP.
DE Modified HIV protein-encoding plasmid DNA #169.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9169;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 755
ID ABK91614 standard; DNA; 9170 BP.
DE Modified HIV protein-encoding plasmid DNA #166.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9170;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 756
ID ABK91607 standard; DNA; 9189 BP.
DE Modified HIV protein-encoding plasmid DNA #159.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9189;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 757
ID ABK91612 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #164.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 24;

ID ABK91611 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #165.
PN WO200232943-A2.

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DE Modified HIV protein-encoding plasmid DNA #163.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 759
ID ABK91623 standard; DNA; 9407 BP.
DE Modified HIV protein-encoding plasmid DNA #175.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9407;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 760
ID ABK91621 standard; DNA; 9782 BP.
DE Modified HIV protein-encoding plasmid DNA #173.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9782;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 761
ID ABK91620 standard; DNA; 9783 BP.
DE Modified HIV protein-encoding plasmid DNA #172.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9783;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 762
ID ABK91624 standard; DNA; 9785 BP.
DE Modified HIV protein-encoding plasmid DNA #176.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9785;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 763
ID ABK91622 standard; DNA; 9788 BP.
DE Modified HIV protein-encoding plasmid DNA #174.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9788;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 764
ID ABK91618 standard; DNA; 9792 BP.
DE Modified HIV protein-encoding plasmid DNA #170.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9792;
Best Local Similarity 47.9%; Pred. No. 24;

RESULT 765
ID ABZ66813 standard; DNA; 10035 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 282.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 10035;
Best Local Similarity 47.6%; Pred. No. 24;

RESULT 766
ID ABK91613 standard; DNA; 12411 BP.
DE Modified HIV protein-encoding plasmid DNA #165.
PN WO200232943-A2.

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PD 25-APR-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (CHAD/) CHADABARTI B K.  
Query Match 4.9%; Score 48.8; DB 6; Length 12411;  
Best Local Similarity 47.9%; Pred. No. 24;  
RESULT 767  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PD WO20027179-A2.  
PD 03-OCT-2002.  
PA (REGC ) UNIV CALIFORNIA.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 4.9%; Score 48.8; DB 10; Length 135638;  
Best Local Similarity 44.7%; Pred. No. 22;  
RESULT 768  
ID ABS63423 standard; cDNA; 528 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PD US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAPA/) RAFALSKI J A.  
Query Match 4.9%; Score 48.6; DB 6; Length 528;  
Best Local Similarity 50.2%; Pred. No. 28;  
RESULT 769  
ID ACA38429 standard; DNA; 687 BP.  
DE Prokaryotic essential gene #20086.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 687;  
Best Local Similarity 45.3%; Pred. No. 28;  
RESULT 770  
ID ACA40639 standard; DNA; 690 BP.  
DE Prokaryotic essential gene #22296.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 690;  
Best Local Similarity 45.3%; Pred. No. 28;  
RESULT 771  
ID ABX56068 standard; DNA; 1320 BP.  
DE M. echinospora calicheamicin biosynthesis gene orfVIII.  
PD WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 4.9%; Score 48.6; DB 8; Length 1320;  
Best Local Similarity 45.1%; Pred. No. 27;  
RESULT 772  
ID ACC82989 standard; DNA; 1397 BP.  
DE HIV-1 subtype C isolate Dui51 reverse transcriptase codon optimised DNA.  
PD WO2003037919-A2.  
PD 08-MAY-2003.  
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
Query Match 4.9%; Score 48.6; DB 8; Length 1397;  
Best Local Similarity 47.8%; Pred. No. 27;  
RESULT 773  
ID AAT90471 standard; cDNA; 1479 BP.  
DE Human agrin cDNA.  
PD WO9721811-A2.  
PD 19-JUN-1997.  
PA (REGE-) REGENERON PHARM INC.  
Query Match 4.9%; Score 48.6; DB 2; Length 1479;  
Best Local Similarity 43.8%; Pred. No. 27;  
RESULT 774  
ID ADL61985 standard; DNA; 1533 BP.  
DE Human ovarian cancer DNA marker #20197.  
PD WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 48.6; DB 5; Length 1533;  
Best Local Similarity 48.4%; Pred. No. 27;

RESULT 775  
ID ABD12608 standard; DNA; 1575 BP.  
DE Pseudomonas aeruginosa polynucleotide #11212.  
PD US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1575;  
Best Local Similarity 46.6%; Pred. No. 27;  
RESULT 776  
ID ABD12542 standard; DNA; 1620 BP.  
DE Pseudomonas aeruginosa polynucleotide #11146.  
PD US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1620;  
Best Local Similarity 46.6%; Pred. No. 27;  
RESULT 777  
ID AAT62137 standard; DNA; 2040 BP.  
DE Leishmania braziliensis Lbhsp83 antigen cDNA.  
PD WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 778  
ID AAV47557 standard; DNA; 2040 BP.  
DE Leishmania antigen Lbhsp83 coding sequence.  
PD WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 779  
ID AAD47114 standard; DNA; 2040 BP.  
DE Leishmania sp. 6H (Lbhsp83) DNA.  
PD WO200272752-A2.  
PD 19-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 780  
ID AAD40284 standard; DNA; 2040 BP.  
DE Leishmania braziliensis hsp83 antigenic protein encoding DNA.  
PD US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 781  
ID AAS96021 standard; cDNA; 2040 BP.  
DE Leishmania antigen Lbhsp83 DNA.  
PD WO200179276-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 782  
ID ABK81732 standard; cDNA; 2040 BP.  
DE Leishmania antigenic polynucleotide #3.  
PD US6365165-B1.  
PD 02-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 27;  
RESULT 783  
ID AAF88523 standard; DNA; 2040 BP.  
DE L. braziliensis Hsp83 antigen DNA SEQ ID 5.  
PD US2002081320-A1.  
PD 27-JUN-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.



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PA (SKEI/) SKEIKY A W.
PA (BHAT/) BHATIA A.
PA (COLE/) COLER R N.
PA (PROB/) PROBST P.
PA (BRAN/) BRANNON M.
  Query Match 4.9%; Score 48.6; DB 6; Length 2040;
  Best Local Similarity 44.4%; Pred. No. 27;
RESULT 784
ID ADB78768 standard; cDNA; 2040 BP.
DE Leishmania DNA encoding antigen Lhsp83.
PN US2002169285-A1.
PD 14-NOV-2002.
PA (REED/) REED S G.
PA (CAMP/) CAMPOS-NETO A.
PA (WEBB/) WEBB J R.
PA (DILL/) DILLON D C.
  Query Match 4.9%; Score 48.6; DB 9; Length 2040;
  Best Local Similarity 44.4%; Pred. No. 27;
RESULT 785
ID AAH14403 standard; cDNA; 2279 BP.
DE Human cDNA sequence SEQ ID NO:11841.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 4.9%; Score 48.6; DB 4; Length 2279;
  Best Local Similarity 47.3%; Pred. No. 27;
RESULT 786
ID ABX08845 standard; cDNA; 2279 BP.
DE Angiogenesis-associated human polynucleotide sequence #107.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match 4.9%; Score 48.6; DB 10; Length 2279;
  Best Local Similarity 47.3%; Pred. No. 27;
RESULT 787
ID AAH17825 standard; cDNA; 2454 BP.
DE Human cDNA sequence SEQ ID NO:17498.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 4.9%; Score 48.6; DB 4; Length 2454;
  Best Local Similarity 47.3%; Pred. No. 27;
RESULT 788
ID ABD12439 standard; DNA; 2472 BP.
DE Pseudomonas aeruginosa polynucleotide #11043.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match 4.9%; Score 48.6; DB 11; Length 2472;
  Best Local Similarity 46.6%; Pred. No. 27;
RESULT 789
ID AAL41592 standard; DNA; 2577 BP.
DE HIV-1 subtype C isolate Dui51 pol gene.
PN WO200204494-A2.
PD 17-JAN-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYCA-) UNIV CAPE TOWN.
PA (UYNC-) UNIV NORTH CAROLINA.
  Query Match 4.9%; Score 48.6; DB 6; Length 2577;
  Best Local Similarity 47.8%; Pred. No. 27;
RESULT 790
ID AAQ06825 standard; DNA; 2712 BP.
DE Streptomyces albidoflavus endochitinase DNA.
PN WO9942594-A1.
PD 26-AUG-1999.
PA (CORR-) CORNELL RES FOUND INC.
  Query Match 4.9%; Score 48.6; DB 2; Length 2712;
  Best Local Similarity 47.6%; Pred. No. 27;
RESULT 791
ID AAH74538 standard; DNA; 2712 BP.
DE Nucleotide sequence of an endochitinase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.
PA (CORR-) CORNELL RES FOUND INC.
  Query Match 4.9%; Score 48.6; DB 4; Length 2712;
  Best Local Similarity 47.6%; Pred. No. 27;
RESULT 792
ID ABA95198 standard; cDNA; 3298 BP.
DE Human MICAPRUB-2 polypeptide encoding cDNA (clone ID: 1593855CB1).
PN WO200216587-A2.
PD 28-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 4.9%; Score 48.6; DB 6; Length 3298;
  Best Local Similarity 47.3%; Pred. No. 26;
RESULT 793
ID ACC82987 standard; DNA; 3687 BP.
DE HIV-1 Gttnc DNA construct.
PN WO2003037919-A2.
PD 08-MAY-2003.
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.
PA (UYCA-) UNIV CAPE TOWN.
  Query Match 4.9%; Score 48.6; DB 8; Length 3687;
  Best Local Similarity 47.8%; Pred. No. 26;
RESULT 794
ID ADO85410 standard; DNA; 3720 BP.
DE Streptomyces phoK/phor::omegaaac double mutant, seq id 5.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS-) CNRS CENT NAT RECH SCI.
  Query Match 4.9%; Score 48.6; DB 12; Length 3720;
  Best Local Similarity 49.4%; Pred. No. 26;
RESULT 795
ID ADC39155 standard; cDNA; 4760 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 97.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
  Query Match 4.9%; Score 48.6; DB 10; Length 4760;
  Best Local Similarity 43.8%; Pred. No. 26;
RESULT 796
ID ADH72283 standard; DNA; 4760 BP.
DE Human gene of the invention NOV60d SEQ ID NO:1179.
PN WO20030102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
  Query Match 4.9%; Score 48.6; DB 12; Length 4760;
  Best Local Similarity 43.8%; Pred. No. 26;
RESULT 797
ID ADO85408 standard; DNA; 4860 BP.
DE Streptomyces phok::omegaaac mutant, seq id 3.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS-) CNRS CENT NAT RECH SCI.
  Query Match 4.9%; Score 48.6; DB 12; Length 4860;
  Best Local Similarity 49.4%; Pred. No. 26;
RESULT 798
ID AAH48730 standard; cDNA; 5065 BP.
DE Human HCN4 cDNA.
PN WO200159153-A2.
PD 16-AUG-2001.
PA (AVER-) AVENTIS PHARMA DEUT GMBH.
  Query Match 4.9%; Score 48.6; DB 4; Length 5065;
  Best Local Similarity 50.6%; Pred. No. 26;
RESULT 799
ID ABA09197 standard; cDNA; 5499 BP.
DE Human cation channel hHCN4 homologue cDNA, SEQ ID NO:973.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 4.9%; Score 48.6; DB 4; Length 5499;
  Best Local Similarity 50.6%; Pred. No. 26;
RESULT 800
ID ADC39153 standard; cDNA; 6224 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 95.
PN WO2003010327-A2.
PD 06-FEB-2003.
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PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 10; Length 6224;  
Query Match 43.8%; Pred. No. 26;  
RESULT 801  
ID ADH72277 standard; DNA; 6224 BP.  
DE Human gene of the invention NOV60a SEQ ID NO:1173.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6224;  
Query Match 43.8%; Pred. No. 26;  
RESULT 802  
ID ADM74234 standard; DNA; 6224 BP.  
DE Human NOV8a gene sequence SeqID73.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6224;  
Query Match 43.8%; Pred. No. 26;  
RESULT 803  
ID ADC39163 standard; cDNA; 6494 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 105.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 10; Length 6494;  
Query Match 43.8%; Pred. No. 26;  
RESULT 804  
ID ADH72291 standard; DNA; 6494 BP.  
DE Human gene of the invention NOV60h SEQ ID NO:1187.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6494;  
Query Match 43.8%; Pred. No. 26;  
RESULT 805  
Query Match 4.9%; Score 48.6; DB 4; Length 110000;  
Best Local Similarity 45.3%; Pred. No. 24;  
RESULT 806  
ID AAV23873 standard; DNA; 562 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 2; Length 562;  
Query Match 49.2%; Pred. No. 30;  
RESULT 807  
ID AA206876 standard; cDNA; 562 BP.  
DE Fine O-methyl transferase (OMT) partial cDNA 2.  
PN US5952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 2; Length 562;  
Query Match 49.2%; Pred. No. 30;  
RESULT 808  
ID AAA69580 standard; cDNA; 562 BP.  
DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 3; Length 562;  
Query Match 49.2%; Pred. No. 30;  
RESULT 809  
ID AAA67960 standard; DNA; 562 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 3; Length 562;  
Query Match

Best Local Similarity 49.2%; Pred. No. 30;  
RESULT 810  
ID ADD41710 standard; DNA; 562 BP.  
DE O-methyl transferase DNA #6.  
PN US2003113173-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKBERG L N.  
PA (HAVU/) HAVUKALA I.  
Query Match 4.9%; Score 48.4; DB 10; Length 562;  
Best Local Similarity 49.2%; Pred. No. 30;  
RESULT 811  
ID AA043032 standard; DNA; 756 BP.  
DE Collagen-like polymer DCP3-C2(AB12)C2 coding sequence.  
PN WO9310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 4.9%; Score 48.4; DB 2; Length 756;  
Best Local Similarity 44.3%; Pred. No. 30;  
RESULT 812  
ID AAT16766 standard; DNA; 756 BP.  
DE Collagen-like polymer sequence D gene 2 encoding unit C2A24C2.  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 4.9%; Score 48.4; DB 2; Length 756;  
Best Local Similarity 44.3%; Pred. No. 30;  
RESULT 813  
ID AA02484 standard; cDNA; 1000 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.  
PN WO958675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC. 4.9%; Score 48.4; DB 3; Length 1000;  
Query Match 33.5%; Pred. No. 29;  
RESULT 814  
ID ADA70207 standard; DNA; 1059 BP.  
DE Rice gene, SEQ ID 3530.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG. 4.9%; Score 48.4; DB 8; Length 1059;  
Query Match 43.8%; Pred. No. 29;  
RESULT 815  
ID ADJ11579 standard; DNA; 1059 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 215.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
Query Match 4.9%; Score 48.4; DB 11; Length 1059;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 816  
ID ADA71187 standard; DNA; 1482 BP.  
DE Rice gene, SEQ ID 4510.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG. 4.9%; Score 48.4; DB 8; Length 1482;  
Query Match 44.0%; Pred. No. 29;  
RESULT 817  
ID AAZ35999 standard; DNA; 1646 BP.  
DE S. kitasatoensis macrolide antibiotic acylation enzyme gene.



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PN JP11285384-A.  
PD 19-OCT-1999.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 4.9%; Score 48.4; DB 3; Length 1646;  
Best Local Similarity 50.4%; Pred. No. 29;  
RESULT 818  
ID ACA37821 standard; DNA; 1650 BP.  
DE Prokaryotic essential gene #19478.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 1650;  
Best Local Similarity 45.0%; Pred. No. 29;  
RESULT 819  
ID ACA27358 standard; DNA; 2523 BP.  
DE Prokaryotic essential gene #9015.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 2523;  
Best Local Similarity 47.4%; Pred. No. 29;  
RESULT 820  
ID ADA70538 standard; DNA; 2562 BP.  
DE Rice gene, SEQ ID 3861.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.9%; Score 48.4; DB 8; Length 2562;  
Best Local Similarity 47.3%; Pred. No. 29;  
RESULT 821  
ID AAS06333 standard; cDNA; 2898 BP.  
DE DNA encoding human glutamate receptor-like protein, MEM2.  
PN WO200144473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.4; DB 4; Length 2898;  
Best Local Similarity 43.0%; Pred. No. 29;  
RESULT 822  
ID AAD07033 standard; DNA; 3690 BP.  
DE Methyllobacterium extorquens PHA synthase DNA.  
PN WO200123596-A2.  
PD 05-APR-2001.  
PA (PION-) PIONEER HI-BRED INT INC.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 4.9%; Score 48.4; DB 4; Length 3690;  
Best Local Similarity 48.2%; Pred. No. 28;  
RESULT 823  
ID AA209496 standard; DNA; 4751 BP.  
DE Human heart tissue Ih ion channel DNA.  
PN WO9942574-A1.  
PD 26-AUG-1999.  
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.  
Query Match 4.9%; Score 48.4; DB 2; Length 4751;  
Best Local Similarity 53.8%; Pred. No. 28;  
RESULT 824  
ID AAD29757 standard; DNA; 4751 BP.  
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 4 DNA.  
PN WO200202630-A2.  
PD 10-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 4.9%; Score 48.4; DB 6; Length 4751;  
Best Local Similarity 53.8%; Pred. No. 28;  
RESULT 825  
ID ACA37735 standard; DNA; 4833 BP.  
DE Prokaryotic essential gene #19392.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 4833;  
Best Local Similarity 50.3%; Pred. No. 28;  
RESULT 826  
ID AAD54223 standard; DNA; 24081 BP.  
DE Streptomyces platensis rosaceus dorrigocin ORF6 DNA.

PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.4; DB 10; Length 24081;  
Best Local Similarity 51.1%; Pred. No. 27;  
RESULT 827  
ID ACA37577 standard; DNA; 31263 BP.  
DE Prokaryotic essential gene #19234.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 31263;  
Best Local Similarity 46.2%; Pred. No. 27;  
RESULT 828  
ID AAD54217 standard; DNA; 52101 BP.  
DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.4; DB 10; Length 52101;  
Best Local Similarity 51.1%; Pred. No. 26;  
RESULT 829  
ID AAD57189 standard; DNA; 600 BP.  
DE Mycobacterium avium subspecies paratuberculosis protein gene #2.  
PN WO2003058248-A2.  
PD 17-JUL-2003.  
PA (IDLE-) ID-LELYSTAD INST DIERHOUDRIJ EN DIERGEZ.  
Query Match 4.9%; Score 48.2; DB 9; Length 600;  
Best Local Similarity 48.4%; Pred. No. 32;  
RESULT 831  
ID ADC30820 standard; cDNA; 663 BP.  
DE Human novel cDNA sequence, SEQ ID NO:902.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 663;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 832  
ID ADK52175 standard; cDNA; 663 BP.  
DE Full length cDNA clone MasP1 clone 3.  
PN WO2004016651-A2.  
PD 26-FEB-2004.  
PA (UYVO-) UNIV YORK.  
Query Match 4.9%; Score 48.2; DB 12; Length 663;  
Best Local Similarity 44.0%; Pred. No. 32;  
RESULT 833  
ID ADJ39458 standard; cDNA; 786 BP.  
DE Plant cDNA #458.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
Query Match 4.9%; Score 48.2; DB 12; Length 786;  
Best Local Similarity 49.8%; Pred. No. 32;  
RESULT 834  
ID ACC68993 standard; cDNA; 811 BP.  
DE Human neurotransmission-associated protein NTRAN-15 cDNA SEQ ID NO:40.  
PN WO2003025129-A2.  
PD 27-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 811;



Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 835  
ID ABD13103 standard; DNA; 822 BP.  
DE Pseudomonas aeruginosa polynucleotide #11707.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 822;  
Best Local Similarity 46.5%; Pred. No. 32;  
RESULT 836  
ID ADG10464 standard; cDNA; 823 BP.  
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:54.  
PN WO200296943-A1.  
PD 05-DEC-2002.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 4.9%; Score 48.2; DB 10; Length 823;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 837  
ID ADG10466 standard; cDNA; 823 BP.  
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:56.  
PN WO200296943-A1.  
PD 05-DEC-2002.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 4.9%; Score 48.2; DB 10; Length 823;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 838  
ID ACA37950 standard; DNA; 825 BP.  
DE Prokaryotic essential gene #19607.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 825;  
Best Local Similarity 48.9%; Pred. No. 32;  
RESULT 839  
ID AAI58255 standard; cDNA; 920 BP.  
DE Human polynucleotide SEQ ID NO 458.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 4; Length 920;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 840  
ID ADQ98462 standard; cDNA; 920 BP.  
DE DNA encoding human GPCR-like protein seqid 132.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 5; Length 920;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 841  
ID ADB48222 standard; cDNA; 920 BP.  
DE Novel human cDNA SEQ ID NO 132.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRNA/) DRMANAC R T.  
Query Match 4.9%; Score 48.2; DB 9; Length 920;  
Best Local Similarity 52.7%; Pred. No. 32;  
RESULT 842  
ID ACA42680 standard; DNA; 930 BP.  
DE Prokaryotic essential gene #24337.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 930;  
Best Local Similarity 48.1%; Pred. No. 32;  
RESULT 843  
ID ABK51403 standard; DNA; 969 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-2.  
PN WO200160973-A2.

PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 844  
ID AAD19381 standard; DNA; 969 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-2 isoform DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 845  
ID ABK51402 standard; DNA; 1038 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-1.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 846  
ID AAD19380 standard; DNA; 1038 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-1 isoform DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 847  
ID AAS14696 standard; DNA; 1038 BP.  
DE Human cDNA encoding transcription factor C/EBPbeta.  
PN WO200174298-A2.  
PD 11-OCT-2001.  
PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
PA (HUGH-) HUGHES HOWARD MED INST.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 848  
ID AAL44084 standard; DNA; 1038 BP.  
DE Human C/EBP-beta protein coding sequence 3.  
PN WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 849  
ID ABK51997 standard; DNA; 1038 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #3.  
PN WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 850  
ID ACF36516 standard; DNA; 1038 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PN WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 851  
ID ABK51410 standard; DNA; 1042 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene mutant.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1042;  
Best Local Similarity 47.2%; Pred. No. 32;  
RESULT 852  
ID ADK71964 standard; DNA; 1260 BP.  
DE Human I Kappa B kinase (IKK) gamma DNA SeqID 22.  
PN WO2004016781-A1.



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DE Human cDNA differentially expressed in granulocytic cells #1134.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (RIKE ) RIKEN KK.  
PA (KAZU-) KAZUSA DNA RES INST.  
Query Match 4.9%; Score 48.2; DB 12; Length 1260;  
Best Local Similarity 47.8%; Pred. No. 32;  
RESULT 853  
ID AAD55721 standard; DNA; 1336 BP.  
DE Argiope trifasciata major ampullate spidroin 2 (MaSp2) DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 4.9%; Score 48.2; DB 8; Length 1336;  
Best Local Similarity 43.2%; Pred. No. 32;  
RESULT 854  
ID ADP09651 standard; DNA; 1413 BP.  
DE Rice cinnamic acid 5-hydroxylase ORF DNA without the T-DNA insert Seq 42.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO.  
PA (POST-) POSTECH FOUND.  
Query Match 4.9%; Score 48.2; DB 12; Length 1413;  
Best Local Similarity 49.8%; Pred. No. 31;  
RESULT 855  
ID ADP75211 standard; cDNA; 1701 BP.  
DE Human ADAMTS2 cDNA splice variant 2.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 1701;  
Best Local Similarity 44.0%; Pred. No. 31;  
RESULT 856  
ID AAA35065 standard; DNA; 1910 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2754.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 857  
ID AAF21187 standard; DNA; 1910 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2754.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 858  
ID ABK51401 standard; DNA; 1910 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 859  
ID AAD19379 standard; DNA; 1910 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 860  
ID AAL44083 standard; DNA; 1910 BP.  
DE Human C/EBP-beta protein coding sequence 2.  
PN WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 861  
ID ABK64563 standard; cDNA; 1910 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1134.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 862  
ID ABL94237 standard; cDNA; 1910 BP.  
DE Human C/EBP beta-encoding cDNA, SEQ ID NO:3.  
PN US6271030-B1.  
PD 07-AUG-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 863  
ID ARK51996 standard; DNA; 1910 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #2.  
PN WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 864  
ID ACF36515 standard; DNA; 1910 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PN WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 865  
ID ABZ96881 standard; DNA; 1910 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 866  
ID ABD20730 standard; DNA; 1910 BP.  
DE Human pulmonary and inflammatory target DNA #341.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 867  
ID AAQ15015 standard; DNA; 1913 BP.  
DE Nuclear factor C/EBP2 DNA.  
PN JP03236782-A.  
PD 22-OCT-1991.  
PA (CHUZ-) CHUZO KISH IMOTO.  
Query Match 4.9%; Score 48.2; DB 2; Length 1913;  
Best Local Similarity 47.2%; Pred. No. 31;  
RESULT 868  
ID ADA44712 standard; DNA; 1975 BP.  
DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.  
PN WO2003031576-A2.  
PD 17-APR-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 1975;  
Best Local Similarity 47.8%; Pred. No. 31;  
RESULT 869  
ID AAC81426 standard; cDNA; 1994 BP.  
DE Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.  
PN JP2000253884-A.  
PD 19-SEP-2000.  
PA (TOAG ) TOA GOSEI CHEM IND LTD.  
Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
Best Local Similarity 47.8%; Pred. No. 31;  
RESULT 870  
ID AAA35027 standard; DNA; 1994 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.



PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 871  
 ID AAF21149 standard; DNA; 1994 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2716.  
 PN WO2000062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (UYEC-) NYCE J W.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 872  
 ID ADA44705 standard; DNA; 1994 BP.  
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.  
 PN WO2003031576-A2.  
 PD 17-APR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 873  
 ID ABZ96843 standard; DNA; 1994 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 874  
 ID ABV75393 standard; DNA; 1994 BP.  
 DE Human NEMO polypeptide encoding DNA.  
 PN WO200292761-A2.  
 PD 21-NOV-2002.  
 PA (IMW) IMMUNEX CORP.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 875  
 ID ABD20692 standard; DNA; 1994 BP.  
 DE Human pulmonary and inflammatory target DNA #303.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 11; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 876  
 ID AAZ07513 standard; DNA; 2009 BP.  
 DE Human RIP-associated protein (RAP-2) encoding DNA.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YEDA) YEDA RES & DEV CO LTD.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2009;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 877  
 ID AAV06593 standard; cDNA; 2023 BP.  
 DE Human N-proteinase (short form) cDNA.  
 PN WO9800555-A1.  
 PD 08-JAN-1998.  
 PA (PROC/) PROCKOP D J.  
 PA (COLI/) COLIGE A.  
 PA (LAPI/) LAPIERE C.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2023;  
 Best Local Similarity 44.0%; Pred. No. 31;  
 RESULT 878  
 ID ABS57455 standard; cDNA; 2023 BP.  
 DE Human short form N-proteinase cDNA.  
 PN US6428998-B1.  
 PD 06-AUG-2002.  
 PA (UYLI-) UNIV LIEGE.  
 Query Match 4.9%; Score 48.2; DB 10; Length 2023;  
 Best Local Similarity 44.0%; Pred. No. 31;

RESULT 879  
 ID AAZ07514 standard; DNA; 2034 BP.  
 DE Human RIP-associated protein (RAP-2) clone #41072 nucleotide sequence.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YEDA) YEDA RES & DEV CO LTD.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2034;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 880  
 ID ACD23012 standard; cDNA; 2035 BP.  
 DE Human NEMO cDNA.  
 PN US2003032055-A1.  
 PD 13-FEB-2003.  
 PA (KENW/) KENWICK S J.  
 PA (WOFF/) WOFFENDIN H.  
 PA (MUNN/) MUNNICH A.  
 PA (SMAH/) SMAHI A.  
 PA (ISRA/) ISRAEL A.  
 PA (POUS/) POUSTKA A.  
 PA (HEIS/) HEISS N.  
 PA (DURS/) D'URSO M.  
 PA (LEWI/) LEWIS R A.  
 PA (NELS/) NELSON D L.  
 PA (ARAD/) ARADHYA S.  
 PA (LEVY/) LEVY M.  
 Query Match 4.9%; Score 48.2; DB 9; Length 2035;  
 Best Local Similarity 47.8%; Pred. No. 31;  
 RESULT 881  
 ID AAA35066 standard; DNA; 2171 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2755.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 31;  
 RESULT 882  
 ID AAF21188 standard; DNA; 2171 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2755.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 31;  
 RESULT 883  
 ID AB296882 standard; DNA; 2171 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 31;  
 RESULT 884  
 ID ABD20731 standard; DNA; 2171 BP.  
 DE Human pulmonary and inflammatory target DNA #342.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 31;  
 RESULT 885  
 ID ACA27128 standard; DNA; 2595 BP.  
 DE Prokaryotic essential gene #8785.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 2595;  
 Best Local Similarity 46.3%; Pred. No. 31;  
 RESULT 886  
 ID AAD28564 standard; DNA; 3350 BP.  
 DE Herpes simplex virus type 2 G10\_UL37consensus DNA.  
 PN WO200202131-A2.



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PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP. 4.9%; Score 48.2; DB 6; Length 3350;  
Query Match 44.5%; Pred. No. 31;  
Best Local Similarity 44.5%; Pred. No. 31;  
RESULT 887  
ID ADG74976 standard; DNA; 3350 BP.  
DE Human herpesvirus 2 isolated clone DNA - SEQ ID 48.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP. 4.9%; Score 48.2; DB 10; Length 3350;  
Query Match 44.5%; Pred. No. 31;  
Best Local Similarity 44.5%; Pred. No. 31;  
RESULT 888  
ID AAS77503 standard; cDNA; 3633 BP.  
DE DNA encoding novel human diagnostic protein #13307.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. 4.9%; Score 48.2; DB 5; Length 3633;  
Query Match 44.0%; Pred. No. 31;  
Best Local Similarity 44.0%; Pred. No. 31;  
RESULT 889  
ID ACC72669 standard; cDNA; 3636 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:8.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. 4.9%; Score 48.2; DB 10; Length 3636;  
Query Match 44.0%; Pred. No. 31;  
Best Local Similarity 44.0%; Pred. No. 31;  
RESULT 890  
ID ACA40841 standard; DNA; 4146 BP.  
DE Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 4.9%; Score 48.2; DB 8; Length 4146;  
Query Match 46.1%; Pred. No. 31;  
Best Local Similarity 46.1%; Pred. No. 31;  
RESULT 891  
ID ACA40804 standard; DNA; 4542 BP.  
DE Prokaryotic essential gene #22461.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 4.9%; Score 48.2; DB 8; Length 4542;  
Query Match 43.2%; Pred. No. 30;  
Best Local Similarity 43.2%; Pred. No. 30;  
RESULT 892  
ID ADP09634 standard; DNA; 4941 BP.  
DE Rice cinnamic acid 5-hydroxylase genomic DNA without the T-DNA SeqID 25.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO. 4.9%; Score 48.2; DB 12; Length 4941;  
PA (POST-) POSTECH FOUND. 49.8%; Pred. No. 30;  
Query Match 49.8%; Pred. No. 30;  
Best Local Similarity 49.8%; Pred. No. 30;  
RESULT 893  
ID AD010048 standard; cDNA; 5204 BP.  
DE Novel human protein Novid cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU/) KEKUDA R. 4.9%; Score 48.2; DB 3; Length 8631;  
PA (ALSO/) ALSOBROOK J P. 47.8%; Pred. No. 30;  
PA (TCHE/) TCHERNEV V T. 4.9%; Score 48.2; DB 3; Length 8631;  
PA (LIUX/) LIU X. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (SPYT/) SPYTEK K A. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (PATI/) PATURAJAN M. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (GROS/) GROSSE W M. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (LEPL/) LEFLEY D M. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (BURG/) BURGESS C E. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (VERN/) VERNET C A M. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (LILL/) LI L. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (GORM/) GORMAN L. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (EDIN/) EDINGER S R. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (SCIO/) SCIORE P. 4.9%; Score 48.2; DB 10; Length 8631;  
PA (ELLE/) ELLERMAN K. 4.9%; Score 48.2; DB 10; Length 8631;

PA (MALY/) MALYANKAR U M. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (ROTH/) ROTHENBERG M E. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (STON/) STONE D J. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (BOLD/) BOLDOG F L. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (GUOX/) GUO X. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (SHEN/) SHENOY S G. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (ANDE/) ANDERSON D W. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (PADI/) PADIGARU M. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (TAUP/) TAUPIER R J. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (MILL/) MILLER C E. 4.9%; Score 48.2; DB 12; Length 5204;  
PA (EISE/) EISEN A. 4.9%; Score 48.2; DB 12; Length 5204;  
Query Match 48.9%; Pred. No. 30;  
Best Local Similarity 48.9%; Pred. No. 30;  
RESULT 894  
ID ADP75209 standard; cDNA; 6642 BP.  
DE Human ADAMTS2 cDNA splice variant 1.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. 4.9%; Score 48.2; DB 11; Length 6642;  
Query Match 44.0%; Pred. No. 30;  
Best Local Similarity 44.0%; Pred. No. 30;  
RESULT 895  
ID AAV06592 standard; cDNA; 6692 BP.  
DE Human N-proteinase (long form) cDNA.  
PN WO9800555-A1.  
PD 08-JAN-1998.  
PA (PROC/) PROCKOP D J. 4.9%; Score 48.2; DB 2; Length 6692;  
PA (COLI/) COLIGE A. 4.9%; Score 48.2; DB 2; Length 6692;  
PA (LAPI/) LAPIERE C. 4.9%; Score 48.2; DB 2; Length 6692;  
Query Match 44.0%; Pred. No. 30;  
Best Local Similarity 44.0%; Pred. No. 30;  
RESULT 896  
ID ABS57451 standard; cDNA; 6692 BP.  
DE Human long form N-proteinase cDNA.  
PN US6428998-B1.  
PD 06-AUG-2002.  
PA (UVLI-) UNIV LIEGE. 4.9%; Score 48.2; DB 10; Length 6692;  
Query Match 44.0%; Pred. No. 30;  
Best Local Similarity 44.0%; Pred. No. 30;  
RESULT 897  
ID AAA35028 standard; DNA; 8631 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA. 4.9%; Score 48.2; DB 3; Length 8631;  
Query Match 47.8%; Pred. No. 30;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 898  
ID AAF21150 standard; DNA; 8631 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2717.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA. 4.9%; Score 48.2; DB 3; Length 8631;  
PA (NYCE/) NYCE J W. 4.9%; Score 48.2; DB 3; Length 8631;  
Query Match 47.8%; Pred. No. 30;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 899  
ID ABZ96844 standard; DNA; 8631 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC. 4.9%; Score 48.2; DB 10; Length 8631;  
Query Match 47.8%; Pred. No. 30;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 900  
ID ABD20693 standard; DNA; 8631 BP.  
DE Human pulmonary and inflammatory target DNA #304.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC. 4.9%; Score 48.2; DB 11; Length 8631;  
Query Match 47.8%; Pred. No. 30;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 901



ID AAD54222 standard; DNA; 9579 BP.  
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF5 DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 9579;  
Best Local Similarity 47.2%; Pred. No. 30;  
RESULT 902  
ID ADC26981 standard; DNA; 20922 BP.  
DE Sorangium cellulosum tmbA gene cluster tmbB DNA.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.9%; Score 48.2; DB 10; Length 20922;  
Best Local Similarity 46.3%; Pred. No. 29;  
RESULT 903  
ID AAD17185 standard; DNA; 27541 BP.  
DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 4.9%; Score 48.2; DB 4; Length 27541;  
Best Local Similarity 47.0%; Pred. No. 29;  
RESULT 904  
ID AAD54217 standard; DNA; 52101 BP.  
DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 52101;  
Best Local Similarity 47.2%; Pred. No. 28;  
RESULT 905  
ID ADC26995 standard; DNA; 67251 BP.  
DE Sorangium cellulosum tmbA gene cluster.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.9%; Score 48.2; DB 10; Length 67251;  
Best Local Similarity 46.4%; Pred. No. 28;  
RESULT 906  
ID AAL60437 standard; DNA; 70383 BP.  
DE Human kinase splice form 1 genomic DNA.  
Query Match 4.9%; Score 48.2; DB 9; Length 70383;  
Best Local Similarity 45.5%; Pred. No. 28;  
RESULT 907  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygroscopicus herbimycin gene cluster, SRQ ID NO:2.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 4.9%; Score 48.2; DB 12; Length 86941;  
Best Local Similarity 45.9%; Pred. No. 28;  
RESULT 908  
Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
Best Local Similarity 43.2%; Pred. No. 28;  
RESULT 909  
Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
Best Local Similarity 43.2%; Pred. No. 28;  
RESULT 910  
ID ABD03629 standard; DNA; 465 BP.  
DE Pseudomonas aeruginosa polynucleotide #2233.  
PN US6551795-B1.

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 465;  
Best Local Similarity 50.0%; Pred. No. 35;  
RESULT 911  
ID ACF39326 standard; DNA; 660 BP.  
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:28.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 4.9%; Score 48; DB 8; Length 660;  
Best Local Similarity 51.4%; Pred. No. 35;  
RESULT 912  
ID ABQ40859 standard; DNA; 712 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27450.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 48; DB 6; Length 712;  
Best Local Similarity 45.5%; Pred. No. 35;  
RESULT 913  
ID ABQ40858 standard; DNA; 712 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27449.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 48; DB 6; Length 712;  
Best Local Similarity 45.5%; Pred. No. 35;  
RESULT 914  
ID AB266735 standard; DNA; 756 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 132.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 10; Length 756;  
Best Local Similarity 48.5%; Pred. No. 35;  
RESULT 915  
ID ABD08476 standard; DNA; 822 BP.  
DE Pseudomonas aeruginosa polynucleotide #7080.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 822;  
Best Local Similarity 45.2%; Pred. No. 34;  
RESULT 916  
ID ABD03843 standard; DNA; 852 BP.  
DE Pseudomonas aeruginosa polynucleotide #2447.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 852;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 917  
ID ABD03031 standard; DNA; 1071 BP.  
DE Pseudomonas aeruginosa polynucleotide #1635.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1071;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 918  
ID AAA02477 standard; cDNA; 1127 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468.  
PN WO9958675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48; DB 3; Length 1127;  
Best Local Similarity 34.2%; Pred. No. 34;  
RESULT 919  
ID AAZ10560 standard; DNA; 1128 BP.  
DE DNA encoding G protein-coupled receptor protein designated SREB1.  
PN WO9946378-A1.



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PD 16-SEP-1999.  
PA (YAMA) YAMANOUCHI PHARM CO LTD.  
Query Match 4.9%; Score 48; DB 2; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 920  
ID AAM46026 standard; cDNA; 1128 BP.  
DE Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17.  
PN WO200022131-A2.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 921  
ID AAD01125 standard; cDNA; 1128 BP.  
DE Human orphan G protein-coupled receptor hGPCR27 cDNA.  
PN WO200031258-A2.  
PD 02-JUN-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 922  
ID AAD27892 standard; DNA; 1128 BP.  
DE Human G-protein coupled receptor 14266 DNA.  
PN WO200212344-A2.  
PD 14-FEB-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 923  
ID AAS98049 standard; DNA; 1128 BP.  
DE Human DNA for potential G protein-coupled receptor #7.  
PN WO200185791-A1.  
PD 15-NOV-2001.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 924  
ID ACA93263 standard; cDNA; 1128 BP.  
DE Human cDNA encoding GPCR hGPCR27.  
PN US2003017528-A1.  
PD 23-JAN-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAN/) LIAN C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 925  
ID AB242853 standard; DNA; 1128 BP.  
DE Human G protein-coupled receptor GPR27 nucleotide SEQ ID NO:493.  
PN WO2000261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 926  
ID ADG98761 standard; cDNA; 1128 BP.  
DE Human orphan GPCR cDNA, GPCR27.  
PN US2003148450-A1.  
PD 07-AUG-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAN/) LIAN C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 10; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 927  
ID ADJ26924 standard; cDNA; 1128 BP.  
DE Human endogenous orphan G-protein coupled receptor (GPCR) 27 cDNA.  
PN US2003175891-A1.  
PD 18-SEP-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.

PA (LIAN/) LIAN C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 928  
ID ADN39803 standard; cDNA; 1128 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:CI75.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 929  
ID ADG86378 standard; DNA; 1128 BP.  
DE Human endogenous orphan GPCR hGPCR27 DNA.  
PN US2003229216-A1.  
PD 11-DEC-2003.  
PA (CHEN/) CHEN R.  
PA (LIAN/) LIAN C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
Query Match 4.9%; Score 48; DB 12; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 930  
ID ADO29912 standard; cDNA; 1128 BP.  
DE Human GPCR GPR27 polynucleotide, SEQ ID NO:1014.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 4.9%; Score 48; DB 12; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 931  
ID ADP20171 standard; cDNA; 1128 BP.  
DE Human G protein coupled receptor hGPCR27 cDNA.  
PN US2004110238-A1.  
PD 10-JUN-2004.  
PA (CHEN/) CHEN R.  
PA (LIAN/) LIAN C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
Query Match 4.9%; Score 48; DB 12; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 932  
ID ACC59401 standard; DNA; 1188 BP.  
DE Microbial resistance gene PA1877 coding sequence.  
PN WO2003041483-A2.  
PD 22-MAY-2003.  
PA (DART-) DARTMOUTH COLLEGE.  
Query Match 4.9%; Score 48; DB 9; Length 1188;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 933  
ID ADC36366 standard; DNA; 1197 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:234.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO-) SUMITOMO CHEM CO LTD.  
Query Match 4.9%; Score 48; DB 10; Length 1197;  
Best Local Similarity 44.1%; Pred. No. 34;  
RESULT 934  
ID ACA37909 standard; DNA; 1275 BP.  
DE Prokaryotic essential gene #19566.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 8; Length 1275;  
Best Local Similarity 46.0%; Pred. No. 34;  
RESULT 935  
ID ABD03924 standard; DNA; 1359 BP.  
DE Pseudomonas aeruginosa polynucleotide #2528.  
PN US6551795-B1.  
PD 22-APR-2003.



PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1359;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 936  
ID ADC36376 standard; DNA; 1411 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:244.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 4.9%; Score 48; DB 10; Length 1411;  
Best Local Similarity 44.1%; Pred. No. 34;  
RESULT 937  
ID ABD03787 standard; DNA; 1473 BP.  
DE Pseudomonas aeruginosa polynucleotide #2391.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1473;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 938  
ID ABD03082 standard; DNA; 1695 BP.  
DE Pseudomonas aeruginosa polynucleotide #1686.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1695;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 939  
ID ABD02888 standard; DNA; 1740 BP.  
DE Pseudomonas aeruginosa polynucleotide #1492.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1740;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 940  
ID AC25954 standard; DNA; 1782 BP.  
DE Prokaryotic essential gene #7611.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 8; Length 1782;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 941  
ID ABD02930 standard; DNA; 1806 BP.  
DE Pseudomonas aeruginosa polynucleotide #1534.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1806;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 942  
ID ADF070581 standard; DNA; 1842 BP.  
DE Orphan receptor ligand-related human protein gene SeqID204.  
PN WO2003071272-A1.  
PD 28-AUG-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 4.9%; Score 48; DB 10; Length 1842;  
Best Local Similarity 45.1%; Pred. No. 34;  
RESULT 943  
ID AAX90924 standard; DNA; 1925 BP.  
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.  
PN WO9947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOPEDIA INC.  
Query Match 4.9%; Score 48; DB 2; Length 1925;  
Best Local Similarity 51.4%; Pred. No. 34;  
RESULT 944  
ID ABD08413 standard; DNA; 1929 BP.  
DE Pseudomonas aeruginosa polynucleotide #7017.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 4.9%; Score 48; DB 11; Length 1929;  
Best Local Similarity 45.2%; Pred. No. 34;  
RESULT 945  
ID ABD08507 standard; DNA; 1947 BP.  
DE Pseudomonas aeruginosa polynucleotide #7111.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1947;  
Best Local Similarity 45.2%; Pred. No. 34;  
RESULT 946  
ID ABD08587 standard; DNA; 2253 BP.  
DE Pseudomonas aeruginosa polynucleotide #7191.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2253;  
Best Local Similarity 45.5%; Pred. No. 34;  
RESULT 947  
ID ABD08649 standard; DNA; 2409 BP.  
DE Pseudomonas aeruginosa polynucleotide #7253.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2409;  
Best Local Similarity 45.5%; Pred. No. 33;  
RESULT 948  
ID ADO24486 standard; cDNA; 2485 BP.  
DE Human PRO87344 encoding cDNA SEQ ID NO:125.  
PN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.9%; Score 48; DB 12; Length 2485;  
Best Local Similarity 45.1%; Pred. No. 33;  
RESULT 949  
ID ABD08843 standard; DNA; 2490 BP.  
DE Pseudomonas aeruginosa polynucleotide #7447.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 2490;  
Best Local Similarity 45.5%; Pred. No. 33;  
RESULT 950  
ID AAS54094 standard; DNA; 3489 BP.  
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #225.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 4; Length 3489;  
Best Local Similarity 45.1%; Pred. No. 33;  
RESULT 951  
ID ACA42240 standard; DNA; 3489 BP.  
DE Prokaryotic essential gene #23897.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48; DB 8; Length 3489;  
Best Local Similarity 45.1%; Pred. No. 33;  
RESULT 952  
ID AAS08699 standard; DNA; 12152 BP.  
DE M. carbonacea DNA encoding Everninomicin biosynthetic enzymes.  
PN WO200151639-A2.  
PD 19-JUL-2001.  
PA (SCHE) SCHERING CORP.  
Query Match 4.9%; Score 48; DB 5; Length 12152;  
Best Local Similarity 48.5%; Pred. No. 32;  
RESULT 953  
ID AAS17367 standard; DNA; 33529 BP.  
DE DNA sequence of S. cellulosum polyketide synthase cosmid, pKOS28-26.  
PN US6280599-B1.  
PD 28-AUG-2001.  
PA (KOSA-) KOSAN BIOSCIENCE.  
Query Match 4.9%; Score 48; DB 5; Length 33529;



Best Local Similarity 46.4%; Pred. No. 31;  
RESULT 954  
ID ABZ66810 standard; DNA; 37116 BP.  
DE Orthocymycin biosynthetic gene cluster SEQ ID NO 279.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 10; Length 37116;  
Best Local Similarity 48.5%; Pred. No. 31;  
RESULT 955  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 12; Length 76994;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 956  
ID ABD08121 standard; DNA; 309 BP.  
DE Pseudomonas aeruginosa polynucleotide #6725.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 309;  
Best Local Similarity 49.4%; Pred. No. 38;  
RESULT 957  
ID ADI42790 standard; DNA; 487 BP.  
DE Plant transcription factor polynucleotide #800.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIANG-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAAR-) HAARKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.  
PA (PINE-) PINEDA O.  
PA (YUGG-) YU G.  
Query Match 4.8%; Score 47.8; DB 12; Length 487;  
Best Local Similarity 45.1%; Pred. No. 38;  
RESULT 958  
ID ABK35609 standard; DNA; 777 BP.  
DE Gene encoding novel human secreted or membrane-associated protein #28.  
PN WO200204600-A2.  
PD 17-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
PA (GLAX-) GLAXO GROUP LTD.  
Query Match 4.8%; Score 47.8; DB 6; Length 777;  
Best Local Similarity 51.8%; Pred. No. 37;  
RESULT 959  
ID ADF58345 standard; cDNA; 777 BP.  
DE Human polynucleotide sequence SEQ ID NO:712.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 47.8; DB 10; Length 777;  
Best Local Similarity 51.8%; Pred. No. 37;  
RESULT 960  
ID ABD17337 standard; DNA; 801 BP.  
DE Pseudomonas aeruginosa polynucleotide #15941.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 801;  
Best Local Similarity 47.5%; Pred. No. 37;

RESULT 961  
ID ABD15977 standard; DNA; 819 BP.  
DE Pseudomonas aeruginosa polynucleotide #14581.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 819;  
Best Local Similarity 47.1%; Pred. No. 37;  
RESULT 962  
ID AAL61183 standard; DNA; 885 BP.  
DE Actinosynnema pretiosum methyltransferase gene #2.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW-) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 885;  
Best Local Similarity 44.9%; Pred. No. 37;  
RESULT 963  
ID ABD08291 standard; DNA; 966 BP.  
DE Pseudomonas aeruginosa polynucleotide #6895.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 966;  
Best Local Similarity 49.4%; Pred. No. 37;  
RESULT 964  
ID ACA37720 standard; DNA; 1029 BP.  
DE Prokaryotic essential gene #19377.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1029;  
Best Local Similarity 45.6%; Pred. No. 37;  
RESULT 965  
ID ADB80220 standard; DNA; 1173 BP.  
DE Mycobacterium tuberculosis nutrient starvation-inducible gene #129.  
PN WO2003004520-A2.  
PD 16-JAN-2003.  
PA (MITCR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 4.8%; Score 47.8; DB 10; Length 1173;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 966  
ID ABD17849 standard; DNA; 1218 BP.  
DE Pseudomonas aeruginosa polynucleotide #16453.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1218;  
Best Local Similarity 47.5%; Pred. No. 37;  
RESULT 967  
ID ACA26886 standard; DNA; 1287 BP.  
DE Prokaryotic essential gene #8543.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1287;  
Best Local Similarity 45.4%; Pred. No. 37;  
RESULT 968  
ID ABL15825 standard; cDNA; 1291 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41957.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 4.8%; Score 47.8; DB 4; Length 1291;  
Best Local Similarity 47.8%; Pred. No. 37;  
RESULT 969  
ID ABA16862 standard; DNA; 1343 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9193.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
Best Local Similarity 51.8%; Pred. No. 37;  
RESULT 970



ID ABA19759 standard; DNA; 1343 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12090.  
FN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
Best Local Similarity 51.8%; Pred. No. 37;  
RESULT 971  
ID ACA37836 standard; DNA; 1404 BP.  
DE Prokaryotic essential gene #19493.  
FN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1404;  
Best Local Similarity 46.8%; Pred. No. 37;  
RESULT 972  
ID ABD08211 standard; DNA; 1485 BP.  
DE Pseudomonas aeruginosa polynucleotide #6815.  
FN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1485;  
Best Local Similarity 49.4%; Pred. No. 37;  
RESULT 973  
ID ABD08326 standard; DNA; 1509 BP.  
DE Pseudomonas aeruginosa polynucleotide #6930.  
FN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1509;  
Best Local Similarity 49.4%; Pred. No. 37;  
RESULT 974  
ID ACA37879 standard; DNA; 1527 BP.  
DE Prokaryotic essential gene #19536.  
FN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1527;  
Best Local Similarity 47.2%; Pred. No. 37;  
RESULT 975  
ID AAD36877 standard; DNA; 1686 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme encoding DNA, ORF15.  
FN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (UVAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 1686;  
Best Local Similarity 46.3%; Pred. No. 37;  
RESULT 976  
ID AAT62138 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-210 antigen cDNA.  
FN WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 977  
ID AAV47558 standard; DNA; 1771 BP.  
DE Leishmania antigen Lt-210 coding sequence.  
FN WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 978  
ID AAZ5621 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt210 nucleotide sequence.  
FN US965142-A.  
PD 12-OCT-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 979

ID AAD40285 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-1 antigenic protein encoding DNA.  
FN US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 980  
ID AAS96022 standard; cDNA; 1771 BP.  
DE Leishmania antigen Lt-1 DNA.  
FN WO200179276-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 981  
ID ABK81733 standard; DNA; 1771 BP.  
DE Leishmania antigenic polynucleotide #4.  
FN US6365165-B1.  
PD 02-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 982  
ID AAF88524 standard; DNA; 1771 BP.  
DE L. tropica Lt-210 antigen DNA SEQ ID 7.  
FN US2002081320-A1.  
PD 27-JUN-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
PA (SKEI/) SKEIKY Y A W.  
PA (BHAT/) BHATIA A.  
PA (COLE/) COLER R N.  
PA (PROB/) PROBST P.  
PA (BRAN/) BRANNON M.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 983  
ID ADB78770 standard; DNA; 1771 BP.  
DE Leishmania DNA encoding antigen Lt-210.  
FN US2002169285-A1.  
PD 14-NOV-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
Query Match 4.8%; Score 47.8; DB 9; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 36;  
RESULT 984  
ID ABD17433 standard; DNA; 1962 BP.  
DE Pseudomonas aeruginosa polynucleotide #16037.  
FN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1962;  
Best Local Similarity 47.5%; Pred. No. 36;  
RESULT 985  
ID ABD17959 standard; DNA; 2526 BP.  
DE Pseudomonas aeruginosa polynucleotide #16563.  
FN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 2526;  
Best Local Similarity 47.5%; Pred. No. 36;  
RESULT 986  
ID AAL61203 standard; DNA; 3018 BP.  
DE Actinosynnema pretiosum cytochrome P450 gene.  
FN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3018;



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Best Local Similarity 47.9%; Pred. No. 36;  
RESULT 987  
ID ABD10462 standard; DNA; 3126 BP.  
DE Pseudomonas aeruginosa polynucleotide #9066.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 3126;  
Best Local Similarity 51.1%; Pred. No. 36;  
RESULT 988  
ID AAL61181 standard; DNA; 3354 BP.  
DE Actinosynnema pretiosum transcriptional regulator gene #1.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3354;  
Best Local Similarity 41.5%; Pred. No. 36;  
RESULT 989  
ID ADQ19781 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2600.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 36;  
RESULT 990  
ID ADQ23914 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6734.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 36;  
RESULT 991  
ID ABD16585 standard; DNA; 5121 BP.  
DE Pseudomonas aeruginosa polynucleotide #15189.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 5121;  
Best Local Similarity 47.1%; Pred. No. 35;  
RESULT 992  
ID ABD16327 standard; DNA; 6327 BP.  
DE Pseudomonas aeruginosa polynucleotide #14931.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 6327;  
Best Local Similarity 47.1%; Pred. No. 35;  
RESULT 993  
ID ACF05731 standard; DNA; 7201 BP.  
DE Plasmid pEAK12d-IPAA44548-6His.  
PN WO2003055913-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7201;  
Best Local Similarity 48.7%; Pred. No. 35;  
RESULT 994  
ID ACF06299 standard; DNA; 7231 BP.  
DE Plasmid pEAK12d-IPAA26841s-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7231;  
Best Local Similarity 48.7%; Pred. No. 35;  
RESULT 995  
ID ACF06300 standard; DNA; 7297 BP.  
DE SigtdIPAA26841s-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7297;  
Best Local Similarity 48.7%; Pred. No. 35;

RESULT 996  
ID ACF05558 standard; DNA; 7429 BP.  
DE Plasmid pEAK12d-IPAA24020-6His.  
PN WO2003055912-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7429;  
Best Local Similarity 48.7%; Pred. No. 35;  
RESULT 997  
ID ACF06298 standard; DNA; 7456 BP.  
DE Plasmid pEAK12d-IPAA26841long-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7456;  
Best Local Similarity 48.7%; Pred. No. 35;  
RESULT 998  
ID ADP28653 standard; DNA; 8973 BP.  
DE Human secreted protein encoding sequence SEQ ID #651.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 8973;  
Best Local Similarity 44.6%; Pred. No. 35;  
RESULT 999  
ID AAD36874 standard; DNA; 29870 BP.  
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 29870;  
Best Local Similarity 46.3%; Pred. No. 34;  
RESULT 1000  
ID AAA29349 standard; DNA; 71989 BP.  
DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.  
Query Match 4.8%; Score 47.8; DB 3; Length 71989;  
Best Local Similarity 48.2%; Pred. No. 33;  
RESULT 1001  
ID AAL61224 standard; DNA; 82746 BP.  
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 82746;  
Best Local Similarity 44.9%; Pred. No. 33;  
RESULT 1002  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 33;  
RESULT 1003  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 45.4%; Pred. No. 33;  
RESULT 1004  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 33;  
RESULT 1005  
ID ACL23251 standard; DNA; 422 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13242.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Query Match 4.8%; Score 47.6; DB 9; Length 422;  
Best Local Similarity 59.7%; Pred. No. 41;  
RESULT 1006  
ID ACA19654 standard; DNA; 921 BP.  
DE Prokaryotic essential gene #1311.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 921;  
Best Local Similarity 47.8%; Pred. No. 40;  
RESULT 1007  
ID ABD17059 standard; DNA; 930 BP.



DE Pseudomonas aeruginosa polynucleotide #15663.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 930;  
Best Local Similarity 47.8%; Pred. No. 40;  
RESULT 1008  
ID ADI45687 standard; cDNA; 1002 BP.  
DE Corn isoprenoid biosynthesis-associated cDNA #30.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) CHASSEMIAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
PA (ZHUT/) ZHU T.  
Query Match 4.8%; Score 47.6; DB 12; Length 1002;  
Best Local Similarity 47.0%; Pred. No. 40;  
RESULT 1009  
ID ADF31999 standard; DNA; 1170 BP.  
DE Transcriptional repressor of the ROK family.  
PN WO2003099993-A2.  
PD 04-DEC-2003.  
PA (AVET-) AVENTIS PHARM INC.  
Query Match 4.8%; Score 47.6; DB 12; Length 1170;  
Best Local Similarity 43.8%; Pred. No. 40;  
RESULT 1010  
ID ADF32000 standard; DNA; 1170 BP.  
DE Transcriptional repressor of the ROK family complement.  
PN WO2003099993-A2.  
PD 04-DEC-2003.  
PA (AVET-) AVENTIS PHARM INC.  
Query Match 4.8%; Score 47.6; DB 12; Length 1170;  
Best Local Similarity 43.8%; Pred. No. 40;  
RESULT 1011  
ID ACA37852 standard; DNA; 1203 BP.  
DE Prokaryotic essential gene #19509.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 1203;  
Best Local Similarity 45.6%; Pred. No. 40;  
RESULT 1012  
ID ABD04031 standard; DNA; 1248 BP.  
DE Pseudomonas aeruginosa polynucleotide #2635.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 1248;  
Best Local Similarity 46.4%; Pred. No. 40;  
RESULT 1013  
ID ABD05292 standard; DNA; 1278 BP.  
DE Pseudomonas aeruginosa polynucleotide #3896.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 1278;  
Best Local Similarity 43.6%; Pred. No. 40;  
RESULT 1014  
ID ACA03563 standard; DNA; 1971 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #46.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 1971;  
Best Local Similarity 46.8%; Pred. No. 39;  
RESULT 1015  
ID ACA03557 standard; DNA; 1971 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #40.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 1971;  
Best Local Similarity 47.6%; Pred. No. 39;  
RESULT 1016  
ID ACCT78513 standard; DNA; 1971 BP.  
DE HIV protInaRT\_YM.opt.SF2 nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 1971;  
Best Local Similarity 47.6%; Pred. No. 39;  
RESULT 1017  
ID ADC13270 standard; DNA; 1971 BP.  
DE DNA of HIV construct protInaRT\_YM-opt\_C SEQ ID NO 49.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 10; Length 1971;  
Best Local Similarity 46.8%; Pred. No. 39;  
RESULT 1018  
ID ABD03593 standard; DNA; 1971 BP.  
DE Pseudomonas aeruginosa polynucleotide #2197.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 1971;  
Best Local Similarity 46.4%; Pred. No. 39;  
RESULT 1019  
ID ABD05320 standard; DNA; 1977 BP.  
DE Pseudomonas aeruginosa polynucleotide #3924.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 1977;  
Best Local Similarity 43.6%; Pred. No. 39;  
RESULT 1020  
ID AAD55732 standard; DNA; 2078 BP.  
DE Dolomides tenebrosus fibroin 2 DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UTWY-) UNIV WYOMING.  
Query Match 4.8%; Score 47.6; DB 8; Length 2078;  
Best Local Similarity 46.2%; Pred. No. 39;  
RESULT 1021  
ID ABD05412 standard; DNA; 2091 BP.  
DE Pseudomonas aeruginosa polynucleotide #4016.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2091;  
Best Local Similarity 43.6%; Pred. No. 39;  
RESULT 1022  
ID ABD03873 standard; DNA; 2211 BP.  
DE Pseudomonas aeruginosa polynucleotide #2477.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2211;  
Best Local Similarity 46.4%; Pred. No. 39;  
RESULT 1023  
ID AAAY0477 standard; DNA; 2305 BP.  
DE HIV FS(+) ProtInact\_RTOpt\_YM coding sequence.  
PN WO200309302-A2.  
PD 06-JUL-2000.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 3; Length 2305;  
Best Local Similarity 47.6%; Pred. No. 39;



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RESULT 1024  
 ID AAY70479 standard; DNA; 2306 BP.  
 DE HIV FS(-) ProtMod Rtppt\_YM coding sequence.  
 PN WO20039302-A2.  
 PD 06-JUL-2000.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 3; Length 2306;  
 Best Local Similarity 47.6%; Pred. No. 39;  
 RESULT 1025  
 ID ACA37615 standard; DNA; 2337 BP.  
 DE Prokaryotic essential gene #19272.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.6; DB 8; Length 2337;  
 Best Local Similarity 46.4%; Pred. No. 39;  
 RESULT 1026  
 ID ACA27167 standard; DNA; 2424 BP.  
 DE Prokaryotic essential gene #8824.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.6; DB 8; Length 2424;  
 Best Local Similarity 43.9%; Pred. No. 39;  
 RESULT 1027  
 ID ACA3547 standard; DNA; 2457 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #30.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 2457;  
 Best Local Similarity 46.8%; Pred. No. 39;  
 RESULT 1028  
 ID ADC13265 standard; DNA; 2457 BP.  
 DE DNA of HIV construct p2Pol-Opt-YM\_C SEQ ID NO 44.  
 PN WO2003004620-A2.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 2457;  
 Best Local Similarity 46.8%; Pred. No. 39;  
 RESULT 1029  
 ID ABL39960 standard; DNA; 2463 BP.  
 DE Synthetic construct PR975YM SEQ ID NO:31.  
 PN WO200204493-A2.  
 PD 17-JAN-2002.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 6; Length 2463;  
 Best Local Similarity 46.8%; Pred. No. 39;  
 RESULT 1030  
 ID ADM3765 standard; DNA; 2463 BP.  
 DE HIV-1 polynucleotide #8.  
 PN US2003223961-A1.  
 PD 04-DEC-2003.  
 PA (MEGE/) MEGEDE J Z.  
 PA (BARV/) BARNETT S W.  
 PA (ENGE/) ENGELBRECHT S.  
 PA (RENS/) RENSBURG E J V.  
 Query Match 4.8%; Score 47.6; DB 12; Length 2463;  
 Best Local Similarity 46.8%; Pred. No. 39;  
 RESULT 1031  
 ID ACA03542 standard; DNA; 2466 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #25.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
 Best Local Similarity 47.6%; Pred. No. 39;  
 RESULT 1032  
 ID ACC78506 standard; DNA; 2466 BP.  
 DE HIV p2Polinaopt.YM.SF2 nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 10-JUN-2004.

PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
 Best Local Similarity 47.6%; Pred. No. 39;  
 RESULT 1033  
 ID AAD28560 standard; DNA; 2481 BP.  
 DE Herpes simplex virus type 2 full-length HSV-2 RL2 gene.  
 PN WO200202131-A2.  
 PD 10-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 6; Length 2481;  
 Best Local Similarity 51.4%; Pred. No. 39;  
 RESULT 1034  
 ID ADG74963 standard; DNA; 2481 BP.  
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 35.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 2481;  
 Best Local Similarity 51.4%; Pred. No. 39;  
 RESULT 1035  
 ID ADG75080 standard; DNA; 3066 BP.  
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 152.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3066;  
 Best Local Similarity 51.4%; Pred. No. 39;  
 RESULT 1036  
 ID ADF30533 standard; cDNA; 3783 BP.  
 DE Rat angiogenesis modulating protein cDNA #24.  
 PN US2003162706-A1.  
 PD 28-AUG-2003.  
 PA (PROC ) PROCTER & GAMBLE CO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3783;  
 Best Local Similarity 43.6%; Pred. No. 39;  
 RESULT 1037  
 ID ADE71207 standard; DNA; 5369 BP.  
 DE Novel human protein coding sequence #23.  
 PN JP2002345493-A.  
 PD 03-DEC-2002.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5369;  
 Best Local Similarity 45.6%; Pred. No. 38;  
 RESULT 1038  
 ID ADK18365 standard; DNA; 5780 BP.  
 DE Human NOVX protein encoding gene #10.  
 PN WO2003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5780;  
 Best Local Similarity 46.4%; Pred. No. 38;  
 RESULT 1039  
 ID ABS78696 standard; DNA; 5802 BP.  
 DE S. kaniharaensis DNA encoding PKSE.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.6; DB 6; Length 5802;  
 Best Local Similarity 46.0%; Pred. No. 38;  
 RESULT 1040  
 ID ADK18367 standard; DNA; 6008 BP.  
 DE Human NOVX protein encoding gene #11.  
 PN WO2003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 38;  
 RESULT 1041  
 ID ADP13461 standard; DNA; 6008 BP.  
 DE Renal cell carcinoma differentially expressed gene #197.  
 PN WO2004048933-A2.  
 PD 10-JUN-2004.



PA (AMHP ) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.  
 Query Match 4.8%; Score 47.6; DB 12; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 38;  
 RESULT 1042  
 ID AAV58939 standard; DNA; 9960 BP.  
 DE Mycobacterium smegmatis embCAB operon.  
 PN WO9841533-A1.  
 PD 24-SEP-1998.  
 Query Match 4.8%; Score 47.6; DB 2; Length 9960;  
 Best Local Similarity 45.1%; Pred. No. 38;  
 RESULT 1043  
 ID AAD17185 standard; DNA; 27541 BP.  
 DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UNVO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAERVIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 4.8%; Score 47.6; DB 4; Length 27541;  
 Best Local Similarity 47.2%; Pred. No. 36;  
 RESULT 1044  
 ID AAS59516 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 4; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 36;  
 RESULT 1045  
 ID ACF64445 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes DNA contig sequence #11.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 36;  
 RESULT 1046  
 ID ADJ12143 standard; DNA; 414 BP.  
 DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 779.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICHE D.  
 Query Match 4.8%; Score 47.4; DB 11; Length 414;  
 Best Local Similarity 47.5%; Pred. No. 44;  
 RESULT 1047  
 ID ADJ44853 standard; cDNA; 504 BP.  
 DE Plant cDNA #5853.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICHE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 4.8%; Score 47.4; DB 12; Length 504;  
 Best Local Similarity 45.2%; Pred. No. 44;  
 RESULT 1048  
 ID ADG93398 standard; DNA; 670 BP.  
 DE Maize lipoxigenase (LOX) DNA #15.  
 PN US2003168855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 4.8%; Score 47.4; DB 10; Length 670;  
 Best Local Similarity 49.0%; Pred. No. 44;  
 RESULT 1049  
 ID ADG933400 standard; DNA; 670 BP.  
 DE Maize lipoxigenase (LOX) DNA #16.  
 PN US2003168855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 4.8%; Score 47.4; DB 10; Length 670;  
 Best Local Similarity 49.0%; Pred. No. 44;  
 RESULT 1050  
 ID ABD10158 standard; DNA; 918 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8762.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 918;  
 Best Local Similarity 46.3%; Pred. No. 43;  
 RESULT 1051  
 ID ABD10588 standard; DNA; 948 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9192.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 948;  
 Best Local Similarity 46.3%; Pred. No. 43;  
 RESULT 1052  
 ID ABD07203 standard; DNA; 954 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5807.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 954;  
 Best Local Similarity 44.2%; Pred. No. 43;  
 RESULT 1053  
 ID AAZ51701 standard; DNA; 1044 BP.  
 DE Burkholderia multivorans recA gene (1).  
 PN WO200014274-A1.  
 PD 16-MAR-2000.  
 PA (UYER-) UNIV BRITISH COLUMBIA.  
 Query Match 4.8%; Score 47.4; DB 3; Length 1044;  
 Best Local Similarity 43.6%; Pred. No. 43;  
 RESULT 1054  
 ID ABD12320 standard; DNA; 1116 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10924.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 1116;  
 Best Local Similarity 48.0%; Pred. No. 43;  
 RESULT 1055  
 ID ABD10379 standard; DNA; 1149 BP.



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DE Pseudomonas aeruginosa polynucleotide #8983.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1149;  
Best Local Similarity 46.3%; Pred. No. 43;  
RESULT 1056  
ID ABD12534 standard; DNA; 1209 BP.  
DE Pseudomonas aeruginosa polynucleotide #11138.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1209;  
Best Local Similarity 48.0%; Pred. No. 43;  
RESULT 1057  
ID ABX56037 standard; DNA; 1248 BP.  
DE M. echinospora calicheamicin biosynthesis gene calM.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 4.8%; Score 47.4; DB 8; Length 1248;  
Best Local Similarity 49.3%; Pred. No. 43;  
RESULT 1058  
ID ABD07240 standard; DNA; 1251 BP.  
DE Pseudomonas aeruginosa polynucleotide #5844.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1251;  
Best Local Similarity 44.2%; Pred. No. 43;  
RESULT 1059  
ID ACA27319 standard; DNA; 1404 BP.  
DE Prokaryotic essential gene #8976.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.4; DB 8; Length 1404;  
Best Local Similarity 44.6%; Pred. No. 43;  
RESULT 1060  
ID ABD04734 standard; DNA; 1650 BP.  
DE Pseudomonas aeruginosa polynucleotide #3338.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1650;  
Best Local Similarity 43.9%; Pred. No. 43;  
RESULT 1061  
ID ACA37851 standard; DNA; 1734 BP.  
DE Prokaryotic essential gene #19508.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.4; DB 8; Length 1734;  
Best Local Similarity 52.8%; Pred. No. 43;  
RESULT 1062  
ID ABD04627 standard; DNA; 1869 BP.  
DE Pseudomonas aeruginosa polynucleotide #3231.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1869;  
Best Local Similarity 43.9%; Pred. No. 42;  
RESULT 1063  
ID ABD12660 standard; DNA; 1881 BP.  
DE Pseudomonas aeruginosa polynucleotide #11264.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1881;  
Best Local Similarity 48.0%; Pred. No. 42;  
RESULT 1064  
ID ABD07163 standard; DNA; 1986 BP.  
DE Pseudomonas aeruginosa polynucleotide #5767.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 1986;  
Best Local Similarity 44.2%; Pred. No. 42;  
RESULT 1065  
ID ABD04694 standard; DNA; 2283 BP.  
DE Pseudomonas aeruginosa polynucleotide #3298.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 2283;  
Best Local Similarity 43.9%; Pred. No. 42;  
RESULT 1066  
ID ADO26117 standard; DNA; 2354 BP.  
DE Corn phenylalanine ammonia synthase (PAL) segid 155.  
PN WO2004046336-A2.  
PD 03-JUN-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Query Match 4.8%; Score 47.4; DB 12; Length 2354;  
Best Local Similarity 47.5%; Pred. No. 42;  
RESULT 1067  
ID ACA25940 standard; DNA; 2463 BP.  
DE Prokaryotic essential gene #7597.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.4; DB 8; Length 2463;  
Best Local Similarity 45.5%; Pred. No. 42;  
RESULT 1068  
ID ABD10506 standard; DNA; 2583 BP.  
DE Pseudomonas aeruginosa polynucleotide #9110.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.4; DB 11; Length 2583;  
Best Local Similarity 46.3%; Pred. No. 42;  
RESULT 1069  
ID AAQ39093 standard; DNA; 2634 BP.  
DE Streptomyces nodosus 2634bp BamHI fragment.  
PN WO9306219-A1.  
PD 01-APR-1993.  
PA (FARH) HOECHST AG.  
Query Match 4.8%; Score 47.4; DB 2; Length 2634;  
Best Local Similarity 44.9%; Pred. No. 42;  
RESULT 1070  
ID ACA23465 standard; DNA; 2883 BP.  
DE Prokaryotic essential gene #5122.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.4; DB 8; Length 2883;  
Best Local Similarity 44.9%; Pred. No. 42;  
RESULT 1071  
ID ADA71066 standard; DNA; 3153 BP.  
DE Rice gene, SEQ ID 4389.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47.4; DB 8; Length 3153;  
Best Local Similarity 46.3%; Pred. No. 42;  
RESULT 1072  
ID ADA69900 standard; DNA; 3252 BP.  
DE Rice gene, SEQ ID 3223.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47.4; DB 8; Length 3252;  
Best Local Similarity 45.4%; Pred. No. 42;  
RESULT 1073  
ID ADC68517 standard; cDNA; 3629 BP.  
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:9.  
PN WO2003040306-A2.



PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Query Match 4.8%; Score 47.4; DB 10; Length 3629;  
Best Local Similarity 46.1%; Pred. No. 42;  
RESULT 1074  
ID ADC68420 standard; cDNA; 3633 BP.  
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:130.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Query Match 4.8%; Score 47.4; DB 10; Length 3633;  
Best Local Similarity 46.1%; Pred. No. 42;  
RESULT 1075  
ID AAD47222 standard; DNA; 19016 BP.  
DE Streptococcus sp. H021 DNA fragment for rabelomycin biosynthetic pathway.  
PN WO200274800-A1.  
PD 26-SEP-2002.  
PA (GALI-) GALILAEUS OY.  
Query Match 4.8%; Score 47.4; DB 8; Length 19016;  
Best Local Similarity 43.3%; Pred. No. 40;  
RESULT 1076  
ID ADB86070 standard; DNA; 47988 BP.  
DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.  
PN WO2003082909-A1.  
PD 09-OCT-2003.  
PA (AMHP) WYETH.  
Query Match 4.8%; Score 47.4; DB 10; Length 47988;  
Best Local Similarity 44.2%; Pred. No. 39;  
RESULT 1077  
ID AAA09469 standard; DNA; 50937 BP.  
DE Streptococcus oleandomycin gene cluster.  
PN WO20026349-A2.  
PD 11-MAY-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
Best Local Similarity 44.7%; Pred. No. 39;  
RESULT 1078  
ID AAA09469 standard; DNA; 50937 BP.  
DE Streptococcus oleandomycin gene cluster.  
PN WO20026349-A2.  
PD 11-MAY-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
Best Local Similarity 45.7%; Pred. No. 39;  
RESULT 1079  
ID ADP74816 standard; DNA; 137560 BP.  
DE Parapoxvirus ovis genome DNA sequence SeqID1.  
Query Match 4.8%; Score 47.4; DB 12; Length 137560;  
Best Local Similarity 47.9%; Pred. No. 38;  
RESULT 1080  
ID ADC76153 standard; DNA; 607 BP.  
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1422.  
PN WO2003020905-A2.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Query Match 4.8%; Score 47.2; DB 10; Length 607;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1081  
ID ADD17151 standard; DNA; 607 BP.  
DE DNA (SeqID 1219) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Query Match 4.8%; Score 47.2; DB 10; Length 607;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1082  
ID ADD17811 standard; DNA; 607 BP.  
DE DNA (SeqID 1879) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.  
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 4.8%; Score 47.2; DB 10; Length 607;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1083  
ID ADK58311 standard; DNA; 607 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #5694.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 4.8%; Score 47.2; DB 10; Length 607;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1084  
ID ABD17417 standard; DNA; 714 BP.  
DE Pseudomonas aeruginosa polynucleotide #16021.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 714;  
Best Local Similarity 48.8%; Pred. No. 47;  
RESULT 1085  
ID ACA23687 standard; DNA; 852 BP.  
DE Prokaryotic essential gene #5344.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.2; DB 8; Length 852;  
Best Local Similarity 47.9%; Pred. No. 47;  
RESULT 1086  
ID ADC76149 standard; DNA; 873 BP.  
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1418.  
PN WO2003020905-A2.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Query Match 4.8%; Score 47.2; DB 10; Length 873;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1087  
ID ADD17156 standard; DNA; 873 BP.  
DE DNA (SeqID 1224) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 4.8%; Score 47.2; DB 10; Length 873;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1088  
ID ADK58312 standard; DNA; 873 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #5695.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 4.8%; Score 47.2; DB 10; Length 873;  
Best Local Similarity 47.8%; Pred. No. 47;  
RESULT 1089  
ID AAT59269 standard; cDNA; 888 BP.  
DE Streptomyces pristinaespiralis papC gene.  
PN WO9601901-A1.  
PD 25-JAN-1996.  
PA (RHON) RHONE POULENC RORER SA.  
Query Match 4.8%; Score 47.2; DB 2; Length 888;  
Best Local Similarity 45.3%; Pred. No. 47;  
RESULT 1090  
ID ABD02366 standard; DNA; 999 BP.  
DE Pseudomonas aeruginosa polynucleotide #970.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 999;  
Best Local Similarity 46.4%; Pred. No. 47;  
RESULT 1091  
ID ADA48950 standard; DNA; 1044 BP.



DE Wheat gene conferring disease resistance in plants.  
PN WO2003000506-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47.2; DB 9; Length 1044;  
Best Local Similarity 44.5%; Pred. No. 47;  
RESULT 1092  
ID ABD02410 standard; DNA; 1110 BP.  
DE Pseudomonas aeruginosa polynucleotide #1014.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 1110;  
Best Local Similarity 46.4%; Pred. No. 47;  
RESULT 1093  
ID ACA26954 standard; DNA; 1134 BP.  
DE Prokaryotic essential gene #8611.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.2; DB 8; Length 1134;  
Best Local Similarity 46.7%; Pred. No. 46;  
RESULT 1094  
ID ABX56038 standard; DNA; 1194 BP.  
DE M. echinospora calicheamicin biosynthesis gene caln.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 4.8%; Score 47.2; DB 8; Length 1194;  
Best Local Similarity 43.0%; Pred. No. 46;  
RESULT 1095  
ID ABD02476 standard; DNA; 1275 BP.  
DE Pseudomonas aeruginosa polynucleotide #1080.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 1275;  
Best Local Similarity 46.4%; Pred. No. 46;  
RESULT 1096  
ID ABX56047 standard; DNA; 1347 BP.  
DE M. echinospora calicheamicin biosynthesis gene calw.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 4.8%; Score 47.2; DB 8; Length 1347;  
Best Local Similarity 47.0%; Pred. No. 46;  
RESULT 1097  
ID ACA23577 standard; DNA; 1374 BP.  
DE Prokaryotic essential gene #5234.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.2; DB 8; Length 1374;  
Best Local Similarity 47.3%; Pred. No. 46;  
RESULT 1098  
ID ACA26528 standard; DNA; 1395 BP.  
DE Prokaryotic essential gene #8185.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.2; DB 8; Length 1395;  
Best Local Similarity 46.6%; Pred. No. 46;  
RESULT 1099  
ID ACA37685 standard; DNA; 1410 BP.  
DE Prokaryotic essential gene #19342.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.2; DB 8; Length 1410;  
Best Local Similarity 45.8%; Pred. No. 46;  
RESULT 1100  
ID ABQ55009 standard; cDNA; 1616 BP.  
DE Human ovarian antigen HUKJ46 cDNA, SEQ ID NO:889.  
PN WO2003020876-A2.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47.2; DB 6; Length 1616;  
Best Local Similarity 45.3%; Pred. No. 46;  
RESULT 1101  
ID ABL39997 standard; DNA; 1680 BP.  
DE Synthetic RT polynucleotide sequence SEQ ID NO:76.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 6; Length 1680;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1102  
ID ADM73810 standard; DNA; 1680 BP.  
DE HIV-1 polynucleotide #45.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBURG E J V.  
Query Match 4.8%; Score 47.2; DB 12; Length 1680;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1103  
ID ACH91868 standard; DNA; 1737 BP.  
DE Human genome derived single exon probe #25063.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 4.8%; Score 47.2; DB 12; Length 1737;  
Best Local Similarity 49.2%; Pred. No. 46;  
RESULT 1104  
ID ACH92275 standard; DNA; 1738 BP.  
DE Human genome derived single exon probe #25470.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 4.8%; Score 47.2; DB 12; Length 1738;  
Best Local Similarity 49.2%; Pred. No. 46;  
RESULT 1105  
ID AAL40132 standard; DNA; 1896 BP.  
DE Isoprenoid related nucleic acid sequence SEQ ID No 16.  
PN WO200226933-A2.  
PD 04-APR-2002.  
PA (CRGI ) CARGILL INC.  
Query Match 4.8%; Score 47.2; DB 6; Length 1896;  
Best Local Similarity 45.3%; Pred. No. 46;  
RESULT 1106  
ID ABD17641 standard; DNA; 1944 BP.  
DE Pseudomonas aeruginosa polynucleotide #16245.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 1944;  
Best Local Similarity 48.8%; Pred. No. 46;  
RESULT 1107  
ID ACA03560 standard; DNA; 1977 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #43.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 1977;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1108  
ID ACC78516 standard; DNA; 1977 BP.  
DE HIV proctri.opt.SF2 nucleotide sequence.  
PN WO2003020876-A2.



PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP. 4.8%; Score 47.2; DB 8; Length 1977;  
Query Match 47.6%; Pred. No. 46;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1109  
ID ADM73804 standard; DNA; 1977 BP.  
DE HIV-1 polynucleotide #39.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBERG E J V.  
Query Match 4.8%; Score 47.2; DB 12; Length 1977;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1110  
ID ABL39991 standard; DNA; 1978 BP.  
DE Synthetic protease and RT polynucleotide sequence SEQ ID NO:70.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR ) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 4.8%; Score 47.2; DB 6; Length 1978;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1111  
ID ACA03571 standard; DNA; 1989 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #54.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 1989;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1112  
ID ACCT78522 standard; DNA; 1989 BP.  
DE HIV RT-opt-SE2 (native) nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 1989;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1113  
ID AB007303 standard; DNA; 2133 BP.  
DE Pseudomonas aeruginosa polynucleotide #5907.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 2133;  
Best Local Similarity 44.1%; Pred. No. 46;  
RESULT 1114  
ID ACA03552 standard; DNA; 2145 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #35.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1115  
ID ACCT78510 standard; DNA; 2145 BP.  
DE HIV pol-opt-SE2 nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1116  
ID AAAY0481 standard; DNA; 2312 BP.  
DE HIV FS(-) ProtMod Rtopt(+) coding sequence.  
PN WO2003039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 3; Length 2312;  
Best Local Similarity 47.6%; Pred. No. 46;  
RESULT 1117

ID ACA03543 standard; DNA; 2472 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #26.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP. 4.8%; Score 47.2; DB 8; Length 2472;  
Query Match 47.6%; Pred. No. 45;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1118  
ID ACCT78507 standard; DNA; 2472 BP.  
DE HIV p2Polopt-SF2 nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP. 4.8%; Score 47.2; DB 8; Length 2472;  
Query Match 47.6%; Pred. No. 45;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1119  
ID ADA69874 standard; DNA; 2529 BP.  
DE Rice gene SEQ ID 3197.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47.2; DB 8; Length 2529;  
Best Local Similarity 44.5%; Pred. No. 45;  
RESULT 1120  
ID ADC72236 standard; DNA; 2691 BP.  
DE Human NR3B gene SEQ ID NO:9.  
PN WO2003016479-A2.  
PD 27-FEB-2003.  
PA (BURN-) BURNHAM INST.  
PA (UYUA ) UNIV YALE.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 4.8%; Score 47.2; DB 10; Length 2691;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1121  
ID ADN49187 standard; cDNA; 2691 BP.  
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.  
PN US2004033500-A1.  
PD 19-FEB-2004.  
PA (BURN-) BURNHAM INST.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 4.8%; Score 47.2; DB 12; Length 2691;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1122  
ID AAL47419 standard; cDNA; 2706 BP.  
DE Human N-methyl-D-aspartate receptor coding sequence.  
PN WO200240538-A2.  
PD 23-MAY-2002.  
PA (FARB ) BAYER AG. 4.8%; Score 47.2; DB 6; Length 2706;  
Query Match 43.7%; Pred. No. 45;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1123  
ID ACC47899 standard; cDNA; 2706 BP.  
DE Human NR3B subunit receptor polypeptide coding sequence.  
PN WO2003033872-A2.  
PD 24-APR-2003.  
PA (RIKE ) RIKEN KK. 4.8%; Score 47.2; DB 8; Length 2706;  
Query Match 43.7%; Pred. No. 45;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1124  
ID ACA38169 standard; DNA; 2751 BP.  
DE Prokaryotic essential gene #19826.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 4.8%; Score 47.2; DB 8; Length 2751;  
Query Match 47.1%; Pred. No. 45;  
Best Local Similarity 47.1%; Pred. No. 45;  
RESULT 1125  
ID ADA69752 standard; DNA; 2763 BP.  
DE Rice gene SEQ ID 3075.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG. 4.8%; Score 47.2; DB 8; Length 2763;  
Query Match



Best Local Similarity 48.2%; Pred. No. 45;  
RESULT 1126  
ID ABD17862 standard; DNA; 2808 BP.  
DE Pseudomonas aeruginosa polynucleotide #16466.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 2808;  
Best Local Similarity 48.8%; Pred. No. 45;  
RESULT 1127  
ID ABD12055 standard; DNA; 2862 BP.  
DE Pseudomonas aeruginosa polynucleotide #10659.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 2862;  
Best Local Similarity 43.1%; Pred. No. 45;  
RESULT 1128  
ID AAT59268 standard; cDNA; 2888 BP.  
DE Streptomyces pristinaespiralis papA and papM intergenic region.  
PN WO9601901-A1.  
PD 25-JAN-1996.  
PA (RHON) RHONE-POULENC RORER SA.  
Query Match 4.8%; Score 47.2; DB 2; Length 2888;  
Best Local Similarity 45.3%; Pred. No. 45;  
RESULT 1129  
ID ADN49407 standard; DNA; 2898 BP.  
DE Human glutamate receptor (MEM2) DNA.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.  
PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PADL/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
Query Match 4.8%; Score 47.2; DB 12; Length 2898;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1130  
ID ABD11810 standard; DNA; 2910 BP.  
DE Pseudomonas aeruginosa polynucleotide #10414.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 2910;  
Best Local Similarity 43.1%; Pred. No. 45;  
RESULT 1131  
ID AAS06334 standard; cDNA; 2916 BP.  
DE DNA encoding human glutamate receptor-like protein, MEM3.  
PN WO20014473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.8%; Score 47.2; DB 4; Length 2916;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1132  
ID ADN49409 standard; DNA; 2916 BP.  
DE Human glutamate receptor (MEM3) DNA.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.  
PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PADL/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
Query Match 4.8%; Score 47.2; DB 12; Length 2916;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1133  
ID AA252054 standard; DNA; 3012 BP.  
DE Codon optimised Human immunodeficiency virus pol coding region.  
PN WO200015819-A1.  
PD 23-MAR-2000.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
Query Match 4.8%; Score 47.2; DB 3; Length 3012;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1134  
ID ABL39983 standard; DNA; 3015 BP.  
DE Synthetic pol polynucleotide sequence SEQ ID NO:62.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 4.8%; Score 47.2; DB 6; Length 3015;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1135  
ID ACA03553 standard; DNA; 3015 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #36.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 3015;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1136  
ID ADM73796 standard; DNA; 3015 BP.  
DE HIV-1 polynucleotide #31.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBURG E J V.  
Query Match 4.8%; Score 47.2; DB 12; Length 3015;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1137  
ID ADC72232 standard; DNA; 3096 BP.  
DE Human NR3B gene SEQ ID NO:5.  
PN WO2003016479-A2.  
PD 27-FEB-2003.  
PA (BURN-) BURNHAM INST.  
PA (UYVA) UNIV YALE.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
Query Match 4.8%; Score 47.2; DB 10; Length 3096;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1138  
ID ADN49183 standard; cDNA; 3096 BP.  
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.  
PN US2004033500-A1.  
PD 19-FEB-2004.  
PA (BURN-) BURNHAM INST.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 4.8%; Score 47.2; DB 12; Length 3096;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1139  
ID ADC72287 standard; DNA; 3097 BP.  
DE Human NR3B gene SEQ ID NO:61.  
PN WO2003016479-A2.  
PD 27-FEB-2003.  
PA (BURN-) BURNHAM INST.  
PA (UYVA) UNIV YALE.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
Query Match 4.8%; Score 47.2; DB 10; Length 3097;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1140  
ID ADN49238 standard; cDNA; 3097 BP.  
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.  
PN US2004033500-A1.  
PD 19-FEB-2004.  
PA (BURN-) BURNHAM INST.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 4.8%; Score 47.2; DB 12; Length 3097;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1141  
ID ABD11900 standard; DNA; 3111 BP.  
DE Pseudomonas aeruginosa polynucleotide #10504.  
PN US5551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 3111;



Best Local Similarity 43.1%; Pred. No. 45;  
RESULT 1142  
ID AAS06335 standard; cDNA; 3132 BP.  
DE DNA encoding human glutamate receptor-like protein, MEM4.  
PN WO20014473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.8%; Score 47.2; DB 4; Length 3132;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1143  
ID AB233750 standard; cDNA; 3132 BP.  
DE Human TRICH encoding cDNA SEQ ID NO 56.  
PN WO200246415-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.8%; Score 47.2; DB 6; Length 3132;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1144  
ID ADN49411 standard; DNA; 3132 BP.  
DE Human glutamate receptor (MEM4) DNA.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.  
PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PAD/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
Query Match 4.8%; Score 47.2; DB 12; Length 3132;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1145  
ID ABD07318 standard; DNA; 3135 BP.  
DE Pseudomonas aeruginosa polynucleotide #5922.  
PN US651795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.2; DB 11; Length 3135;  
Best Local Similarity 44.1%; Pred. No. 45;  
RESULT 1146  
ID AAC76703 standard; cDNA; 3207 BP.  
DE Human ORFX ORF2258 polynucleotide sequence SEQ ID NO:4515.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.8%; Score 47.2; DB 3; Length 3207;  
Best Local Similarity 43.7%; Pred. No. 45;  
RESULT 1147  
ID ACA03544 standard; DNA; 3639 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #27.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1148  
ID ACC78508 standard; DNA; 3639 BP.  
DE HIV p24RevNeg.Opt.native\_B nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1149  
ID ADM02119 standard; cDNA; 3955 BP.  
DE Human cDNA of the invention SEQ ID NO:804.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 4.8%; Score 47.2; DB 11; Length 3955;  
Best Local Similarity 49.2%; Pred. No. 45;  
RESULT 1150  
ID AAA70414 standard; DNA; 4319 BP.  
DE HIV Gag-polymerase expression cassette coding sequence GagPol.ModSP.  
PN WO200039302-A2.

PD 06-JUL-2000.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.8%; Score 47.2; DB 3; Length 4319;  
Best Local Similarity 47.6%; Pred. No. 45;  
RESULT 1151  
ID ADI60576 standard; DNA; 4532 BP.  
DE Secreted polypeptide encoding gene #115.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 4532;  
Best Local Similarity 49.2%; Pred. No. 45;  
RESULT 1152  
ID ADO24366 standard; cDNA; 4973 BP.  
DE Human PRO87327 encoding cDNA SEQ ID NO:5.  
PN WO2004043397-A2.  
PD 27-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 4.8%; Score 47.2; DB 12; Length 4973;  
Best Local Similarity 49.2%; Pred. No. 45;  
RESULT 1153  
ID AAV21186 standard; DNA; 5676 BP.  
DE Amycolatopsis mediterranei strain wt3136 5.7 kb KpnI DNA fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS-) NOVARTIS AG.  
Query Match 4.8%; Score 47.2; DB 2; Length 5676;  
Best Local Similarity 44.9%; Pred. No. 44;  
RESULT 1154  
ID ADS53354 standard; DNA; 6402 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3896.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 6402;  
Best Local Similarity 43.0%; Pred. No. 44;  
RESULT 1155  
ID AA252055 standard; DNA; 8908 BP.  
DE Packaging construct PHDMHgm2 DNA.  
PN WO200015819-A1.  
PD 23-MAR-2000.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
Query Match 4.8%; Score 47.2; DB 3; Length 8908;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1156  
ID AA287298 standard; DNA; 11220 BP.  
DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.  
PN WO20000620-A2.  
PD 06-JAN-2000.  
PA (MINU-) UNIV MINNESOTA.  
Query Match 4.8%; Score 47.2; DB 3; Length 11220;  
Best Local Similarity 47.3%; Pred. No. 44;  
RESULT 1157  
ID ADJ91917 standard; DNA; 11220 BP.  
DE Streptomyces macrolide biosynthetic protein (PikAII) coding sequence.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 4.8%; Score 47.2; DB 12; Length 11220;  
Best Local Similarity 47.3%; Pred. No. 44;  
RESULT 1158  
ID ADJ72366 standard; DNA; 23949 BP.  
DE Streptomyces roseosporus daptomycin biosynthesis gene fragment.  
PN WO2003014297-A2.  
PD 20-FEB-2003.  
PA (CUBI-) CUBIST PHARM INC.  
Query Match 4.8%; Score 47.2; DB 10; Length 23949;  
Best Local Similarity 44.7%; Pred. No. 43;  
RESULT 1159  
ID ADC26979 standard; DNA; 27705 BP.



DE Sorangium cellulosum tmbA gene cluster tmbA DNA.  
PN US2003054547-A1.  
PD 20-MAR-2003.  
PA (JULI/) JULIEN B.  
Query Match 4.8%; Score 47.2; DB 10; Length 27705;  
Best Local Similarity 46.1%; Pred. No. 43;  
RESULT 1160  
ID AAV21187 standard; DNA; 53789 BP.  
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS) NOVARTIS AG.  
Query Match 4.8%; Score 47.2; DB 2; Length 53789;  
Best Local Similarity 44.9%; Pred. No. 42;  
RESULT 1161  
ID ABD16054 standard; DNA; 441 BP.  
DE Pseudomonas aeruginosa polynucleotide #14658.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47; DB 11; Length 441;  
Best Local Similarity 46.1%; Pred. No. 52;  
RESULT 1162  
ID ADB68842 standard; DNA; 536 BP.  
DE Minority luxI consensus sequence DNA 14.  
PN WO2003057902-A2.  
PD 17-JUL-2003.  
PA (FRAU) FRAUNHOFER USA INC.  
Query Match 4.8%; Score 47; DB 10; Length 536;  
Best Local Similarity 12.9%; Pred. No. 51;  
RESULT 1163  
ID ADC08861 standard; DNA; 597 BP.  
DE Corn DNA sequence seq ID1166 related to grain filling.  
PN WO2003000905-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.8%; Score 47; DB 10; Length 597;  
Best Local Similarity 49.8%; Pred. No. 51;  
RESULT 1164  
ID ACA26778 standard; DNA; 675 BP.  
DE Prokaryotic essential gene #8435.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47; DB 8; Length 675;  
Best Local Similarity 47.0%; Pred. No. 51;  
RESULT 1165  
ID ADO63457 standard; DNA; 715 BP.  
DE Transcription factor G3083 orthologous sequence, SEQ ID 1924.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 4.8%; Score 47; DB 12; Length 715;  
Best Local Similarity 48.1%; Pred. No. 51;  
RESULT 1166  
ID ABO78042 standard; cDNA; 758 BP.  
DE Maize SCIP-1 orthologue encoding cDNA SEQ ID NO 5.  
PN US2002069428-A1.  
PD 06-JUN-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 4.8%; Score 47; DB 6; Length 758;  
Best Local Similarity 46.9%; Pred. No. 51;  
RESULT 1167  
ID ABX12766 standard; DNA; 930 BP.  
DE DNA encoding murine ischaemia activated protein (IAP).  
PN US2002160495-A1.  
PD 31-OCT-2002.  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Query Match 4.8%; Score 47; DB 8; Length 930;  
Best Local Similarity 50.7%; Pred. No. 50;  
RESULT 1168  
ID ADL17042 standard; cDNA; 1120 BP.  
DE Streptomyces coelicolor Bcl-2 domain cDNA #1.

PN US2004023866-A1.  
PD 05-FEB-2004.  
PA (GODZ/) GODZIK A.  
PA (REED/) REED J C.  
Query Match 4.8%; Score 47; DB 12; Length 1120;  
Best Local Similarity 48.7%; Pred. No. 50;  
RESULT 1169  
ID ABD15922 standard; DNA; 1260 BP.  
DE Pseudomonas aeruginosa polynucleotide #14526.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47; DB 11; Length 1260;  
Best Local Similarity 46.1%; Pred. No. 50;  
RESULT 1170  
ID ABL16234 standard; DNA; 1260 BP.  
DE Pseudomonas aeruginosa polynucleotide #14838.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47; DB 11; Length 1260;  
Best Local Similarity 46.1%; Pred. No. 50;  
RESULT 1171  
ID AB266692 standard; DNA; 1293 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 46.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.8%; Score 47; DB 10; Length 1293;  
Best Local Similarity 44.1%; Pred. No. 50;  
RESULT 1172  
ID AAO22481 standard; DNA; 1320 BP.  
DE groEL-1 gene partial sequence.  
PN WO9204452-A.  
PD 19-MAR-1992.  
PA (INSP) INST PASTEUR.  
Query Match 4.8%; Score 47; DB 2; Length 1320;  
Best Local Similarity 44.2%; Pred. No. 50;  
RESULT 1173  
ID ABQ54643 standard; cDNA; 1354 BP.  
DE Human ovarian antigen HE2KN09 cDNA, SEQ ID NO:523.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 47; DB 6; Length 1354;  
Best Local Similarity 44.6%; Pred. No. 50;  
RESULT 1174  
ID AAV20099 standard; DNA; 1416 BP.  
DE Pseudomonas LipR kinase coding sequence.  
PN WO9806836-A2.  
PD 19-FEB-1998.  
PA (GENV) GENENCOR INT INC.  
Query Match 4.8%; Score 47; DB 2; Length 1416;  
Best Local Similarity 45.7%; Pred. No. 50;  
RESULT 1175  
ID AAAL3891 standard; DNA; 1416 BP.  
DE Pseudomonas alcaligenes LipR nucleotide sequence SEQ ID NO:3.  
PN US6048710-A.  
PD 11-APR-2000.  
PA (GENV) GENENCOR INT INC.  
Query Match 4.8%; Score 47; DB 3; Length 1416;  
Best Local Similarity 45.7%; Pred. No. 50;  
RESULT 1176  
ID AAD22868 standard; DNA; 1416 BP.  
DE Pseudomonas alcaligenes LipR DNA.  
PN US6313283-B1.  
PD 06-NOV-2001.  
PA (GENV) GENENCOR INT INC.  
Query Match 4.8%; Score 47; DB 6; Length 1416;  
Best Local Similarity 45.7%; Pred. No. 50;  
RESULT 1177  
ID ACA27226 standard; DNA; 1536 BP.  
DE Prokaryotic essential gene #8883.



PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 1536;  
 Best Local Similarity 51.1%; Pred. No. 50;  
 RESULT 1178  
 ID AAQ22482 standard; DNA; 1620 BP.  
 DE groEL-1 gene coding region.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 1620;  
 Best Local Similarity 44.2%; Pred. No. 50;  
 RESULT 1179  
 ID ABX56033 standard; DNA; 1707 BP.  
 DE M. echinospora calicheamicin biosynthesis gene call.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47; DB 8; Length 1707;  
 Best Local Similarity 48.0%; Pred. No. 50;  
 RESULT 1180  
 ID AAG4515 standard; cDNA; 1722 BP.  
 DE Nucleotide sequence of truncated FEZ1 transcript G3612.  
 PN WO200050585-A2.  
 PD 31-AUG-2000.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 Query Match 4.8%; Score 47; DB 3; Length 1722;  
 Best Local Similarity 45.9%; Pred. No. 50;  
 RESULT 1181  
 ID ADA71120 standard; DNA; 1790 BP.  
 DE Rice gene, SEQ ID 4443.  
 PN WO200300898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47; DB 8; Length 1790;  
 Best Local Similarity 50.2%; Pred. No. 50;  
 RESULT 1182  
 ID ACA23626 standard; DNA; 1968 BP.  
 DE Prokaryotic essential gene #5283.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 1968;  
 Best Local Similarity 45.2%; Pred. No. 49;  
 RESULT 1183  
 ID AAN92408 standard; DNA; 2061 BP.  
 DE Sequence encoding pseudorabies virus (PRV) glycoprotein gH.  
 PN WO8910965-A.  
 PD 16-NOV-1989.  
 PA (UPJO) UPJOHN CO.  
 Query Match 4.8%; Score 47; DB 1; Length 2061;  
 Best Local Similarity 44.7%; Pred. No. 49;  
 RESULT 1184  
 ID AAQ22484 standard; DNA; 2167 BP.  
 DE gro es el operon with promoter sequence.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2167;  
 Best Local Similarity 44.2%; Pred. No. 49;  
 RESULT 1185  
 ID ADD22490 standard; DNA; 2335 BP.  
 DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 140.  
 PN JP2003111595-A.  
 PD 15-APR-2003.  
 PA (ITOY/) ITO Y.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 49;  
 RESULT 1186  
 ID ADL15967 standard; cDNA; 2335 BP.  
 DE Human PP 100 cDNA.  
 PN WO2003008450-A1.

PD 30-JAN-2003.  
 PA (ITOY/) ITOH K.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 49;  
 RESULT 1187  
 ID AAQ22485 standard; DNA; 2668 BP.  
 DE groEL-1 gene.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2668;  
 Best Local Similarity 44.2%; Pred. No. 49;  
 RESULT 1188  
 ID AAV23493 standard; DNA; 4377 BP.  
 DE Pseudomonas LipQ, LipR, OrfV operon.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GENV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 2; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 48;  
 RESULT 1189  
 ID AAL13904 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:28.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GENV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 3; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 48;  
 RESULT 1190  
 ID AAF30869 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes LipQ, LipR and OrfZ gene region.  
 PN US6225106-B1.  
 PD 01-MAY-2001.  
 PA (GENV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 4; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 48;  
 RESULT 1191  
 ID AAD22881 standard; DNA; 4377 BP.  
 DE P. alcaligenes DNA comprising cosmids #71, #201, #505 and #726.  
 PN US6131283-B1.  
 PD 06-NOV-2001.  
 PA (GENV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 48;  
 RESULT 1192  
 ID AAF88336 standard; DNA; 6459 BP.  
 DE S. spinosa DNA fragment encoding ORF19, SEQ ID 43.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 6459;  
 Best Local Similarity 46.9%; Pred. No. 48;  
 RESULT 1193  
 ID ABK52418 standard; DNA; 6868 BP.  
 DE DNA encoding propionibacterium associated proteins.  
 PN JP2002112790-A.  
 PD 16-APR-2002.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 4.8%; Score 47; DB 6; Length 6868;  
 Best Local Similarity 51.7%; Pred. No. 48;  
 RESULT 1194  
 ID AAF88313 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 2.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 45;  
 RESULT 1195  
 ID AAF88316 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 5.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.



PA (FARB ) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 45;  
 RESULT 1196  
 ID AA221501 standard; DNA; 80161 BP.  
 DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.  
 Query Match 4.8%; Score 47; DB 2; Length 80161;  
 Best Local Similarity 46.9%; Pred. No. 45;  
 RESULT 1197  
 ID AD139159 standard; DNA; 85692 BP.  
 DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
 PN WO2003106853-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 PA (REID/) REID R C.  
 Query Match 4.8%; Score 47; DB 12; Length 85692;  
 Best Local Similarity 43.9%; Pred. No. 45;  
 RESULT 1198  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 44;  
 RESULT 1199  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 44;  
 RESULT 1200  
 ID AAA68102 standard; DNA; 296 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 4.7%; Score 46.8; DB 3; Length 296;  
 Best Local Similarity 54.7%; Pred. No. 56;  
 RESULT 1201  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKALA I.  
 Query Match 4.7%; Score 46.8; DB 10; Length 296;  
 Best Local Similarity 54.7%; Pred. No. 56;  
 RESULT 1202  
 ID ABZ13007 standard; DNA; 768 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 812.  
 PN WO200216855-A2.  
 PD 28-FEB-2002.  
 PA (SCRI) SCRIPPS RES INST.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.7%; Score 46.8; DB 6; Length 768;  
 Best Local Similarity 46.0%; Pred. No. 55;  
 RESULT 1203  
 ID ABD06367 standard; DNA; 792 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4971.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 792;  
 Best Local Similarity 50.4%; Pred. No. 55;  
 RESULT 1204  
 ID AAV73801 standard; DNA; 801 BP.  
 DE KSHV LUR terminal repeat unit DNA.  
 PN US5849564-A.  
 PD 15-DEC-1998.  
 PA (UYCO) UNIV COLUMBIA NEW YORK.  
 Query Match 4.7%; Score 46.8; DB 2; Length 801;  
 Best Local Similarity 45.3%; Pred. No. 55;  
 RESULT 1205  
 ID AAA30291 standard; DNA; 801 BP.  
 DE Rhadino virus cis-acting element, RVCAE.  
 PN WO200029626-A1.  
 PD 25-MAY-2000.  
 PA (KIEFF) KIEFF E D.  
 PA (BALL/) BALLESTAS M E.

PA (KAYE/) KAYE K M.  
 Query Match 4.7%; Score 46.8; DB 3; Length 801;  
 Best Local Similarity 45.3%; Pred. No. 55;  
 RESULT 1206  
 ID ABA93488 standard; DNA; 801 BP.  
 DE Kaposi's sarcoma-associated herpesvirus terminal repeat unit.  
 PN US6322792-B1.  
 PD 27-NOV-2001.  
 PA (KIEFF) KIEFF E D.  
 Query Match 4.7%; Score 46.8; DB 6; Length 801;  
 Best Local Similarity 45.3%; Pred. No. 55;  
 RESULT 1207  
 ID ADJ65097 standard; DNA; 801 BP.  
 DE HHV8 terminal repeat region, TR.  
 PN US2004037847-A1.  
 PD 26-FEB-2004.  
 PA (KIEFF) KIEFF E D.  
 PA (BALL/) BALLESTAS M E.  
 PA (KAYE/) KAYE K M.  
 Query Match 4.7%; Score 46.8; DB 12; Length 801;  
 Best Local Similarity 45.3%; Pred. No. 55;  
 RESULT 1208  
 ID ADL17814 standard; DNA; 872 BP.  
 DE WO2003020741-A1.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.  
 PA (DOWC) DOW AGROSCIENCES LLC.  
 Query Match 4.7%; Score 46.8; DB 10; Length 872;  
 Best Local Similarity 48.8%; Pred. No. 55;  
 RESULT 1209  
 ID ACA37750 standard; DNA; 984 BP.  
 DE Prokaryotic essential gene #19407.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.8; DB 8; Length 984;  
 Best Local Similarity 50.4%; Pred. No. 54;  
 RESULT 1210  
 ID ABD06351 standard; DNA; 1071 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4955.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 1071;  
 Best Local Similarity 50.4%; Pred. No. 54;  
 RESULT 1211  
 ID ABD06390 standard; DNA; 1131 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4994.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 1131;  
 Best Local Similarity 50.4%; Pred. No. 54;  
 RESULT 1212  
 ID ABD06380 standard; DNA; 1215 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4984.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 1215;  
 Best Local Similarity 50.4%; Pred. No. 54;  
 RESULT 1213  
 ID ADA45210 standard; cDNA; 1358 BP.  
 DE Recombinant Max & JLP N-terminal region protein, M2L2II coding sequence.  
 PN WO2003066652-A2.  
 PD 14-AUG-2003.  
 PA (UTEM) UNIV TEMPLE.  
 Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
 Best Local Similarity 54.1%; Pred. No. 54;  
 RESULT 1214  
 ID ADA45206 standard; cDNA; 1358 BP.  
 DE Recombinant Max and JLP N-terminal region protein, M2, coding sequence.



PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 54;  
RESULT 1215  
ID ADA45208 standard; cDNA; 1358 BP.  
DE Recombinant Max and JLP N-terminal region protein, M2LZI coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 54;  
RESULT 1216  
ID ACA40293 standard; DNA; 1464 BP.  
DE Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 1464;  
Best Local Similarity 42.2%; Pred. No. 54;  
RESULT 1217  
ID ACA37666 standard; DNA; 2739 BP.  
DE Prokaryotic essential gene #19323.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 2739;  
Best Local Similarity 45.1%; Pred. No. 53;  
RESULT 1218  
ID ABD08987 standard; DNA; 3171 BP.  
DE Pseudomonas aeruginosa polynucleotide #7591.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 3171;  
Best Local Similarity 43.4%; Pred. No. 53;  
RESULT 1219  
ID ABD09358 standard; DNA; 3210 BP.  
DE Pseudomonas aeruginosa polynucleotide #7962.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 3210;  
Best Local Similarity 43.4%; Pred. No. 53;  
RESULT 1220  
ID AAH47802 standard; DNA; 3535 BP.  
DE Chimeric CBD-fused FR901379 acylase DNA.  
PN WO200131038-A1.  
PD 03-MAY-2001.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 4.7%; Score 46.8; DB 4; Length 3535;  
Best Local Similarity 49.3%; Pred. No. 53;  
RESULT 1221  
ID AA157831 standard; cDNA; 4176 BP.  
DE Human polynucleotide SEQ ID NO 34.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 46.8; DB 4; Length 4176;  
Best Local Similarity 49.4%; Pred. No. 52;  
RESULT 1222  
ID AAQ95540 standard; DNA; 4356 BP.  
DE Cardiac adenylyl cyclase gene.  
PN TW243453-A.  
PD 21-MAR-1995.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Query Match 4.7%; Score 46.8; DB 2; Length 4356;  
Best Local Similarity 45.9%; Pred. No. 52;  
RESULT 1223  
ID ADA45191 standard; cDNA; 4667 BP.  
DE Murine JLP coding sequence.  
PN WO2003066652-A2.

PD 14-AUG-2003.  
PA (UTEM ) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 4667;  
Best Local Similarity 54.1%; Pred. No. 52;  
RESULT 1224  
ID ADC10001 standard; DNA; 5220 BP.  
DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
PN WO2003000842-A2.  
PD 03-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.7%; Score 46.8; DB 10; Length 5220;  
Best Local Similarity 42.6%; Pred. No. 52;  
RESULT 1225  
ID AAF32248 standard; DNA; 5692 BP.  
DE Streptomyces sp. cyclic lipopeptide acylase encoding DNA SEQ ID NO:1.  
PN WO200102585-A1.  
PD 11-JAN-2001.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 4.7%; Score 46.8; DB 4; Length 5692;  
Best Local Similarity 49.3%; Pred. No. 52;  
RESULT 1226  
ID AAD54224 standard; DNA; 5862 BP.  
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF7 DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.7%; Score 46.8; DB 10; Length 5862;  
Best Local Similarity 46.8%; Pred. No. 52;  
RESULT 1227  
ID ACA37617 standard; DNA; 10232 BP.  
DE Prokaryotic essential gene #19274.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 10232;  
Best Local Similarity 44.0%; Pred. No. 51;  
RESULT 1228  
ID AAA58472 standard; DNA; 18660 BP.  
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.  
PN WO200040704-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.7%; Score 46.8; DB 3; Length 18660;  
Best Local Similarity 47.5%; Pred. No. 50;  
RESULT 1229  
ID ABL68348 standard; DNA; 25000 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6685.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 4.7%; Score 46.8; DB 6; Length 25000;  
Best Local Similarity 47.3%; Pred. No. 50;  
RESULT 1230  
ID AAAL1992 standard; DNA; 37856 BP.  
DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
PN DE19846493-A1.  
PD 13-APR-2000.  
PA (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Query Match 4.7%; Score 46.8; DB 3; Length 37856;  
Best Local Similarity 48.2%; Pred. No. 49;  
RESULT 1231  
Query Match 4.7%; Score 46.8; DB 4; Length 110000;  
Best Local Similarity 42.2%; Pred. No. 48;  
RESULT 1232  
ID ABD15774 standard; DNA; 270 BP.  
DE Pseudomonas aeruginosa polynucleotide #14378.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 270;  
Best Local Similarity 50.2%; Pred. No. 61;  
RESULT 1233  
ID ABD01848 standard; DNA; 489 BP.



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DE Pseudomonas aeruginosa polynucleotide #452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 489;
Best Local Similarity 47.9%; Pred. No. 60;
RESULT 1234
ID ACA38033 standard; DNA; 723 BP.
DE Prokaryotic essential gene #19690.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.6; DB 8; Length 723;
Best Local Similarity 45.3%; Pred. No. 59;
RESULT 1235
ID ABD13964 standard; DNA; 777 BP.
DE Pseudomonas aeruginosa polynucleotide #12569.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 777;
Best Local Similarity 53.6%; Pred. No. 59;
RESULT 1236
ID ABD14635 standard; DNA; 786 BP.
DE Pseudomonas aeruginosa polynucleotide #13239.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 786;
Best Local Similarity 53.6%; Pred. No. 59;
RESULT 1237
ID ACC59353 standard; DNA; 948 BP.
DE R ruber esterase estA coding sequence #1.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 948;
Best Local Similarity 46.0%; Pred. No. 59;
RESULT 1238
ID ACC59354 standard; DNA; 948 BP.
DE R ruber esterase estA coding sequence #2.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 948;
Best Local Similarity 46.0%; Pred. No. 59;
RESULT 1239
ID ABD01827 standard; DNA; 981 BP.
DE Pseudomonas aeruginosa polynucleotide #431.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 981;
Best Local Similarity 47.9%; Pred. No. 59;
RESULT 1240
ID ABD11883 standard; DNA; 981 BP.
DE Pseudomonas aeruginosa polynucleotide #10487.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 981;
Best Local Similarity 47.7%; Pred. No. 59;
RESULT 1241
ID ABD08147 standard; DNA; 1062 BP.
DE Pseudomonas aeruginosa polynucleotide #6751.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1062;
Best Local Similarity 47.2%; Pred. No. 59;
RESULT 1242
ID ABD04953 standard; DNA; 1947 BP.
DE Pseudomonas aeruginosa polynucleotide #3557.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1947;
Best Local Similarity 45.1%; Pred. No. 58;
RESULT 1243
ID AAD53021 standard; DNA; 1299 BP.
DE Streptomyces species emas gene.
PN WO200292801-A2.
PD 21-NOV-2002.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 46.6; DB 10; Length 1299;
Best Local Similarity 48.0%; Pred. No. 58;
RESULT 1244
ID ABD04946 standard; DNA; 1380 BP.
DE Pseudomonas aeruginosa polynucleotide #3550.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1380;
Best Local Similarity 45.1%; Pred. No. 58;
RESULT 1245
ID ABZ71149 standard; DNA; 1473 BP.
DE S. murayamaensis ATCC 21414 kinamycin encoding DNA SEQ ID NO:36.
PN WO200302066-A2.
PD 09-JAN-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 4.7%; Score 46.6; DB 8; Length 1473;
Best Local Similarity 46.4%; Pred. No. 58;
RESULT 1246
ID ACC59357 standard; DNA; 1494 BP.
DE R ruber vector pMSS12 coding sequence insert #4.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 1494;
Best Local Similarity 46.0%; Pred. No. 58;
RESULT 1247
ID ACC59352 standard; DNA; 1494 BP.
DE R ruber vector pMSS12 coding sequence insert #2.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 1494;
Best Local Similarity 46.0%; Pred. No. 58;
RESULT 1248
ID ABD08270 standard; DNA; 1530 BP.
DE Pseudomonas aeruginosa polynucleotide #6874.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1530;
Best Local Similarity 47.2%; Pred. No. 58;
RESULT 1249
ID AAL61148 standard; DNA; 1710 BP.
DE Human mutant ARX gene #1.
PN WO2003045989-A1.
PD 05-JUN-2003.
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Query Match 4.7%; Score 46.6; DB 9; Length 1710;
Best Local Similarity 46.3%; Pred. No. 58;
RESULT 1250
ID ABD04953 standard; DNA; 1947 BP.
DE Pseudomonas aeruginosa polynucleotide #3557.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1947;
Best Local Similarity 45.1%; Pred. No. 58;

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RESULT 1251  
ID ABD4312 standard; DNA; 2325 BP.  
DE Pseudomonas aeruginosa polynucleotide #12916.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 2325;  
Best Local Similarity 53.6%; Pred. No. 57;  
RESULT 1252  
ID ADB87421 standard; DNA; 2500 BP.  
DE Transgene expression regulatory element, STAR66F.  
PN WO2003004704-A2.  
PD 16-JAN-2003.  
PA (CHRO-) CHROMAGENICS BV.  
Query Match 4.7%; Score 46.6; DB 10; Length 2500;  
Best Local Similarity 46.1%; Pred. No. 57;  
RESULT 1253  
ID ADJ35230 standard; DNA; 2500 BP.  
DE Human stabilizing anti-repression, STAR, element #66.  
PN WO2003106674-A2.  
PD 24-DEC-2003.  
PA (CHRO-) CHROMAGENICS BV.  
Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
Best Local Similarity 46.1%; Pred. No. 57;  
RESULT 1254  
ID ADL96848 standard; DNA; 2500 BP.  
DE Stabilizing Anti-Repressor DNA sequence, T2F STAR 66F.  
PN WO2003106684-A2.  
PD 24-DEC-2003.  
PA (CHRO-) CHROMAGENICS BV.  
Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
Best Local Similarity 46.1%; Pred. No. 57;  
RESULT 1255  
ID ACC44572 standard; cDNA; 3285 BP.  
DE Alpha-amylase/glucosylase fusion nucleotide sequence SEQ ID NO:46.  
PN WO2003018766-A2.  
PD 06-MAR-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.7%; Score 46.6; DB 8; Length 3285;  
Best Local Similarity 48.7%; Pred. No. 57;  
RESULT 1256  
ID ABL15824 standard; cDNA; 3790 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41954.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NV.  
Query Match 4.7%; Score 46.6; DB 4; Length 3790;  
Best Local Similarity 47.2%; Pred. No. 57;  
RESULT 1257  
ID ACA26449 standard; DNA; 3963 BP.  
DE Prokaryotic essential gene #8106.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.6; DB 8; Length 3963;  
Best Local Similarity 43.1%; Pred. No. 57;  
RESULT 1258  
ID AAL61172 standard; DNA; 4770 BP.  
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #3.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.7%; Score 46.6; DB 8; Length 4770;  
Best Local Similarity 44.8%; Pred. No. 56;  
RESULT 1259  
ID ADC10001 standard; DNA; 5220 BP.  
DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
PN WO2003000842-A2.  
PD 03-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.7%; Score 46.6; DB 10; Length 5220;  
Best Local Similarity 44.2%; Pred. No. 56;  
RESULT 1260

ID ABS78655 standard; DNA; 5811 BP.  
DE S. macromyceticus DNA encoding PKSE protein macromomycin.  
PN CA2387401-A1.  
PD 04-SEP-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.7%; Score 46.6; DB 6; Length 5811;  
Best Local Similarity 47.6%; Pred. No. 56;  
RESULT 1261  
ID ABD01877 standard; DNA; 7419 BP.  
DE Pseudomonas aeruginosa polynucleotide #481.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 7419;  
Best Local Similarity 47.9%; Pred. No. 56;  
RESULT 1262  
ID ABD01792 standard; DNA; 7449 BP.  
DE Pseudomonas aeruginosa polynucleotide #396.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 7449;  
Best Local Similarity 47.9%; Pred. No. 56;  
RESULT 1263  
ID ABL66291 standard; DNA; 14800 BP.  
DE Lung cancer related gene sequence SEQ ID NO:4628.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 4.7%; Score 46.6; DB 6; Length 14800;  
Best Local Similarity 44.8%; Pred. No. 54;  
RESULT 1264  
ID ADP13447 standard; DNA; 14800 BP.  
DE Renal cell carcinoma differentially expressed gene #183.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Query Match 4.7%; Score 46.6; DB 12; Length 14800;  
Best Local Similarity 44.8%; Pred. No. 54;  
RESULT 1265  
ID AAS94858 standard; DNA; 14835 BP.  
DE Human DNA sequence #113 expressed during foam cell differentiation.  
PN WO200177389-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.7%; Score 46.6; DB 6; Length 14835;  
Best Local Similarity 44.8%; Pred. No. 54;  
RESULT 1266  
ID AAD54223 standard; DNA; 24081 BP.  
DE Streptomyces platensis subspecies roseaceus dorrigocin ORF6 DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.7%; Score 46.6; DB 10; Length 24081;  
Best Local Similarity 46.7%; Pred. No. 54;  
RESULT 1267  
ID ADQ07566 standard; DNA; 25467 BP.  
DE Streptomyces kanamyceticus kanamycin biosynthesis genes SEQ ID NO:1.  
PN JP2004173537-A.  
PD 24-JUN-2004.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 4.7%; Score 46.6; DB 12; Length 25467;  
Best Local Similarity 46.9%; Pred. No. 54;  
RESULT 1268  
ID ABZ71131 standard; DNA; 36321 BP.  
DE Streptomyces murayamaensis ATCC 21414 kinamycin related DNA SEQ ID NO:1.  
PN WO2003002066-A2.



PD 09-JAN-2003.  
PA (DIVE-) DIVERSA CORP. 4.7%; Score 46.6; DB 8; Length 36321;  
Query Match 46.4%; Pred. No. 53;  
Best Local Similarity 46.4%; Pred. No. 53;  
RESULT 1269  
ID ACF30939 standard; DNA; 53905 BP.  
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
PN WO2003027290-A1.  
PD 03-APR-2003.  
PA (NLSB) JAPAN TOBACCO INC.  
PA (SYGN) SYNGENTA LTD.  
Query Match 4.7%; Score 46.6; DB 8; Length 53905;  
Best Local Similarity 46.2%; Pred. No. 53;  
RESULT 1270  
ID ADI09998 standard; DNA; 53905 BP.  
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
PN WO2004005515-A1.  
PD 15-JAN-2004.  
PA (NLSB) JAPAN TOBACCO INC.  
PA (SYGN) SYNGENTA LTD.  
Query Match 4.7%; Score 46.6; DB 12; Length 53905;  
Best Local Similarity 46.2%; Pred. No. 53;  
RESULT 1271  
ID ABL59157 standard; cDNA; 1072 BP.  
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
PN US2002031506-A1.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1280  
ID ABL59157 standard; cDNA; 1072 BP.  
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
PN US2002031506-A1.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1281  
ID AAI58027 standard; cDNA; 1100 BP.  
DE Human polynucleotide SEQ ID NO 230.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1100;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1282  
ID AAI59813 standard; cDNA; 1205 BP.  
DE Human polynucleotide SEQ ID NO 3802.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1205;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1283  
ID ADI42681 standard; DNA; 1219 BP.  
DE Plant transcription factor polynucleotide #735.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIAN-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAKE-) HAAKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.  
PA (PINE-) PINEDA O.  
PA (YUGG-) YU G.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 44.2%; Pred. No. 63;  
RESULT 1284  
ID ADO02930 standard; cDNA; 1219 BP.  
DE Corn orthologue of Thalea transcription factor, cDNA #98.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN-) ZHANG J.  
PA (FROM-) FROMM M E.

PD 09-JAN-2003.  
PA (DIVE-) DIVERSA CORP. 4.7%; Score 46.6; DB 8; Length 36321;  
Query Match 46.4%; Pred. No. 53;  
Best Local Similarity 46.4%; Pred. No. 53;  
RESULT 1269  
ID ACF30939 standard; DNA; 53905 BP.  
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
PN WO2003027290-A1.  
PD 03-APR-2003.  
PA (NLSB) JAPAN TOBACCO INC.  
PA (SYGN) SYNGENTA LTD.  
Query Match 4.7%; Score 46.6; DB 8; Length 53905;  
Best Local Similarity 46.2%; Pred. No. 53;  
RESULT 1270  
ID ADI09998 standard; DNA; 53905 BP.  
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
PN WO2004005515-A1.  
PD 15-JAN-2004.  
PA (NLSB) JAPAN TOBACCO INC.  
PA (SYGN) SYNGENTA LTD.  
Query Match 4.7%; Score 46.6; DB 12; Length 53905;  
Best Local Similarity 46.2%; Pred. No. 53;  
RESULT 1271  
ID ABL59157 standard; cDNA; 1072 BP.  
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
PN US2002031506-A1.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1280  
ID ABL59157 standard; cDNA; 1072 BP.  
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
PN US2002031506-A1.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1281  
ID AAI58027 standard; cDNA; 1100 BP.  
DE Human polynucleotide SEQ ID NO 230.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1100;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1282  
ID AAI59813 standard; cDNA; 1205 BP.  
DE Human polynucleotide SEQ ID NO 3802.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1205;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1283  
ID ADI42681 standard; DNA; 1219 BP.  
DE Plant transcription factor polynucleotide #735.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER-) SHERMAN B K.  
PA (RIEC-) RIECHMANN J L.  
PA (JIAN-) JIANG C.  
PA (HEAR-) HEARD J E.  
PA (HAKE-) HAAKE V.  
PA (CREE-) CREELMAN R A.  
PA (RATC-) RATCLIFFE O.  
PA (ADAM-) ADAM L J.  
PA (REUB-) REUBER T L.  
PA (KEDD-) KEDDIE J.  
PA (BROU-) BROUN P E.  
PA (PILG-) PILGRIM M L.  
PA (DUBE-) DUBELL A N.  
PA (PINE-) PINEDA O.  
PA (YUGG-) YU G.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 44.2%; Pred. No. 63;  
RESULT 1284  
ID ADO02930 standard; cDNA; 1219 BP.  
DE Corn orthologue of Thalea transcription factor, cDNA #98.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN-) ZHANG J.  
PA (FROM-) FROMM M E.



PA (HEAR/) HEARD J E. 4.7%; Score 46.4; DB 12; Length 1219;  
PA (RIEG/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 44.2%; Pred. No. 63;  
RESULT 1285  
ID AA265013 standard; cDNA; 1227 BP.  
DE Membrane-bound protein PRO828 encoding cDNA.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 3; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1286  
ID AA846137 standard; cDNA; 1227 BP.  
DE Human DNA encoding PRO polypeptide sequence #213.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 4; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1287  
ID AAF44159 standard; cDNA; 1227 BP.  
DE Human PRO828 (UNQ469) nucleotide sequence SEQ ID NO:188.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 5; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1288  
ID ABJ88133 standard; cDNA; 1227 BP.  
DE Human PRO828 cDNA sequence SEQ ID NO:123.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 6; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1289  
ID ABK28599 standard; cDNA; 1227 BP.  
DE Human DNA57037-1444 encoding PRO828.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 6; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1290  
ID ABJ95622 standard; cDNA; 1227 BP.  
DE Human angiogenesis related cDNA PRO828 SEQ ID NO: 123.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERR/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 4.7%; Score 46.4; DB 6; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1291  
ID ACA89587 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1292  
ID ACA73597 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1293  
ID ACA05912 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1294  
ID ACA66746 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO protein #213.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1295  
ID ACA64292 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 63;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1296  
ID ACF20321 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1297  
ID ACF19707 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1298  
ID ACD21995 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1299  
ID ACF13160 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036160-A1.  
PD 20-FEB-2003.



Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1300  
ID ACD25263 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1301  
ID ACF00312 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1302  
ID ACA72369 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1303  
ID ACD04893 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1304  
ID ACD18354 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1305  
ID ACD08361 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1306  
ID ACA88795 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1307  
ID ACA70237 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1308  
ID ACD12459 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1309  
ID ACC74374 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;

RESULT 1310  
ID ACD16002 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1311  
ID ACD25570 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1312  
ID ACD18047 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1313  
ID ACC88334 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1314  
ID ACD21688 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1315  
ID ACD18755 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1316  
ID ABX98365 standard; cDNA; 1227 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 425.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1317  
ID ACD14116 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1318  
ID ACD09896 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1319  
ID ACC88641 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1320  
ID ACD21381 standard; cDNA; 1227 BP.



DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1321  
ID ABX75753 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO828.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1322  
ID ABX797956 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1323  
ID ACA97432 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1324  
ID ACA57895 standard; cDNA; 1227 BP.  
DE Human PRO828 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1325  
ID ACD14423 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1326  
ID ACC91206 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1327  
ID ACC88948 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1328  
ID ACD07145 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1329  
ID ACA67596 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1330  
ID ACC81651 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1331  
ID ACC89255 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1332  
ID ACC86611 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1333  
ID ACC89869 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1334  
ID ACC93048 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1335  
ID ABX80751 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1336  
ID ACA72676 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1337  
ID ACA89194 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1338  
ID ACA69930 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1339  
ID ACA97073 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1340  
ID ACA91069 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032108-A1.



PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1351  
ID ACA74677 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
FN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1352  
ID ACA70544 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
FN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1353  
ID ACD14730 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
FN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1354  
ID ACA68402 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1355  
ID ABX98867 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1356  
ID ACC81344 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1357  
ID ACA95668 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1358  
ID ACD04586 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003022996-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1359  
ID ACC88027 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1360  
ID ACF12689 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
PD 20-FEB-2003.

PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1341  
ID ACA70851 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
FN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1342  
ID ACA95361 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1343  
ID ACD44260 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO828 polypeptide.  
FN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1344  
ID ACC86304 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1345  
ID ACC90176 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1346  
ID ACD12784 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
FN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1347  
ID ACF20014 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
FN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1348  
ID ABX76958 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
FN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1349  
ID ACA71290 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1350  
ID ACA68933 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
FN US2003036136-A1.  
PD 20-FEB-2003.



RESULT 1361  
ID ABX79431 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1362  
ID ACA96404 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1363  
ID ACA65178 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1364  
ID ACA73904 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1365  
ID ACA74316 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1366  
ID ACA96711 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1367  
ID ACD10817 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1368  
ID ACC91513 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1369  
ID ACA93452 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032187-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1370  
ID ACD02848 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US20030322301-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1371  
ID ACC87413 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1372  
ID ACC85997 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1373  
ID ABX81134 standard; DNA; 1227 BP.  
DE Human secreted or transmembrane protein related PCR primer #48.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1374  
ID ACA65485 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1375  
ID ACA94302 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1376  
ID ACA98046 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1377  
ID ACA91548 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1378  
ID ACA90762 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1379  
ID ACD16309 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1380  
ID ACD17470 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1381  
ID ACC92127 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040069-A1.



PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1382  
ID AC74984 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US200302293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1383  
ID AC91855 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1384  
ID AC71499 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1385  
ID ACC90899 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1386  
ID AC365909 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO protein #213.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1387  
ID AC92950 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1388  
ID AC95054 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1389  
ID AC16616 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1390  
ID AC15695 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1391  
ID ABX17034 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #47.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;

Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1392  
ID ABX16798 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane protein #213.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;  
RESULT 1393  
ID AC67889 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1394  
ID AC97739 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1395  
ID AC99188 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1396  
ID ACC91820 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1397  
ID AC11231 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1398  
ID AC15081 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1399  
ID AC88338 standard; cDNA; 1227 BP.  
DE Human secreted and transmembrane polypeptide PRO828 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1400  
ID AC81845 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO828 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1401  
ID AC11845 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032118-A1.



PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1402  
ID ACC95974 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1403  
ID ACF16537 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1404  
ID ACF02655 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1405  
ID ACF02962 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1406  
ID ACF21549 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1407  
ID ACF10233 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1408  
ID ACF78126 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1409  
ID ACD46831 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1410  
ID ACD49594 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1411  
ID ACF28361 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1412  
ID ACD89051 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1413  
ID ACD84446 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1414  
ID ACD99220 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1415  
ID ADA78177 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1416  
ID ACF48962 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1417  
ID ACD09282 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1418  
ID ACF12075 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1419  
ID ACF41309 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;  
RESULT 1420  
ID ACF15923 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.



Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1430				
ID ACF50497 standard; cDNA; 1227 BP.				
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.				
PN US2003104549-A1.				
PD 05-JUN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1431				
ID ACH07968 standard; cDNA; 1227 BP.				
DE Human secreted/transmembrane protein (PRO) cDNA #213.				
PN US2003049749-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1432				
ID ACF13774 standard; cDNA; 1227 BP.				
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.				
PN US2003064462-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1433				
ID ACD411700 standard; cDNA; 1227 BP.				
DE Human secreted/transmembrane protein (PRO) cDNA #213.				
PN US2003065159-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1434				
ID ADA37699 standard; cDNA; 1227 BP.				
DE Human cDNA encoding secreted/transmembrane protein PRO828.				
PN US2003008297-A1.				
PD 09-JAN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1435				
ID ACF32113 standard; cDNA; 1227 BP.				
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.				
PN US2003064447-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1436				
ID ACF23391 standard; cDNA; 1227 BP.				
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.				
PN US2003073184-A1.				
PD 17-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1437				
ID ACF45603 standard; cDNA; 1227 BP.				
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.				
PN US2003064451-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1438				
ID ACD45603 standard; cDNA; 1227 BP.				
DE Human secreted/transmembrane protein (PRO) cDNA #213.				
PN US2003064451-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1439				
ID ACD45603 standard; cDNA; 1227 BP.				
DE Human secreted/transmembrane protein (PRO) cDNA #213.				
PN US2003064451-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		
RESULT 1440				
ID ACD45603 standard; cDNA; 1227 BP.				
DE Human secreted/transmembrane protein (PRO) cDNA #213.				
PN US2003064451-A1.				
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	4.7%;	Score 46.4;	DB 9;	Length 1227;
Best Local Similarity	50.0%;	Pred. No. 63;		



Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1439  
ID ACF53260 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1440  
ID ACF727440 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1441  
ID ACF45278 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1442  
ID ACF29896 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1443  
ID ACD89972 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1444  
ID ACD84753 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1445  
ID ACD98913 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1446  
ID ACF77205 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1447  
ID ACF76898 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1448

ID ACF49883 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1449  
ID ACF50190 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1450  
ID ADA21385 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO828.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1451  
ID ACD09589 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1452  
ID ACD08668 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1453  
ID ACF12382 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1454  
ID ACC94890 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1455  
ID ACD22609 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1456  
ID ACF15309 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1457  
ID ACC97404 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1458  
ID ACC92434 standard; cDNA; 1227 BP.



DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003059880-A1.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1459  
 ID ACF14081 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003064465-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1460  
 ID ACF14388 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003054478-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1461  
 ID ADA10172 standard; cDNA; 1227 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO828.  
 PN US2003059831-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1462  
 ID ACF09619 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003068718-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1463  
 ID ACD45910 standard; cDNA; 1227 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #213.  
 PN US2003064454-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1464  
 ID ACD48059 standard; cDNA; 1227 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #213.  
 PN US2003064461-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1465  
 ID ACD67790 standard; cDNA; 1227 BP.  
 DE cDNA encoding human PRO polypeptide #213.  
 PN US2003068724-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1466  
 ID ACF25598 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003068727-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1467  
 ID ACF29282 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003068772-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1468  
 ID ACD85060 standard; cDNA; 1227 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #213.  
 PN US2003068714-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1469  
 ID ACD84139 standard; cDNA; 1227 BP.  
 DE Human PRO polynucleotide #213.  
 PN US2003068758-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1470  
 ID ACD88130 standard; cDNA; 1227 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #213.  
 PN US2003068776-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1471  
 ID ACF30817 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003069407-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1472  
 ID ACF32420 standard; cDNA; 1227 BP.  
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
 PN US2003104555-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1473  
 ID ACHI2080 standard; cDNA; 1227 BP.  
 DE cDNA encoding human PRO polypeptide #213.  
 PN US2003049768-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1474  
 ID ACHI2387 standard; cDNA; 1227 BP.  
 DE cDNA encoding human PRO polypeptide #213.  
 PN US2003049771-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1475  
 ID ACD40779 standard; cDNA; 1227 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #213.  
 PN US2003032134-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;  
 Best Local Similarity 50.0%; Pred. No. 63;  
 RESULT 1476  
 ID ADA17716 standard; cDNA; 1227 BP.  
 DE cDNA encoding human PRO828 polypeptide.  
 PN US2003054987-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;  
 Query Match Similarity 50.0%; Pred. No. 63;



Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1477  
ID ACF18251 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1478  
ID ACF08698 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1479  
ID ACF311499 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1480  
ID ACF52339 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1481  
ID ACD50208 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1482  
ID ACF38911 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1483  
ID ACF26826 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1484  
ID ACF24926 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1485  
ID ACF46506 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1486  
ID ACF28054 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1487  
ID ACD89358 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1488  
ID ACF63930 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1489  
ID ACF60570 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1490  
ID ACH12694 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1491  
ID ACH10117 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1492  
ID ACD03972 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1493  
ID ACD10510 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1494  
ID ACD12152 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1495  
ID ACF42537 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054480-A1.  
PD 20-MAR-2003.



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PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1496  
ID ADA27824 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO828.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1497  
ID ACF18558 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1498  
ID ACF02348 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1499  
ID ACF21856 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;  
RESULT 1500  
ID ACF10540 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 4.7%; Score 46.4; DB 9; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 63;